

TASSEL: software for association mapping of complex t

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Gene-Based Sequence Diversity Analysis of Field Pea ( <i>Pisum</i> ). <i>Genetics</i> , 2007, 177, 2263-2275.	2.9	74
2	Genetic diversity among oat varieties of worldwide origin and associations of AFLP markers with quantitative traits. <i>Theoretical and Applied Genetics</i> , 2008, 117, 1041-1053.	3.6	79
3	NATURAL SELECTION ALONG AN ENVIRONMENTAL GRADIENT: A CLASSIC CLINE IN MOUSE PIGMENTATION. <i>Evolution; International Journal of Organic Evolution</i> , 2008, 62, 1555-1570.	2.3	144
4	Demographic processes shaping genetic variation. <i>Current Opinion in Plant Biology</i> , 2008, 11, 103-109.	7.1	31
5	Polymorphisms of IFS1 and IFS2 gene are associated with isoflavone concentrations in soybean seeds. <i>Plant Science</i> , 2008, 175, 505-512.	3.6	41
6	Status and Prospects of Association Mapping in Plants. <i>Plant Genome</i> , 2008, 1, .	2.8	1,118
7	Patterns of Molecular Evolution Associated With Two Selective Sweeps in the Tb1â€Dwarf8 Region in Maize. <i>Genetics</i> , 2008, 180, 1107-1121.	2.9	32
8	Key Impact of <i>Vgt1</i> on Flowering Time Adaptation in Maize: Evidence From Association Mapping and Ecogeographical Information. <i>Genetics</i> , 2008, 178, 2433-2437.	2.9	129
9	Efficient Mapping of Plant Height Quantitative Trait Loci in a Sorghum Association Population With Introgressed Dwarfing Genes. <i>Genetics</i> , 2008, 180, 629-637.	2.9	138
10	Dominant male-sterile populations for association mapping and introgression of exotic wheat germplasm. <i>Australian Journal of Agricultural Research</i> , 2008, 59, 470.	1.5	4
11	Genome-Wide and Mla Locus-Specific Characterisation of Latvian Barley Varieties. <i>Proceedings of the Latvian Academy of Sciences</i> , 2008, 62, 103-109.	0.1	1
12	Genome-Wide Reduction of Genetic Diversity in Wheat Breeding. <i>Crop Science</i> , 2009, 49, 161-168.	1.8	124
13	Sweet Sorghum Genetic Diversity and Association Mapping for Brix and Height. <i>Plant Genome</i> , 2009, 2, .	2.8	168
14	Genome-wide association mapping of quantitative traits in sorghum ( <i>Sorghum bicolor</i> (L.) Moench) by using multiple models. <i>Breeding Science</i> , 2009, 59, 217-227.	1.9	43
15	Allelic diversities in rice starch biosynthesis lead to a diverse array of rice eating and cooking qualities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 21760-21765.	7.1	469
16	Epistatic Interactions between <i>Opaque2</i> Transcriptional Activator and Its Target Gene <i>CyPPDK1</i> Control Kernel Trait Variation in Maize. <i>Plant Physiology</i> , 2009, 150, 506-520.	4.8	45
17	Software engineering the mixed model for genome-wide association studies on large samples. <i>Briefings in Bioinformatics</i> , 2009, 10, 664-675.	6.5	96
18	Starch as a major integrator in the regulation of plant growth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 10348-10353.	7.1	467

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19	Fine Mapping and Haplotype Structure Analysis of a Major Flowering Time Quantitative Trait Locus on Maize Chromosome 10. <i>Genetics</i> , 2009, 183, 1555-1563.	2.9	60
20	Genetic Characterization and Linkage Disequilibrium Estimation of a Global Maize Collection Using SNP Markers. <i>PLoS ONE</i> , 2009, 4, e8451.	2.5	338
21	Bayesian Quantitative Trait Locus Mapping Based on Reconstruction of Recent Genetic Histories. <i>Genetics</i> , 2009, 183, 709-721.	2.9	5
22	Identification of a <i>Cis</i> -Acting Regulatory Polymorphism in a Eucalypt <i>COBRA</i> -Like Gene Affecting Cellulose Content. <i>Genetics</i> , 2009, 183, 1153-1164.	2.9	89
23	Gramene QTL database: development, content and applications. <i>Database: the Journal of Biological Databases and Curation</i> , 2009, 2009, bap005.	3.0	95
24	Association mapping and marker-assisted selection of the lettuce dieback resistance gene <i>Tvr1</i> . <i>BMC Plant Biology</i> , 2009, 9, 135.	3.6	47
25	Linkage disequilibrium and population structure in wild and domesticated populations of <i>Phaseolus vulgaris</i> L.. <i>Evolutionary Applications</i> , 2009, 2, 504-522.	3.1	139
26	Association mapping of stigma and spikelet characteristics in rice ( <i>Oryza sativa</i> L.). <i>Molecular Breeding</i> , 2009, 24, 277-292.	2.1	96
27	Genetics of dietary fibre in bread wheat. <i>Euphytica</i> , 2009, 170, 155.	1.2	41
28	Association mapping and marker development of the candidate genes (1 <sup>st</sup> ), (1 <sup>st</sup> )- $\beta$ -D-Glucan-4-glucanohydrolase and (1 <sup>st</sup> )- $\beta$ -Xylan-endohydrolase 1 for malting quality in barley. <i>Euphytica</i> , 2009, 170, 109-122.		14
29	Linkage disequilibrium based association mapping of fiber quality traits in <i>G. hirsutum</i> L. variety germplasm. <i>Genetica</i> , 2009, 136, 401-417.	1.1	144
30	Structure of genetic diversity in the two major gene pools of common bean ( <i>Phaseolus vulgaris</i> L.) Tj ETQq1 1 0.784314 rgBT / Overlock 3.6 280	3.6	280
31	Identification of associations between SSR markers and fiber traits in an exotic germplasm derived from multiple crosses among <i>Gossypium</i> tetraploid species. <i>Theoretical and Applied Genetics</i> , 2009, 119, 93-103.	3.6	66
32	Population structure and association mapping on chromosome 7 using a diverse panel of Chinese germplasm of rice ( <i>Oryza sativa</i> L.). <i>Theoretical and Applied Genetics</i> , 2009, 119, 459-470.	3.6	55
33	Genetic variants of HvCbf14 are statistically associated with frost tolerance in a European germplasm collection of <i>Hordeum vulgare</i> . <i>Theoretical and Applied Genetics</i> , 2009, 119, 1335-1348.	3.6	54
34	Fine mapping, physical mapping and development of diagnostic markers for the <i>Rrs2</i> scald resistance gene in barley. <i>Theoretical and Applied Genetics</i> , 2009, 119, 1507-1522.	3.6	40
35	Molecular characterization of global maize breeding germplasm based on genome-wide single nucleotide polymorphisms. <i>Theoretical and Applied Genetics</i> , 2009, 120, 93-115.	3.6	201
36	Introgression from modern hybrid varieties into landrace populations of maize ( <i>Zea mays</i> ssp.) Tj ETQq1 1 0.784314 rgBT / Overlock 3.9 55	3.9	55

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37	Association mapping of straighthead disorder induced by arsenic in <i>Oryza sativa</i> . Plant Breeding, 2009, 128, 551-558.	1.9	31
38	Association mapping of cadmium, copper and hydrogen peroxide tolerance of roots and translocation capacities of cadmium and copper in <i>Arabidopsis thaliana</i> . Physiologia Plantarum, 2009, 137, 235-248.	5.2	10
39	Association Mapping of Malting Quality Data from Western Canadian Two-row Barley Cooperative Trials. Crop Science, 2010, 50, 1649-1663.	1.8	30
40	Nucleotide diversity and molecular evolution of the PSY1 gene in Zea mays compared to some other grass species. Theoretical and Applied Genetics, 2010, 120, 709-720.	3.6	36
41	Genetic variation at bx1 controls DIMBOA content in maize. Theoretical and Applied Genetics, 2010, 120, 721-734.	3.6	49
42	Cloning and characterization of a putative GS3 ortholog involved in maize kernel development. Theoretical and Applied Genetics, 2010, 120, 753-763.	3.6	126
43	Inferring population structure and genetic diversity of broad range of wild diploid alfalfa (Medicago) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262	3.6	60
44	Genetic analysis and characterization of a new maize association mapping panel for quantitative trait loci dissection. Theoretical and Applied Genetics, 2010, 121, 417-431.	3.6	176
45	Genetic diversity and population structure of a diverse set of rice germplasm for association mapping. Theoretical and Applied Genetics, 2010, 121, 475-487.	3.6	172
46	Carotenoid biosynthesis genes provide evidence of geographical subdivision and extensive linkage disequilibrium in the carrot. Theoretical and Applied Genetics, 2010, 121, 659-672.	3.6	32
47	Structure, allelic diversity and selection of Asr genes, candidate for drought tolerance, in Oryza sativa L. and wild relatives. Theoretical and Applied Genetics, 2010, 121, 769-787.	3.6	68
48	Variability of grain quality in sorghum: association with polymorphism in Sh2, Bt2, Sssl, Ae1, Wx and O2. Theoretical and Applied Genetics, 2010, 121, 1171-1185.	3.6	33
49	Genetic diversity and marker-trait associations in a collection of Pak-choi (Brassica rapa L. ssp.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262	1.4	15
50	Polymorphisms of soybean isoflavone synthase and flavanone 3-hydroxylase genes are associated with soybean mosaic virus resistance. Molecular Breeding, 2010, 25, 13-24.	2.1	20
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52	Association mapping of late maturity $\alpha$ -amylase (LMA) activity in a collection of synthetic hexaploid wheat. Molecular Breeding, 2010, 26, 39-49.	2.1	62
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54	Population structure and genetic diversity in elite sugar beet germplasm investigated with SSR markers. Euphytica, 2010, 175, 35-42.	1.2	33

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56	Association genetics in crop improvement. <i>Current Opinion in Plant Biology</i> , 2010, 13, 174-180.	7.1	410
57	Single feature polymorphism (SFP)-based selective sweep identification and association mapping of growth-related metabolic traits in <i>Arabidopsis thaliana</i> . <i>BMC Genomics</i> , 2010, 11, 188.	2.8	11
58	Genome-wide SNPs and re-sequencing of growth habit and inflorescence genes in barley: implications for association mapping in germplasm arrays varying in size and structure. <i>BMC Genomics</i> , 2010, 11, 707.	2.8	81
59	Relationship, evolutionary fate and function of two maize co-orthologs of rice GW2 associated with kernel size and weight. <i>BMC Plant Biology</i> , 2010, 10, 143.	3.6	179
60	Association genetics of traits controlling lignin and cellulose biosynthesis in black cottonwood ( <i>Populus trichocarpa</i> , Salicaceae) secondary xylem. <i>New Phytologist</i> , 2010, 188, 515-532.	7.3	134
61	Genes underlying quantitative variation in ecologically important traits: <i>PHYTOCHROME</i> Tj ETQq0 0 0 rgBT /Overlock 10 set in <i>Arabidopsis thaliana</i> . <i>Molecular Ecology</i> , 2010, 19, 1187-1199.	3.9	43
62	Mixed linear model approach adapted for genome-wide association studies. <i>Nature Genetics</i> , 2010, 42, 355-360.	21.4	2,022
63	Rare genetic variation at <i>Zea mays crtRB1</i> increases $\beta^2$ -carotene in maize grain. <i>Nature Genetics</i> , 2010, 42, 322-327.	21.4	421
64	Towards identifying genes underlying ecologically relevant traits in <i>Arabidopsis thaliana</i> . <i>Nature Reviews Genetics</i> , 2010, 11, 867-879.	16.3	297
65	Genetic diversity and association analysis of protein and oil content in food-grade soybeans from Asia and the United States. <i>Plant Breeding</i> , 2010, 129, 250-256.	1.9	44
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67	Genetic Diversity, Population Structure, and Linkage Disequilibrium in U.S. Elite Winter Wheat. <i>Plant Genome</i> , 2010, 3, .	2.8	103
68	Association and Linkage Analysis of Aluminum Tolerance Genes in Maize. <i>PLoS ONE</i> , 2010, 5, e9958.	2.5	91
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70	Association genetics reveal candidate gene SNPs affecting wood properties in <i>Pinus radiata</i> . <i>Australian Forestry</i> , 2010, 73, 185-190.	0.9	7
71	Metabolic Networks: How to Identify Key Components in the Regulation of Metabolism and Growth. <i>Plant Physiology</i> , 2010, 152, 428-444.	4.8	155
72	Joint linkage-linkage disequilibrium mapping is a powerful approach to detecting quantitative trait loci underlying drought tolerance in maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19585-19590.	7.1	202

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74	Gene Conversion and DNA Sequence Polymorphism in the Sex-Determination Gene <i>fog-2</i> and Its Paralog <i>ftt-1</i> in <i>Caenorhabditis elegans</i> . Molecular Biology and Evolution, 2010, 27, 1561-1569.	8.9	13
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76	Allelic Variation in Cell Wall Candidate Genes Affecting Solid Wood Properties in Natural Populations and Land Races of <i>Pinus radiata</i> . Genetics, 2010, 185, 1477-1487.	2.9	74
77	Parallel adaptive evolution of Atlantic cod on both sides of the Atlantic Ocean in response to temperature. Proceedings of the Royal Society B: Biological Sciences, 2010, 277, 3725-3734.	2.6	206
78	Landscape genetics of plants. Trends in Plant Science, 2010, 15, 675-683.	8.8	129
79	Artificial selection for determinate growth habit in soybean. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 8563-8568.	7.1	330
80	Methodologies and Results in Grapevine Research. , 2010, , .		20
81	Marker Development for Important Grapevine Traits by Genetic Diversity Studies and Investigation of Differential Gene Expression. , 2010, , 375-387.		1
82	Genome-wide association analyses of common wheat ( <i>Triticum aestivum</i> L.) germplasm identifies multiple loci for aluminium resistance This article is one of a selection of papers from the conference "Exploiting Genome-wide Association in Oilseed Brassicas: a model for genetic improvement of major OECD crops for sustainable farming". Genome, 2010, 53, 957-966.	2.0	70
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88	Nucleotide diversity and linkage disequilibrium of nine genes with putative effects on flowering time in perennial ryegrass ( <i>Lolium perenne</i> L.). Plant Science, 2011, 180, 228-237.	3.6	41
89	Association of simple sequence repeat (SSR) markers with submergence tolerance in diverse populations of perennial ryegrass. Plant Science, 2011, 180, 391-398.	3.6	36
90	Genetic Diversity of a Maize Association Population with Restricted Phenology. Crop Science, 2011, 51, 704-715.	1.8	81

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92	Wheat genetic resources - how to exploit?. <i>Czech Journal of Genetics and Plant Breeding</i> , 2011, 47, S43-S48.	0.8	2
93	Genetic Variation of HvCBF Genes and Their Association with Salinity Tolerance in Tibetan Annual Wild Barley. <i>PLoS ONE</i> , 2011, 6, e22938.	2.5	90
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98	Association of a Novel <i>Pinus monticola</i> Chitinase Gene (<i>PmCh4B</i>) with Quantitative Resistance to <i>Cronartium ribicola</i>. <i>Phytopathology</i> , 2011, 101, 904-911.	2.2	28
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100	Ridge Regression and Other Kernels for Genomic Selection with R Package rrBLUP. <i>Plant Genome</i> , 2011, 4, 250-255.	2.8	1,588
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102	Towards marker-assisted selection in pulses: a review. <i>Plant Breeding</i> , 2011, 130, 297-313.	1.9	156
103	Association analysis of vegetable soybean quality traits with SSR markers. <i>Plant Breeding</i> , 2011, 130, 444-449.	1.9	29
104	Association between nonsynonymous mutations of <i>starch synthase IIa</i> and starch quality in rice (<i>Oryza sativa</i>). <i>New Phytologist</i> , 2011, 189, 593-601.	7.3	19
105	The molecular basis of quantitative variation in foliar secondary metabolites in <i>Eucalyptus globulus</i>. <i>New Phytologist</i> , 2011, 191, 1041-1053.	7.3	82
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108	Overview of techniques to account for confounding due to population stratification and cryptic relatedness in genomic data association analyses. <i>Heredity</i> , 2011, 106, 511-519.	2.6	70
109	Population structure of hyperinvasive serotype 12F, clonal complex 218 <i>Streptococcus pneumoniae</i> revealed by multilocus <i>boxB</i> sequence typing. <i>Infection, Genetics and Evolution</i> , 2011, 11, 1929-1939.	2.3	21



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111	DNA methylation polymorphism in flue-cured tobacco and candidate markers for tobacco mosaic virus resistance. <i>Journal of Zhejiang University: Science B</i> , 2011, 12, 935-942.	2.8	5
112	Altitudinal and Climatic Adaptation Is Mediated by Flowering Traits and <i>FRI</i> , <i>FLC</i> , and <i>PHYC</i> Genes in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2011, 157, 1942-1955.	4.8	171
113	Variation in flowering time in sorghum core collection and mapping of QTLs controlling flowering time by association analysis. <i>Genetic Resources and Crop Evolution</i> , 2011, 58, 983-989.	1.6	15
114	Genetic diversity and association mapping in a collection of selected Chinese soybean accessions based on SSR marker analysis. <i>Conservation Genetics</i> , 2011, 12, 1145-1157.	1.5	36
115	Genome-wide association mapping: a case study in bread wheat ( <i>Triticum aestivum</i> L.). <i>Molecular Breeding</i> , 2011, 27, 37-58.	2.1	278
116	Association mapping of quantitative resistance for <i>Leptosphaeria maculans</i> in oilseed rape ( <i>Brassica</i> ) Tj ETQq0 0 0 r gBT /Overlock 10 Tf	2.1	86
117	Genome-wide association mapping of <i>Fusarium</i> head blight resistance in contemporary barley breeding germplasm. <i>Molecular Breeding</i> , 2011, 27, 439-454.	2.1	142
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120	Contrasted patterns of selection since maize domestication on duplicated genes encoding a starch pathway enzyme. <i>Theoretical and Applied Genetics</i> , 2011, 122, 705-722.	3.6	16
121	Functional markers developed from multiple loci in <i>GS3</i> for fine marker-assisted selection of grain length in rice. <i>Theoretical and Applied Genetics</i> , 2011, 122, 905-913.	3.6	97
122	Association mapping of grain color, phenolic content, flavonoid content and antioxidant capacity in dehulled rice. <i>Theoretical and Applied Genetics</i> , 2011, 122, 1005-1016.	3.6	98
123	Resistance to Soil-borne cereal mosaic virus in durum wheat is controlled by a major QTL on chromosome arm 2BS and minor loci. <i>Theoretical and Applied Genetics</i> , 2011, 123, 527-544.	3.6	25
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129	Flowering time variation in oilseed rape ( <i>Brassica napus</i> L.) is associated with allelic variation in the FRIGIDA homologue BnaA.FRI.a. Journal of Experimental Botany, 2011, 62, 5641-5658.	4.8	114
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140	Genome-Wide Association Mapping in Tomato ( <i>Solanum lycopersicum</i> ) Is Possible Using Genome Admixture of <i>Solanum lycopersicum</i> var. <i>cerasiforme</i> . G3: Genes, Genomes, Genetics, 2012, 2, 853-864.	1.8	77
141	Evaluation of soybean germplasm conserved in NIAS genebank and development of mini core collections. Breeding Science, 2012, 61, 566-592.	1.9	121
142	A candidate gene-based association study of tocopherol content and composition in rapeseed ( <i>Brassica napus</i> ). Frontiers in Plant Science, 2012, 3, 129.	3.6	58
143	Genome wide linkage disequilibrium in Chinese asparagus bean ( <i>Vigna. unguiculata</i> ssp. <i>sesquipedialis</i> ) germplasm: implications for domestication history and genome wide association studies. Heredity, 2012, 109, 34-40.	2.6	35
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147	SNP in starch biosynthesis genes associated with nutritional and functional properties of rice. <i>Scientific Reports</i> , 2012, 2, 557.	3.3	93
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150	Association Mapping for Grain Quality in a Diverse Sorghum Collection. <i>Plant Genome</i> , 2012, 5, .	2.8	113
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160	Genetic dissection of the temperature dependent emergence processes in sorghum using a cumulative emergence model and stability parameters. <i>Theoretical and Applied Genetics</i> , 2012, 125, 1647-1661.	3.6	25
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162	Genome-wide association analysis detecting significant single nucleotide polymorphisms for chlorophyll and chlorophyll fluorescence parameters in soybean ( <i>Glycine max</i> ) landraces. <i>Euphytica</i> , 2012, 186, 919-931.	1.2	85
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296	Polymorphism of TaSAP1-A1 and its association with agronomic traits in wheat. <i>Planta</i> , 2013, 237, 1495-1508.	3.2	83
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299	Identification of genetic markers linked to anthracnose resistance in sorghum using association analysis. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1649-1657.	3.6	43
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721	Genetic diversity and association mapping of cadmium tolerance in bermudagrass [ <i>Cynodon dactylon</i> (L.) Pers.]. <i>Plant and Soil</i> , 2015, 390, 307-321.	3.7	14
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733	Phenotypic population screen identifies a new mutation in bovine DGAT1 responsible for unsaturated milk fat. <i>Scientific Reports</i> , 2015, 5, 8484.	3.3	14
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735	Modelling the genetic architecture of flowering time control in barley through nested association mapping. <i>BMC Genomics</i> , 2015, 16, 290.	2.8	192
736	Population structure and marker-trait association studies of iron, zinc and selenium concentrations in seed of field pea ( <i>Pisum sativum</i> L.). <i>Molecular Breeding</i> , 2015, 35, 1.	2.1	68
737	Accumulation of 5-hydroxynorvaline in maize ( <i>Zea mays</i> ) leaves is induced by insect feeding and abiotic stress. <i>Journal of Experimental Botany</i> , 2015, 66, 593-602.	4.8	36
738	From association to prediction: statistical methods for the dissection and selection of complex traits in plants. <i>Current Opinion in Plant Biology</i> , 2015, 24, 110-118.	7.1	166
739	Identification of a gene controlling variation in the salt tolerance of rapeseed ( <i>Brassica napus</i> L.). <i>Planta</i> , 2015, 242, 313-326.	3.2	45
740	Marker-trait association study for sucrose and yield contributing traits in sugarcane ( <i>Saccharum</i> spp.) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.2	93
741	MAGIC populations in crops: current status and future prospects. <i>Theoretical and Applied Genetics</i> , 2015, 128, 999-1017.	3.6	230
742	Genome-wide DArT and SNP scan for QTL associated with resistance to stripe rust ( <i>Puccinia</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10	3.6	91



#	ARTICLE	IF	CITATIONS
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748	A transposable element in a NAC gene is associated with drought tolerance in maize seedlings. <i>Nature Communications</i> , 2015, 6, 8326.	12.8	392
749	Association analysis of grain traits with SSR markers between <i>Aegilops tauschii</i> and hexaploid wheat ( <i>Triticum aestivum</i> L.). <i>Journal of Integrative Agriculture</i> , 2015, 14, 1936-1948.	3.5	11
750	Genome-wide association mapping reveals novel sources of resistance to northern corn leaf blight in maize. <i>BMC Plant Biology</i> , 2015, 15, 206.	3.6	74
751	PSIKO2: a fast and versatile tool to infer population stratification on various levels in GWAS: Table 1.. <i>Bioinformatics</i> , 2015, 31, 3552-3554.	4.1	2
752	Genetic characteristics of soybean resistance to HG type 0 and HG type 1.2.3.5.7 of the cyst nematode analyzed by genome-wide association mapping. <i>BMC Genomics</i> , 2015, 16, 598.	2.8	104
753	Evolution and selection of <i>hg1</i> , a copy number variant nematode resistance locus. <i>Molecular Ecology</i> , 2015, 24, 1774-1791.	3.9	66
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756	Genome-wide association of drought-related and biomass traits with HapMap SNPs in <i>Medicago truncatula</i> . <i>Plant, Cell and Environment</i> , 2015, 38, 1997-2011.	5.7	69
757	Identification of genomic regions involved in tolerance to drought stress and drought stress induced leaf senescence in juvenile barley. <i>BMC Plant Biology</i> , 2015, 15, 125.	3.6	92
758	Dynamic Quantitative Trait Locus Analysis of Plant Phenomic Data. <i>Trends in Plant Science</i> , 2015, 20, 822-833.	8.8	57
759	Grouping of early maturing quality protein maize inbreds based on SNP markers and combining ability under multiple environments. <i>Field Crops Research</i> , 2015, 183, 169-183.	5.1	63
760	Maize Homologs of HCT, a Key Enzyme in Lignin Biosynthesis, Bind the NLR Rp1 Proteins to Modulate the Defense Response. <i>Plant Physiology</i> , 2015, 169, pp.00703.2015.	4.8	48
761	Prediction accuracies for growth and wood attributes of interior spruce in space using genotyping-by-sequencing. <i>BMC Genomics</i> , 2015, 16, 370.	2.8	86



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769	Genome-wide association analysis of symbiotic nitrogen fixation in common bean. <i>Theoretical and Applied Genetics</i> , 2015, 128, 1999-2017.	3.6	91
770	Comparison of Sub1 markers and their combinations for submergence tolerance and analysis of adaptation strategies of rice in rainfed lowland ecology. <i>Comptes Rendus - Biologies</i> , 2015, 338, 650-659.	0.2	14
771	A candidate gene-based association study reveals SNPs significantly associated with bud burst in European beech ( <i>Fagus sylvatica</i> L.). <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	1.6	19
772	Association of single nucleotide polymorphisms in LpIRI1 gene with freezing tolerance traits in perennial ryegrass. <i>Euphytica</i> , 2015, 204, 523-534.	1.2	15
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776	A haplotype block associated with thousandâ€kernel weight on chromosome 5DS in common wheat (<i>Triticum aestivum</i> L.). <i>Journal of Integrative Plant Biology</i> , 2015, 57, 662-672.	8.5	10
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778	Genome wide association mapping of agro-morphological and disease resistance traits in sugarcane. <i>Euphytica</i> , 2015, 202, 269-284.	1.2	62
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784	Identification of significant single nucleotide polymorphisms for resistance to maize rough dwarf disease in elite maize ( <i>Zea mays</i> L.) inbred lines. <i>Euphytica</i> , 2015, 203, 109-120.	1.2	18
785	A genome-wide association study platform built on iPlant cyberinfrastructure. <i>Concurrency Computation Practice and Experience</i> , 2015, 27, 420-432.	2.2	5
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789	QTL Analysis Coupled with PTR-ToF-MS and Candidate Gene-Based Association Mapping Validate the Role of Md-AAT1 as a Major Gene in the Control of Flavor in Apple Fruit. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 239-252.	1.8	19
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799	Association Analyses to Genetically Improve Drought and Freezing Tolerance of Faba Bean ( <i>Vicia</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	1.8	33
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821	Association analysis of resistance to cereal cyst nematodes (<i>Heterodera avenae</i>) and root lesion nematodes (<i>Pratylenchus neglectus</i> and <i>P. thornei</i>) in CIMMYT advanced spring wheat lines for semi-arid conditions. <i>Breeding Science</i> , 2016, 66, 692-702.	1.9	41
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828	Genome-Wide Association Study Reveals the Genetic Basis of Stalk Cell Wall Components in Maize. <i>PLoS ONE</i> , 2016, 11, e0158906.	2.5	40
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835	Characterizing Variation of Branch Angle and Genome-Wide Association Mapping in Rapeseed ( <i>Brassica</i> ) Tj ETQq1 1 0.784314 rgBT /Ov	3.6	44
836	Development and Identification of SSR Markers Associated with Starch Properties and Î²-Carotene Content in the Storage Root of Sweet Potato ( <i>Ipomoea batatas</i> L.). <i>Frontiers in Plant Science</i> , 2016, 7, 223.	3.6	19
837	Association Mapping for Fiber-Related Traits and Digestibility in Alfalfa ( <i>Medicago sativa</i> ). <i>Frontiers in Plant Science</i> , 2016, 7, 331.	3.6	19
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845	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.	3.6	117
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848	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.	3.6	75
849	Multigenic Control of Pod Shattering Resistance in Chinese Rapeseed Germplasm Revealed by Genome-Wide Association and Linkage Analyses. <i>Frontiers in Plant Science</i> , 2016, 7, 1058.	3.6	25
850	Molecular Evolution and Association of Natural Variation in ZmARF31 with Low Phosphorus Tolerance in Maize. <i>Frontiers in Plant Science</i> , 2016, 7, 1076.	3.6	12
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854	Association Studies in <i>Populus tomentosa</i> Reveal the Genetic Interactions of Pto-MIR156c and Its Targets in Wood Formation. <i>Frontiers in Plant Science</i> , 2016, 7, 1159.	3.6	12
855	QTL Detection and Elite Alleles Mining for Stigma Traits in <i>Oryza sativa</i> by Association Mapping. <i>Frontiers in Plant Science</i> , 2016, 7, 1188.	3.6	26
856	Genome-Wide Association Study of Resistance to Soybean Cyst Nematode ( <i>Heterodera glycines</i> ) HG Type 2.5.7 in Wild Soybean ( <i>Glycine soja</i> ). <i>Frontiers in Plant Science</i> , 2016, 7, 1214.	3.6	68
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874	Genetic variations and miRNA-target interactions contribute to natural phenotypic variations in <i>Populus</i> . New Phytologist, 2016, 212, 150-160.	7.3	17
875	Root trait diversity, molecular marker diversity, and trait-marker associations in a core collection of <i>Lupinus angustifolius</i> . Journal of Experimental Botany, 2016, 67, 3683-3697.	4.8	20
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955	Genetic dissection of heading date and yield under Mediterranean dry climate in barley ( <i>Hordeum</i> ) Tj ETQq1 1 0.784314 rgBT <sub>12</sub> /Overlook	1.2	12
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1027	A resistance locus in the American heirloom rice variety Carolina Gold Select is triggered by <sc>TAL</sc> effectors with diverse predicted targets and is effective against African strains of <i>Xanthomonas oryzae</i> pv. <i>oryzicola</i>. Plant Journal, 2016, 87, 472-483.	5.7	76
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1029	Genomic heterozygosity and hybrid breakdown in cotton (Gossypium): different traits, different effects. BMC Genetics, 2016, 17, 58.	2.7	9
1030	Genome-wide association mapping for root traits in a panel of rice accessions from Vietnam. BMC Plant Biology, 2016, 16, 64.	3.6	52
1031	Association mapping and favorable allele mining for node of first fruiting/sympodial branch and its height in Upland cotton (Gossypium hirsutum L.). Euphytica, 2016, 210, 57-68.	1.2	8

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1032	Genotyping-by-sequencing to remap QTL for type II Fusarium head blight and leaf rust resistance in a wheat-tall wheatgrass introgression recombinant inbred population. <i>Molecular Breeding</i> , 2016, 36, 1.	2.1	7
1033	The genetic diversity and structure of indica rice in China as detected by single nucleotide polymorphism analysis. <i>BMC Genetics</i> , 2016, 17, 53.	2.7	37
1034	Genome-wide study refines the quantitative trait locus for number of ribs in a Large White-Minzu intercross pig population and reveals a new candidate gene. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1885-1890.	2.1	28
1035	Genome-wide association study for semen quality traits in German Warmblood stallions. <i>Animal Reproduction Science</i> , 2016, 171, 81-86.	1.5	25
1036	Single nucleotide polymorphism in sugar pathway and disease resistance genes in sugarcane. <i>Plant Cell Reports</i> , 2016, 35, 1629-1653.	5.6	5
1037	Population Genomics of Fungal and Oomycete Pathogens. <i>Annual Review of Phytopathology</i> , 2016, 54, 323-346.	7.8	96
1038	Specific peroxidases differentiate <i>Brachypodium distachyon</i> accessions and are associated with drought tolerance traits. <i>Annals of Botany</i> , 2016, 118, 259-270.	2.9	8
1039	Polymorphism and association analysis of a drought-resistant gene TaLTP-s in wheat. <i>Journal of Integrative Agriculture</i> , 2016, 15, 1198-1206.	3.5	3
1040	Fine-mapping of qGW4.05, a major QTL for kernel weight and size in maize. <i>BMC Plant Biology</i> , 2016, 16, 81.	3.6	47
1041	Uncovering novel loci for mesocotyl elongation and shoot length in indica rice through genome-wide association mapping. <i>Planta</i> , 2016, 243, 645-657.	3.2	91
1042	Fine mapping of qKW7, a major QTL for kernel weight and kernel width in maize, confirmed by the combined analytic approaches of linkage and association analysis. <i>Euphytica</i> , 2016, 210, 221-232.	1.2	21
1043	Genome-wide association study of grain yield and related traits using a collection of advanced indica rice breeding lines for irrigated ecosystems. <i>Field Crops Research</i> , 2016, 193, 70-86.	5.1	17
1044	Functional mechanisms of drought tolerance in maize through phenotyping and genotyping under well watered and water stressed conditions. <i>European Journal of Agronomy</i> , 2016, 79, 43-57.	4.1	31
1045	Screening of whole genome sequences identified high-impact variants for stallion fertility. <i>BMC Genomics</i> , 2016, 17, 288.	2.8	21
1046	Genetic features of red and green junglefowls and relationship with Indonesian native chickens Sumatera and Kedu Hitam. <i>BMC Genomics</i> , 2016, 17, 320.	2.8	40
1047	Expression profiling of genes involved in drought stress and leaf senescence in juvenile barley. <i>BMC Plant Biology</i> , 2016, 16, 3.	3.6	57
1048	SNP-based analysis of genetic diversity reveals important alleles associated with seed size in rice. <i>BMC Plant Biology</i> , 2016, 16, 93.	3.6	42
1049	Bioinformatics for agriculture in the Next-Generation sequencing era. <i>Chemical and Biological Technologies in Agriculture</i> , 2016, 3, .	4.6	31

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1051	Microsatellite markers used for genome-wide association mapping of partial resistance to <i>Sclerotinia sclerotiorum</i> in a world collection of <i>Brassica napus</i> . <i>Molecular Breeding</i> , 2016, 36, 72.	2.1	64
1052	Genome-wide association study on stem rust resistance in Kazakh spring barley lines. <i>BMC Plant Biology</i> , 2016, 16, 6.	3.6	41
1053	Association mapping of leaf traits in spinach ( <i>Spinacia oleracea</i> L.). <i>Plant Breeding</i> , 2016, 135, 399-404.	1.9	21
1054	Genome-wide association mapping of sexual incompatibility genes in cacao ( <i>Theobroma cacao</i> L.). <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	1.6	22
1055	Molecular marker based detection of leaf rust resistance gene Lr34 in Indian bread wheat ( <i>Triticum</i> ) Tj ETQq1 1 0.784314 rgBT /Overl	1.0	6
1056	Hybridization and introgression in two ecologically dissimilar <i>Fundulus</i> hybrid zones. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 1051-1063.	2.3	17
1057	Imputing Genotypes in Biallelic Populations from Low-Coverage Sequence Data. <i>Genetics</i> , 2016, 202, 487-495.	2.9	59
1058	Association studies reveal the effect of genetic variation in lncRNA UGTRL and its putative target PtoUGT88A1 on wood formation in <i>Populus tomentosa</i> . <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	1.6	8
1059	Association genetics in <i>Populus</i> reveals the interactions between Pto-miR160a and its target Pto-ARF16. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1069-1082.	2.1	22
1060	Identification of Quantitative Trait Loci for the Phenolic Acid Contents and Their Association with Agronomic Traits in Tibetan Wild Barley. <i>Journal of Agricultural and Food Chemistry</i> , 2016, 64, 980-987.	5.2	10
1061	Identification of single nucleotide polymorphisms in soybean associated with resistance to common cutworm ( <i>Spodoptera litura</i> Fabricius). <i>Euphytica</i> , 2016, 209, 49-62.	1.2	22
1062	Variation in genomic methylation in natural populations of <i>Populus simonii</i> is associated with leaf shape and photosynthetic traits. <i>Journal of Experimental Botany</i> , 2016, 67, 723-737.	4.8	34
1063	Effects of ambient and preceding temperatures and metabolic genes on flight metabolism in the Glanville fritillary butterfly. <i>Journal of Insect Physiology</i> , 2016, 85, 23-31.	2.0	16
1064	Analytical and Decision Support Tools for Genomics-Assisted Breeding. <i>Trends in Plant Science</i> , 2016, 21, 354-363.	8.8	70
1065	Discovery of QTLs for water mining and water use efficiency traits in rice under water-limited condition through association mapping. <i>Molecular Breeding</i> , 2016, 36, 1.	2.1	21
1066	Association mapping of germinability and seedling vigor in sorghum under controlled low-temperature conditions. <i>Genome</i> , 2016, 59, 137-145.	2.0	38
1067	Genome-Wide Association Study in <i>Arabidopsis thaliana</i> of Natural Variation in Seed Oil Melting Point: A Widespread Adaptive Trait in Plants. <i>Journal of Heredity</i> , 2016, 107, 257-265.	2.4	10

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1069	Introgression and Exploitation of QTL for Yield and Yield Components from Related Wild Species in Rice Cultivars. Sustainable Development and Biodiversity, 2016, , 171-202.	1.7	2
1070	Linkage disequilibrium in wild and cultured populations of Pacific oyster ( <i>Crassostrea gigas</i> ). Journal of Ocean University of China, 2016, 15, 327-333.	1.2	3
1071	Underlying Mechanisms of Zymographic Diversity in Starch Synthase I and Pullulanase in Rice-Developing Endosperm. Journal of Agricultural and Food Chemistry, 2016, 64, 2030-2037.	5.2	27
1072	Molecular characterization of CIMMYT maize inbred lines with genotyping-by-sequencing SNPs. Theoretical and Applied Genetics, 2016, 129, 753-765.	3.6	94
1073	Strigolactone pathway genes and plant architecture: association analysis and QTL detection for horticultural traits in chrysanthemum. Molecular Genetics and Genomics, 2016, 291, 957-969.	2.1	20
1074	Loci and candidate gene identification for resistance to <i>Phytophthora sojae</i> via association analysis in soybean [ <i>Glycine max</i> (L.) Merr.]. Molecular Genetics and Genomics, 2016, 291, 1095-1103.	2.1	29
1075	Fine mapping of qKL1.07, a major QTL for kernel length in maize. Molecular Breeding, 2016, 36, 1.	2.1	21
1076	A genome-wide association study reveals novel elite allelic variations in seed oil content of <i>Brassica napus</i> . Theoretical and Applied Genetics, 2016, 129, 1203-1215.	3.6	185
1077	Association mapping for drought tolerance in barley at the reproductive stage. Comptes Rendus - Biologies, 2016, 339, 51-59.	0.2	26
1078	Association analysis of cowpea bacterial blight resistance in USDA cowpea germplasm. Euphytica, 2016, 208, 143-155.	1.2	39
1079	Population genomic analysis of gibberellin-responsive long non-coding RNAs in <i>Populus</i> . Journal of Experimental Botany, 2016, 67, 2467-2482.	4.8	98
1080	Evolution of DUF1313 family members across plant species and their association with maize photoperiod sensitivity. Genomics, 2016, 107, 199-207.	2.9	9
1081	SNP discovery in common bean by restriction-associated DNA (RAD) sequencing for genetic diversity and population structure analysis. Molecular Genetics and Genomics, 2016, 291, 1277-1291.	2.1	18
1082	Metabolomic Assessment of Key Maize Resources: GC-MS and NMR Profiling of Grain from B73 Hybrids of the Nested Association Mapping (NAM) Founders and of Geographically Diverse Landraces. Journal of Agricultural and Food Chemistry, 2016, 64, 2162-2172.	5.2	28
1083	Combined linkage and association mapping identifies a major QTL (qRts8-1), conferring tar spot complex resistance in maize. Theoretical and Applied Genetics, 2016, 129, 1217-1229.	3.6	45
1084	Identification of putative candidate genes for red rot resistance in sugarcane ( <i>Saccharum</i> species) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.1	36
1085	Harnessing the power of RADseq for ecological and evolutionary genomics. Nature Reviews Genetics, 2016, 17, 81-92.	16.3	1,169

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1087	Fusarium head blight resistance loci in a stratified population of wheat landraces and varieties. <i>Euphytica</i> , 2016, 207, 551-561.	1.2	20
1088	SNP diversity within and among <i>Brassica rapa</i> accessions reveals no geographic differentiation. <i>Genome</i> , 2016, 59, 11-21.	2.0	15
1089	Association analysis of grapevine bunch traits using a comprehensive approach. <i>Theoretical and Applied Genetics</i> , 2016, 129, 227-242.	3.6	28
1090	Genome-wide association-mapping for fruit quality traits in tomato. <i>Euphytica</i> , 2016, 207, 439-451.	1.2	47
1091	A genome-wide association study of plant height and primary branch number in rapeseed ( <i>Brassica</i> ) Tj ETQq1 1 0.784314 rgBT/Overbo	3.6	144
1092	Population genomic scans suggest novel genes underlie convergent flowering time evolution in the introduced range of <i>Arabidopsis thaliana</i> . <i>Molecular Ecology</i> , 2017, 26, 92-106.	3.9	24
1093	Genotyping-by-sequencing-based genome-wide association studies on Verticillium wilt resistance in autotetraploid alfalfa ( <i>Medicago sativa</i> L.). <i>Molecular Plant Pathology</i> , 2017, 18, 187-194.	4.2	30
1094	Analysis of genetic diversity, population structure and linkage disequilibrium in Iranian wheat landraces using SSR markers. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2017, 15, 327-334.	0.8	14
1095	Development of a multiple-hybrid population for genome-wide association studies: theoretical consideration and genetic mapping of flowering traits in maize. <i>Scientific Reports</i> , 2017, 7, 40239.	3.3	29
1096	Mapping QTLs Controlling Agronomic Traits in the 'Attila'—'CDC Go' Spring Wheat Population under Organic Management using 90K SNP Array. <i>Crop Science</i> , 2017, 57, 365-377.	1.8	30
1097	Validating Genome-Wide Association Candidates Controlling Quantitative Variation in Nodulation. <i>Plant Physiology</i> , 2017, 173, 921-931.	4.8	71
1098	Genetic divergence in two tropical maize composites after four cycles of reciprocal recurrent selection. <i>Plant Breeding</i> , 2017, 136, 41-49.	1.9	12
1099	Molecular diversity and identification of alleles for Verticillium wilt resistance in elite cotton ( <i>Gossypium hirsutum</i> L.) germplasm. <i>Euphytica</i> , 2017, 213, 1.	1.2	15
1100	Genetic dissection of powdery mildew resistance in interspecific half-sib grapevine families using SNP-based maps. <i>Molecular Breeding</i> , 2017, 37, 1.	2.1	82
1101	Genetic diversity, population structure and association analysis in linseed ( <i>Linum usitatissimum</i> L.). <i>Physiology and Molecular Biology of Plants</i> , 2017, 23, 207-219.	3.1	25
1102	Fast-GBS: a new pipeline for the efficient and highly accurate calling of SNPs from genotyping-by-sequencing data. <i>BMC Bioinformatics</i> , 2017, 18, 5.	2.6	99
1103	Joint genome-wide association and transcriptome sequencing reveals a complex polygenic network underlying hypocotyl elongation in rapeseed ( <i>Brassica napus</i> L.). <i>Scientific Reports</i> , 2017, 7, 41561.	3.3	12

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1105	Identification of favorable alleles in the non-yellow coloring 1 gene by association mapping in maize. <i>Euphytica</i> , 2017, 213, 1.	1.2	2
1106	Genome-wide association analysis of seed germination percentage and germination index in <i>Brassica napus</i> L. under salt and drought stresses. <i>Euphytica</i> , 2017, 213, 1.	1.2	37
1107	Molecular genetic diversity and association mapping of nut and kernel traits in Slovenian hazelnut ( <i>Corylus avellana</i> ) germplasm. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	1.6	25
1108	Association mapping of aphid resistance in USDA cowpea ( <i>Vigna unguiculata</i> L. Walp.) core collection using SNPs. <i>Euphytica</i> , 2017, 213, 1.	1.2	26
1109	Genome-wide association analysis of seedling traits in diverse <i>Sorghum</i> germplasm under thermal stress. <i>BMC Plant Biology</i> , 2017, 17, 12.	3.6	80
1110	Frequency and fertility restoration efficiency of <i>Rf3</i> and <i>Rf4</i> genes in Indian rice. <i>Plant Breeding</i> , 2017, 136, 74-82.	1.9	9
1111	Genetic architecture of seed longevity in bread wheat ( <i>Triticum aestivum</i> L.). <i>Journal of Biosciences</i> , 2017, 42, 81-89.	1.1	31
1112	Allelic variation and effects of 16 candidate genes on disease resistance in western Canadian spring wheat cultivars. <i>Molecular Breeding</i> , 2017, 37, 1.	2.1	11
1113	Phenotypic and genotypic screening for rust resistance in common bean germplasm in Uganda. <i>Euphytica</i> , 2017, 213, 1.	1.2	3
1114	Development of a maize 55K SNP array with improved genome coverage for molecular breeding. <i>Molecular Breeding</i> , 2017, 37, 20.	2.1	82
1115	Field-based high throughput phenotyping rapidly identifies genomic regions controlling yield components in rice. <i>Scientific Reports</i> , 2017, 7, 42839.	3.3	74
1116	Genome-wide association study of yield components and fibre quality traits in a cotton germplasm diversity panel. <i>Euphytica</i> , 2017, 213, 1.	1.2	42
1117	Association analysis of molecular markers with traits under drought stress in safflower. <i>Crop and Pasture Science</i> , 2017, 68, 167.	1.5	26
1118	Genome-wide association study (GWAS) of salt tolerance in worldwide soybean germplasm lines. <i>Molecular Breeding</i> , 2017, 37, 1.	2.1	82
1119	Genotyping-by-sequencing of waxy and glossy near-isogenic broccoli lines. <i>Euphytica</i> , 2017, 213, 1.	1.2	7
1120	The genomic basis of adaptation in plants. <i>Current Opinion in Plant Biology</i> , 2017, 36, 88-94.	7.1	68
1121	Molecular genetic characterization and association mapping in spelt wheat. <i>Plant Breeding</i> , 2017, 136, 214-223.	1.9	17

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1123	Genetic Analysis of Cadmium Accumulation in Shoots of Sorghum Landraces. Crop Science, 2017, 57, 22-31.	1.8	8
1124	Asymmetric subgenome selection and cis-regulatory divergence during cotton domestication. Nature Genetics, 2017, 49, 579-587.	21.4	367
1125	Saturated genic <i>SNP</i> mapping identified functional candidates and selection tools for the <i>Pinus monticola</i> Cr2 locus controlling resistance to white pine blister rust. Plant Biotechnology Journal, 2017, 15, 1149-1162.	8.3	33
1126	Association genetics of phenolic needle compounds in Norway spruce with variable susceptibility to needle bladder rust. Plant Molecular Biology, 2017, 94, 229-251.	3.9	30
1127	Genome-wide association study for performance traits in chickens using genotype by sequencing approach. Scientific Reports, 2017, 7, 41748.	3.3	33
1128	Association mapping utilizing diverse barley lines reveals net form net blotch seedling resistance/susceptibility loci. Theoretical and Applied Genetics, 2017, 130, 915-927.	3.6	37
1129	CW5 acts in the brassinosteroid signalling pathway to regulate grain width and weight in rice. Nature Plants, 2017, 3, 17043.	9.3	386
1130	A genome-wide association study of seed composition traits in wild soybean ( <i>Glycine soja</i> ). BMC Genomics, 2017, 18, 18.	2.8	113
1131	Genome-wide association study for soybean cyst nematode resistance in Chinese elite soybean cultivars. Molecular Breeding, 2017, 37, 1.	2.1	22
1132	Dissecting the genetic architecture of <i>Fusarium verticillioides</i> seed rot resistance in maize by combining QTL mapping and genome-wide association analysis. Scientific Reports, 2017, 7, 46446.	3.3	41
1133	Validation of Seed Weight-Associated SSR Markers and Their Usefulness in Distinguishing Chickpea Genotypes According to Seed Size. Agricultural Research, 2017, 6, 130-138.	1.7	5
1134	Cassava haplotype map highlights fixation of deleterious mutations during clonal propagation. Nature Genetics, 2017, 49, 959-963.	21.4	208
1135	Genotyping-by-sequencing of pear ( <i>Pyrus</i> spp.) accessions unravels novel patterns of genetic diversity and selection footprints. Horticulture Research, 2017, 4, 17015.	6.3	56
1136	Natural antisense transcripts are significantly involved in regulation of drought stress in maize. Nucleic Acids Research, 2017, 45, 5126-5141.	14.5	53
1137	<i>ETHQV6.3</i> is involved in melon climacteric fruit ripening and is encoded by a <i>NAC</i> domain transcription factor. Plant Journal, 2017, 91, 671-683.	5.7	71
1138	Differential expression of a <i>WRKY</i> gene between wild and cultivated soybeans correlates to seed size. Journal of Experimental Botany, 2017, 68, 2717-2729.	4.8	65
1139	Gene Fractionation and Function in the Ancient Subgenomes of Maize. Molecular Biology and Evolution, 2017, 34, 1825-1832.	8.9	61



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1141	Comparison and confirmation of SNP-bud burst associations in European beech populations in Germany. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	1.6	12
1142	Association genetics of growth and adaptive traits in loblolly pine ( <i>Pinus taeda</i> L.) using whole-exome-discovered polymorphisms. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	1.6	29
1143	Integrated high-density consensus genetic map of <i>Pyrus</i> and anchoring of the "Bartlett" v1.0 ( <i>Pyrus communis</i> ) genome. <i>DNA Research</i> , 2017, 24, dsw063.	3.4	28
1144	The adaptive genomic landscape of beak morphology in Darwin's finches. <i>Molecular Ecology</i> , 2017, 26, 4978-4989.	3.9	33
1145	Genome-wide Association Analysis Tracks Bacterial Leaf Blight Resistance Loci In Rice Diverse Germplasm. <i>Rice</i> , 2017, 10, 8.	4.0	49
1146	The next generation of carotenoid studies in carrot ( <i>Daucus carota</i> L.). <i>Acta Horticulturae</i> , 2017, , 93-100.	0.2	3
1147	Genotyping-by-sequencing targeting of a novel downy mildew resistance gene Pl 20 from wild <i>Helianthus argophyllus</i> for sunflower ( <i>Helianthus annuus</i> L.). <i>Theoretical and Applied Genetics</i> , 2017, 130, 1519-1529.	3.6	47
1148	Genetic diversity and association mapping of agronomic yield traits in eighty six synthetic hexaploid wheat. <i>Euphytica</i> , 2017, 213, 1.	1.2	15
1149	Genetic variation architecture of mitochondrial genome reveals the differentiation in Korean landrace and weedy rice. <i>Scientific Reports</i> , 2017, 7, 43327.	3.3	13
1150	Adjusting for Familial Relatedness in the Analysis of GWAS Data. <i>Methods in Molecular Biology</i> , 2017, 1526, 175-190.	0.9	7
1151	Analysis of Quantitative Trait Loci. <i>Methods in Molecular Biology</i> , 2017, 1526, 191-203.	0.9	1
1152	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.	3.6	39
1153	Functional natural allelic variants of flavonoid 3,5-hydroxylase gene governing catechin traits in tea plant and its relatives. <i>Planta</i> , 2017, 245, 523-538.	3.2	30
1154	Phenotypic and genome-wide association analysis of spike ethylene in diverse wheat genotypes under heat stress. <i>New Phytologist</i> , 2017, 214, 271-283.	7.3	96
1155	Molecular dissection of QTL governing grain size traits employing association and linkage mapping in Basmati rice. <i>Molecular Breeding</i> , 2017, 37, 1.	2.1	6
1156	A 191-bp insertion/deletion in GBSS1 region is responsible for the changes in grain amylose content in barley ( <i>Hordeum vulgare</i> L.). <i>Molecular Breeding</i> , 2017, 37, 1.	2.1	8
1157	Preliminary evidence for associations between molecular markers and quantitative traits in a set of bread wheat ( <i>Triticum aestivum</i> L.) cultivars and breeding lines. <i>Comptes Rendus - Biologies</i> , 2017, 340, 307-313.	0.2	4

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1158	Genetic diversity of tropical maize inbred lines combining resistance to <i>Striga hermonthica</i> with drought tolerance using SNP markers. <i>Plant Breeding</i> , 2017, 136, 338-343.	1.9	24
1159	Identification of favorable SNP alleles and candidate genes for seedlessness in <i>Vitis vinifera</i> L. using genome-wide association mapping. <i>Euphytica</i> , 2017, 213, 1.	1.2	34
1160	Construction of genotyping-by-sequencing based high-density genetic maps and QTL mapping for fusarium wilt resistance in pigeonpea. <i>Scientific Reports</i> , 2017, 7, 1911.	3.3	55
1161	Genetics of mycorrhizal symbiosis in winter wheat ( <i>Triticum aestivum</i> ). <i>New Phytologist</i> , 2017, 215, 779-791.	7.3	76
1162	Association analysis for pomological traits in mango ( <i>Mangifera indica</i> L.) by genic-SSR markers. <i>Trees - Structure and Function</i> , 2017, 31, 1391-1409.	1.9	18
1163	A genome-wide association study of 23 agronomic traits in Chinese wheat landraces. <i>Plant Journal</i> , 2017, 91, 861-873.	5.7	152
1164	SSR markers associated with fiber yield traits in ramie ( <i>Boehmeria nivea</i> L. Gaudich). <i>Industrial Crops and Products</i> , 2017, 107, 439-445.	5.2	18
1165	Genome-wide association study of outcrossing in cytoplasmic male sterile lines of rice. <i>Scientific Reports</i> , 2017, 7, 3223.	3.3	13
1166	A High-Throughput, Field-Based Phenotyping Technology for Tall Biomass Crops. <i>Plant Physiology</i> , 2017, 174, 2008-2022.	4.8	118
1167	Genetic and transcriptomic analyses of lignin- and lodging-related traits in <i>Brassica napus</i> . <i>Theoretical and Applied Genetics</i> , 2017, 130, 1961-1973.	3.6	64
1168	Nucleotide polymorphisms associated with climate, phenology and physiological traits in European beech ( <i>Fagus sylvatica</i> L.). <i>New Forests</i> , 2017, 48, 463-477.	1.7	15
1169	Genome-wide sequence variations between wild and cultivated tomato species revisited by whole genome sequence mapping. <i>BMC Genomics</i> , 2017, 18, 430.	2.8	24
1170	Increased Power To Dissect Adaptive Traits in Global Sorghum Diversity Using a Nested Association Mapping Population. <i>Genetics</i> , 2017, 206, 573-585.	2.9	152
1171	Whole-genome resequencing of 292 pigeonpea accessions identifies genomic regions associated with domestication and agronomic traits. <i>Nature Genetics</i> , 2017, 49, 1082-1088.	21.4	218
1172	Genotyping-by-sequencing of three mapping populations for identification of candidate genomic regions for resistance to sterility mosaic disease in pigeonpea. <i>Scientific Reports</i> , 2017, 7, 1813.	3.3	48
1173	Association genetics of essential oil traits in <i>Eucalyptus loxophleba</i> : explaining variation in oil yield. <i>Molecular Breeding</i> , 2017, 37, 1.	2.1	9
1174	Additive QTLs on three chromosomes control flowering time in woodland strawberry ( <i>Fragaria vesca</i> )	6.3	29
1175	High-throughput SNP genotyping of modern and wild emmer wheat for yield and root morphology using a combined association and linkage analysis. <i>Functional and Integrative Genomics</i> , 2017, 17, 667-685.	3.5	42

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1176	Association mapping to discover significant marker-trait associations for resistance against fusarium wilt variant 2 in pigeonpea [ <i>Cajanus cajan</i> (L.) Millspaugh] using SSR markers. <i>Journal of Applied Genetics</i> , 2017, 58, 307-319.	1.9	19
1177	Genetic Control of Plasticity in Root Morphology and Anatomy of Rice in Response to Water Deficit. <i>Plant Physiology</i> , 2017, 174, 2302-2315.	4.8	112
1178	Identification of bakanae disease resistance loci in japonica rice through genome wide association study. <i>Rice</i> , 2017, 10, 29.	4.0	43
1179	Genotyping-by-Sequencing Facilitates a High-Density Consensus Linkage Map for <i>Aegilops umbellulata</i> , a Wild Relative of Cultivated Wheat. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1551-1561.	1.8	43
1180	Development and Evaluation of Near-Isogenic Lines with Different Blast Resistance Alleles at the <i>Piz</i> Locus in <i>japonica</i> Rice from the Lower Region of the Yangtze River, China. <i>Plant Disease</i> , 2017, 101, 1283-1291.	1.4	11
1181	Deciphering the genetic control of fruit texture in apple by multiple family-based analysis and genome-wide association. <i>Journal of Experimental Botany</i> , 2017, 68, 1451-1466.	4.8	50
1182	Genotyping by sequencing reveals a new locus for pig teat number. <i>Animal Genetics</i> , 2017, 48, 470-472.	1.7	13
1183	Genome-wide association analysis identifies loci governing mercury accumulation in maize. <i>Scientific Reports</i> , 2017, 7, 247.	3.3	11
1184	Novel Sources of Leaf Rust Resistance in Winter Wheat. <i>Crop Science</i> , 2017, 57, 865-876.	1.8	4
1185	All roads lead to weediness: Patterns of genomic divergence reveal extensive recurrent weedy rice origins from South Asian <i>Oryza</i> . <i>Molecular Ecology</i> , 2017, 26, 3151-3167.	3.9	51
1186	Genotyping-by-Sequencing-Based Investigation of the Genetic Architecture Responsible for a $\sim 1/4$ Sevenfold Increase in Soybean Seed Stearic Acid. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 299-308.	1.8	18
1187	Natural Variation in the Promoter of GSE5 Contributes to Grain Size Diversity in Rice. <i>Molecular Plant</i> , 2017, 10, 685-694.	8.3	253
1188	Population structure analysis and association mapping of bacterial blight resistance in indica rice ( <i>Oryza sativa</i> L.) accessions. <i>Plant Growth Regulation</i> , 2017, 82, 21-35.	3.4	1
1189	Insect herbivory ( <i>Choristoneura fumiferana</i> , Tortricidea) underlies tree population structure ( <i>Picea</i> ) Tj ETQq1 1 0.784314 rgBT/Overlook	3.3	15
1190	Population structure and genetic basis of the agronomic traits of upland cotton in China revealed by a genome-wide association study using high-density <i>scp</i> SNP s. <i>Plant Biotechnology Journal</i> , 2017, 15, 1374-1386.	8.3	196
1191	Fine-scale genetic structure due to adaptive divergence among microhabitats. <i>Heredity</i> , 2017, 118, 594-604.	2.6	24
1192	Analysis of QTL for seed oil content in <i>Brassica napus</i> by association mapping and QTL mapping. <i>Euphytica</i> , 2017, 213, 1.	1.2	24
1193	Microsatellite based linkage disequilibrium analyses reveal Saltol haplotype fragmentation and identify novel QTLs for seedling stage salinity tolerance in rice ( <i>Oryza sativa</i> L.). <i>Journal of Plant Biochemistry and Biotechnology</i> , 2017, 26, 310-320.	1.7	12

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1194	Identification of marker-trait associations for morphological descriptors and yield component traits in sugarcane. <i>Physiology and Molecular Biology of Plants</i> , 2017, 23, 185-196.	3.1	24
1195	Behavioural response to song and genetic divergence in two subspecies of white-crowned sparrows ( <i>Zonotrichia leucophrys</i> ). <i>Molecular Ecology</i> , 2017, 26, 3011-3027.	3.9	61
1196	Overcoming the Law of the Hidden in Cyberinfrastructures. <i>Trends in Plant Science</i> , 2017, 22, 117-123.	8.8	10
1197	The Evolution of Soybean Knowledge Base (SoyKB). <i>Methods in Molecular Biology</i> , 2017, 1533, 149-159.	0.9	25
1198	Genetic architecture of flag leaf length and width in rice ( <i>Oryza sativa</i> L.) revealed by association mapping. <i>Genes and Genomics</i> , 2017, 39, 341-352.	1.4	12
1200	Deciphering the <i>Theobroma cacao</i> self-incompatibility system: from genomics to diagnostic markers for self-compatibility. <i>Journal of Experimental Botany</i> , 2017, 68, 4775-4790.	4.8	42
1201	Identification of new loci for body weight traits in F2 chicken population using genome-wide association study. <i>Livestock Science</i> , 2017, 206, 125-131.	1.6	16
1202	Genome-wide association mapping of genomic regions associated with phenotypic traits in Canadian western spring wheat. <i>Molecular Breeding</i> , 2017, 37, 1.	2.1	30
1203	Novel Loci Underlie Natural Variation in Vitamin E Levels in Maize Grain. <i>Plant Cell</i> , 2017, 29, 2374-2392.	6.6	93
1204	Signatures of polygenic adaptation associated with climate across the range of a threatened fish species with high genetic connectivity. <i>Molecular Ecology</i> , 2017, 26, 6253-6269.	3.9	34
1205	Effects of assortative mate choice on the genomic and morphological structure of a hybrid zone between two bird subspecies. <i>Molecular Ecology</i> , 2017, 26, 6430-6444.	3.9	34
1206	Association analysis of the glutelin synthesis genes GluA and GluB1 in a Japonica rice collection. <i>Molecular Breeding</i> , 2017, 37, 1.	2.1	4
1207	Finding loci associated to partial resistance to white pine blister rust in sugar pine ( <i>Pinus lambertiana</i> ) Tj ETQq0 0 0,rgBT /Overclock 10 Tf	1.8	11
1208	Rice molecular markers and genetic mapping: Current status and prospects. <i>Journal of Integrative Agriculture</i> , 2017, 16, 1879-1891.	3.5	21
1209	Association mapping for seed cotton yield, yield components and fibre quality traits in upland cotton ( <i>Gossypium hirsutum</i> L.) genotypes. <i>Plant Breeding</i> , 2017, 136, 958-968.	1.9	10
1210	Association of candidate genes with heading date in a diverse <i>Dactylis glomerata</i> population. <i>Plant Science</i> , 2017, 265, 146-153.	3.6	13
1211	A genome-wide survey with different rapeseed ecotypes uncovers footprints of domestication and breeding. <i>Journal of Experimental Botany</i> , 2017, 68, 4791-4801.	4.8	52
1212	Genome-Wide Association Mapping of Stem Rust Resistance in <i>Hordeum vulgare</i> subsp. <i>spontaneum</i> . <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3491-3507.	1.8	30

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1213	Breeding Avenues in Fruit Crops for Imparting Resistance Against Insect Pests. , 2017, , 289-322.		0
1214	Associations between the $\delta^5$ -terpineol synthase gene and $\delta^5$ -terpineol content in different grapevine varieties. Biotechnology and Biotechnological Equipment, 2017, 31, 1100-1105.	1.3	5
1215	DARtseq molecular markers for resistance to Phytophthora cinnamomi in pineapple (Ananas comosus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.9	4
1216	A Simple Package to Script and Simulate Breeding Schemes: The Breeding Scheme Language. Crop Science, 2017, 57, 1347-1354.	1.8	29
1217	Crop-model assisted phenomics and genome-wide association study for climate adaptation of indica rice. 1. Phenology. Journal of Experimental Botany, 2017, 68, 4369-4388.	4.8	16
1218	Crop-model assisted phenomics and genome-wide association study for climate adaptation of indica rice. 2. Thermal stress and spikelet sterility. Journal of Experimental Botany, 2017, 68, 4389-4406.	4.8	26
1219	Genome-wide association study and gene set analysis for understanding candidate genes involved in salt tolerance at the rice seedling stage. Molecular Genetics and Genomics, 2017, 292, 1391-1403.	2.1	37
1220	QTL mapping of general combining abilities of four traits in maize using a high-density genetic map. Journal of Integrative Agriculture, 2017, 16, 1700-1707.	3.5	5
1221	Genetic diversity and association mapping of forage quality in diverse bermudagrass accessions. Euphytica, 2017, 213, 1.	1.2	9
1222	Candidate gene sequencing and validation of SNP markers linked to carotenoid content in cassava (Manihot esculenta Crantz). Molecular Breeding, 2017, 37, 1.	2.1	15
1223	Genome-wide Association Analysis of Powdery Mildew Resistance in U.S. Winter Wheat. Scientific Reports, 2017, 7, 11743.	3.3	29
1224	Association analysis of cowpea mosaic virus (CPMV) resistance in the USDA cowpea germplasm collection. Euphytica, 2017, 213, 1.	1.2	7
1225	Linkage disequilibrium based association mapping of micronutrients in common bean (Phaseolus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.2	18
1226	Engineering Quantitative Trait Variation for Crop Improvement by Genome Editing. Cell, 2017, 171, 470-480.e8.	28.9	797
1227	Selinene Volatiles Are Essential Precursors for Maize Defense Promoting Fungal Pathogen Resistance. Plant Physiology, 2017, 175, 1455-1468.	4.8	61
1228	From Hype to Hope: Genome-Wide Association Studies in Soybean. Compendium of Plant Genomes, 2017, , 95-109.	0.5	0
1229	Genome-Wide Linkage-Disequilibrium Mapping to the Candidate Gene Level in Melon (Cucumis melo). Scientific Reports, 2017, 7, 9770.	3.3	62
1230	Metabolomics and genomics combine to unravel the pathway for the presence of fragrance in rice. Scientific Reports, 2017, 7, 8767.	3.3	36

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1232	Genome-wide association mapping of canopy wilting in diverse soybean genotypes. <i>Theoretical and Applied Genetics</i> , 2017, 130, 2203-2217.	3.6	65
1233	Genotyping-by-Sequencing-Based Genetic Analysis of African Rice Cultivars and Association Mapping of Blast Resistance Genes Against <i>Magnaporthe oryzae</i> Populations in Africa. <i>Phytopathology</i> , 2017, 107, 1039-1046.	2.2	14
1234	Genome-wide Association Study Reveals that the Aquaporin NIP1;1 Contributes to Variation in Hydrogen Peroxide Sensitivity in <i>Arabidopsis thaliana</i> . <i>Molecular Plant</i> , 2017, 10, 1082-1094.	8.3	30
1235	Genetic variation and associations involving Fusarium head blight and deoxynivalenol accumulation in cultivated oat ( <i>Avena sativa</i> L.). <i>Plant Breeding</i> , 2017, 136, 620-636.	1.9	20
1236	Association mapping revealed SNP markers for adaptation to low phosphorus conditions and rock phosphate response in USDA cowpea ( <i>Vigna unguiculata</i> (L.) Walp.) germplasm. <i>Euphytica</i> , 2017, 213, 1.	1.2	19
1237	Brassinosteroid and gibberellin control of seedling traits in maize ( <i>Zea mays</i> L.). <i>Plant Science</i> , 2017, 263, 132-141.	3.6	25
1238	Breeding experiments and genome-wide association analysis elucidate two genetically different forms of non-syndromic congenital cleft lip and jaw in Vorderwald Ä Montbéliarde cattle. <i>Animal Genetics</i> , 2017, 48, 523-530.	1.7	2
1239	The identification of new candidate genes <i>Triticum aestivum</i> <i>FLOWERING LOCUS T3</i> and <i>TaFT3a</i> and <i>TARGET OF EAT1</i> ( <i>TaTOE1a</i> ) controlling the short-day photoperiod response in bread wheat. <i>Plant, Cell and Environment</i> , 2017, 40, 2678-2690.	5.7	45
1240	Genetic architecture of wild soybean ( <i>Glycine soja</i> ) response to soybean cyst nematode (Heterodera) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5	2.1	37
1241	Association mapping analysis of fiber yield and quality traits in Upland cotton ( <i>Gossypium hirsutum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.1	20
1242	Genome-wide association mapping of latex yield and girth in Amazonian accessions of <i>Hevea brasiliensis</i> grown in a suboptimal climate zone. <i>Genomics</i> , 2017, 109, 475-484.	2.9	30
1243	Candidate loci involved in domestication and improvement detected by a published 90K wheat SNP array. <i>Scientific Reports</i> , 2017, 7, 44530.	3.3	50
1244	Genomic evidence for local adaptation in the ovoviparous marine fish <i>Sebastiscus marmoratus</i> with a background of population homogeneity. <i>Scientific Reports</i> , 2017, 7, 1562.	3.3	32
1245	Effective Dispersal of Caribbean Reef Fish is Smaller than Current Spacing Among Marine Protected Areas. <i>Scientific Reports</i> , 2017, 7, 4689.	3.3	15
1246	Maize ( <i>Zea mays</i> L.) genome size indicated by 180-bp knob abundance is associated with flowering time. <i>Scientific Reports</i> , 2017, 7, 5954.	3.3	24
1247	Marker-trait association analysis of frost tolerance of 672 worldwide pea ( <i>Pisum sativum</i> L.) collections. <i>Scientific Reports</i> , 2017, 7, 5919.	3.3	23
1248	Genomic patterns in <i>Acropora cervicornis</i> show extensive population structure and variable genetic diversity. <i>Ecology and Evolution</i> , 2017, 7, 6188-6200.	1.9	45

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1249	Genetic diversity and population structure of <i>Striga hermonthica</i> populations from Kenya and Nigeria. <i>Weed Research</i> , 2017, 57, 293-302.	1.7	23
1250	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.	2.8	69
1251	Associations between the 1-deoxy-d-xylulose-5-phosphate synthase gene and aroma in different grapevine varieties. <i>Genes and Genomics</i> , 2017, 39, 1059-1067.	1.4	10
1252	HopBase: a unified resource for <i>Humulus</i> genomics. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	3.0	31
1253	Surveying the Maize community for their diversity and pedigree visualization needs to prioritize tool development and curation. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	3.0	4
1254	The Conserved and Unique Genetic Architecture of Kernel Size and Weight in Maize and Rice. <i>Plant Physiology</i> , 2017, 175, 774-785.	4.8	114
1255	Strategies and tools to improve crop productivity by targeting photosynthesis. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160377.	4.0	19
1256	An InDel in the Promoter of <i>AI-ACTIVATED MALATE TRANSPORTER9</i> Selected during Tomato Domestication Determines Fruit Malate Contents and Aluminum Tolerance. <i>Plant Cell</i> , 2017, 29, 2249-2268.	6.6	207
1257	Genomic estimation of complex traits reveals ancient maize adaptation to temperate North America. <i>Science</i> , 2017, 357, 512-515.	12.6	169
1258	Can asexuality confer a short-term advantage? Investigating apparent biogeographic success in the apomictic triploid fern <i>Myriopteris gracilis</i> . <i>American Journal of Botany</i> , 2017, 104, 1254-1265.	1.7	7
1259	Genetic Diversity and Association Study of Aromatics in Grapevine. <i>Journal of the American Society for Horticultural Science</i> , 2017, 142, 225-231.	1.0	17
1260	Detecting the QTL-allele system conferring flowering date in a nested association mapping population of soybean using a novel procedure. <i>Theoretical and Applied Genetics</i> , 2017, 130, 2297-2314.	3.6	70
1261	Mapping resistance responses to <i>Sclerotinia</i> infestation in introgression lines of <i>Brassica juncea</i> carrying genomic segments from wild Brassicaceae <i>B. fruticulosa</i> . <i>Scientific Reports</i> , 2017, 7, 5904.	3.3	56
1262	Genomic variation across two barn swallow hybrid zones reveals traits associated with divergence in sympatry and allopatry. <i>Molecular Ecology</i> , 2017, 26, 5676-5691.	3.9	48
1263	Growth response of 98 barley ( <i>Hordeum vulgare</i> L.) genotypes to elevated CO <sub>2</sub> and identification of related quantitative trait loci using genome-wide association studies. <i>Plant Breeding</i> , 2017, 136, 483-497.	1.9	15
1264	A SNP-based association analysis for plant growth habit in worldwide cowpea ( <i>Vigna unguiculata</i> (L.) Tj ETQq1 1 0,784314 rgBT /Over	1.2	0
1265	Cloning, molecular evolution and functional characterization of ZmbHLH16, the maize ortholog of OsTIP2 (OsbHLH142). <i>Biology Open</i> , 2017, 6, 1654-1663.	1.2	12
1266	A cost-benefit analysis to select the most effective method for positional cloning: genotyping by sequencing versus allele-specific PCR. <i>Euphytica</i> , 2017, 213, 1.	1.2	0



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1268	Assessment of SNP and InDel Variations Among Rice Lines of Tulaipanji x Ranjit. Rice Science, 2017, 24, 336-348.	3.9	5
1269	Genome-wide association study for resistance to the southern root-knot nematode (Meloidogyne) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	2.1	35
1270	Genetic diversity, population structure, and linkage disequilibrium of elite and local apple accessions from Belgium using the IRSC array. Tree Genetics and Genomes, 2017, 13, 1.	1.6	31
1271	Marker traits association of agronomical traits correlated with stagnant flooding tolerance in rice. Journal of Physics: Conference Series, 2017, 835, 012002.	0.4	0
1272	Genetic mapping of a major codominant QTL associated with $\beta^2$ -carotene accumulation in watermelon. Molecular Breeding, 2017, 37, 1.	2.1	57
1273	Genetic dissection of adventitious shoot regeneration in roses by employing genome-wide association studies. Plant Cell Reports, 2017, 36, 1493-1505.	5.6	21
1274	Identification of quantitative trait loci associated with resistance to net form net blotch in a collection of Nordic barley germplasm. Theoretical and Applied Genetics, 2017, 130, 2025-2043.	3.6	19
1275	Characterization of twenty Camelina spp. accessions using single nucleotide polymorphism genotyping. Horticulture Environment and Biotechnology, 2017, 58, 187-194.	2.1	4
1276	Quantitative trait locus (QTL) analysis of fruit-quality traits for mandarin breeding in Japan. Tree Genetics and Genomes, 2017, 13, 1.	1.6	26
1277	Candidate gene based association mapping in Fusarium culmorum for field quantitative pathogenicity and mycotoxin production in wheat. BMC Genetics, 2017, 18, 49.	2.7	14
1278	Genotyping-by-sequencing of a melon (Cucumis melo L.) germplasm collection from a secondary center of diversity highlights patterns of genetic variation and genomic features of different gene pools. BMC Genomics, 2017, 18, 59.	2.8	72
1279	Genomic characterization of a core set of the USDA-NPGS Ethiopian sorghum germplasm collection: implications for germplasm conservation, evaluation, and utilization in crop improvement. BMC Genomics, 2017, 18, 108.	2.8	41
1280	Impact of novel SNPs identified in Cynara cardunculus genes on functionality of proteins regulating phenylpropanoid pathway and their association with biological activities. BMC Genomics, 2017, 18, 183.	2.8	11
1281	Association mapping of loci controlling genetic and environmental interaction of soybean flowering time under various photo-thermal conditions. BMC Genomics, 2017, 18, 415.	2.8	58
1282	Transcriptomic resources for the medicinal legume Mucuna pruriens: de novo transcriptome assembly, annotation, identification and validation of EST-SSR markers. BMC Genomics, 2017, 18, 409.	2.8	34
1283	Loci and candidate genes conferring resistance to soybean cyst nematode HG type 2.5.7. BMC Genomics, 2017, 18, 462.	2.8	37
1284	The development and use of a molecular model for soybean maturity groups. BMC Plant Biology, 2017, 17, 91.	3.6	70

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1285	Identification of genetic loci associated with crude protein and mineral concentrations in alfalfa ( <i>Medicago sativa</i> ) using association mapping. <i>BMC Plant Biology</i> , 2017, 17, 97.	3.6	24
1286	Identification of genes related to salt stress tolerance using intron-length polymorphic markers, association mapping and virus-induced gene silencing in cotton. <i>Scientific Reports</i> , 2017, 7, 528.	3.3	30
1287	Development of EST-SSR markers through de novo RNA sequencing and application for biomass productivity in kenaf ( <i>Hibiscus cannabinus</i> L.). <i>Genes and Genomics</i> , 2017, 39, 1139-1156.	1.4	11
1288	Genetic mapping with testcrossing associations and F2:3 populations reveals the importance of heterosis in chilling tolerance at maize seedling stage. <i>Scientific Reports</i> , 2017, 7, 3232.	3.3	18
1289	Fine Mapping, Transcriptome Analysis, and Marker Development for <i>Y2</i> , the Gene That Conditions Î²-Carotene Accumulation in Carrot ( <i>Daucus carota</i> L.). <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2665-2675.	1.8	48
1290	Genome-wide Association Analysis for Drought Tolerance and Associated Traits in Common Bean. <i>Plant Genome</i> , 2017, 10, plantgenome2015.12.0122.	2.8	74
1291	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.	3.6	38
1292	Association mapping of leaf rust resistance loci in a spring wheat core collection. <i>Theoretical and Applied Genetics</i> , 2017, 130, 345-361.	3.6	41
1293	Association mapping for floral traits in cultivated <i>Paeonia rockii</i> based on SSR markers. <i>Molecular Genetics and Genomics</i> , 2017, 292, 187-200.	2.1	21
1294	Construction of an SSR and RAD Marker-Based Genetic Linkage Map for Carnation ( <i>Dianthus</i> ) Tj ETQq1 1 0.784314 r/gBT / Overlock 10 T	1.8	22
1295	High rates of extra-pair paternity in a socially monogamous beetle with biparental care. <i>Ecological Entomology</i> , 2017, 42, 1-10.	2.2	23
1296	Deletion of an Endoplasmic Reticulum Stress Response Element in a ZmPP2C-A Gene Facilitates Drought Tolerance of Maize Seedlings. <i>Molecular Plant</i> , 2017, 10, 456-469.	8.3	107
1297	Genome-wide association study reveals genetic architecture of coleoptile length in wheat. <i>Theoretical and Applied Genetics</i> , 2017, 130, 391-401.	3.6	52
1298	Genotyping-by-sequencing approaches to characterize crop genomes: choosing the right tool for the right application. <i>Plant Biotechnology Journal</i> , 2017, 15, 149-161.	8.3	240
1299	Natural variations in stearoyl-acp desaturase genes affect the conversion of stearic to oleic acid in maize kernel. <i>Theoretical and Applied Genetics</i> , 2017, 130, 151-161.	3.6	23
1300	Genome resources for climate-resilient cowpea, an essential crop for food security. <i>Plant Journal</i> , 2017, 89, 1042-1054.	5.7	199
1301	Genetic diversity and association analysis of Chinese chestnut ( <i>Castanea mollissima</i> Blume) cultivars based on SSR markers. <i>Revista Brasileira De Botanica</i> , 2017, 40, 235-246.	1.3	5
1302	Genomic regions, cellular components and gene regulatory basis underlying pod length variations in cowpea ( <i>V.Ânguiculata</i> L. Walp). <i>Plant Biotechnology Journal</i> , 2017, 15, 547-557.	8.3	68

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1303	Genetic architecture of plant stress resistance: multi-trait genome-wide association mapping. <i>New Phytologist</i> , 2017, 213, 1346-1362.	7.3	144
1304	Identification of loci controlling forage yield and nutritive value in diploid alfalfa using GBS-CWAS. <i>Theoretical and Applied Genetics</i> , 2017, 130, 261-268.	3.6	58
1306	Mapping Resistance to <i>Alternaria cucumerina</i> in <i>Cucumis melo</i> . <i>Phytopathology</i> , 2017, 107, 427-432.	2.2	17
1307	Genome-Wide Association Study of Spot Form of Net Blotch Resistance in the Upper Midwest Barley Breeding Programs. <i>Phytopathology</i> , 2017, 107, 100-108.	2.2	22
1308	Exploring and exploiting phenotypic and genetic diversity in peach: identification of major genes and QTLs by GWAS. <i>Acta Horticulturae</i> , 2017, , 419-424.	0.2	1
1309	Numericware i: Identical by State Matrix Calculator. <i>Evolutionary Bioinformatics</i> , 2017, 13, 117693431668866.	1.2	6
1310	The <i>Medicago truncatula</i> GRAS protein RAD1 supports arbuscular mycorrhiza symbiosis and <i>Phytophthora palmivora</i> susceptibility. <i>Journal of Experimental Botany</i> , 2017, 68, 5871-5881.	4.8	42
1311	Genome wide association study of two phenology traits (flowering time and maturity date) in apple. <i>Acta Horticulturae</i> , 2017, , 411-418.	0.2	1
1312	A SNP-enabled assessment of genetic diversity, evolutionary relationships and the identification of candidate genes in chrysanthemum. <i>Genome Biology and Evolution</i> , 2017, 8, evw270.	2.5	38
1313	Genome-wide association study for agronomic and physiological traits in spring wheat evaluated in a range of heat prone environments. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1819-1835.	3.6	117
1314	Population structure and association mapping of traits related to reproductive development in field pea. <i>Euphytica</i> , 2017, 213, 1.	1.2	12
1315	Population Structure and Genetic Diversity Analysis of Germplasm from the Winter Wheat Eastern European Regional Yield Trial (WWEERYT). <i>Crop Science</i> , 2017, 57, 812-820.	1.8	3
1316	Association mapping of agronomic traits of canola ( <i>Brassica napus</i> L.) subject to heat stress under field conditions. <i>Australian Journal of Crop Science</i> , 2017, 11, 1094-1105.	0.3	8
1317	New Candidate Genes Affecting Rice Grain Appearance and Milling Quality Detected by Genome-Wide and Gene-Based Association Analyses. <i>Frontiers in Plant Science</i> , 2016, 7, 1998.	3.6	55
1318	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.	3.6	23
1319	Genome-Wide Association and Transcriptome Analyses Reveal Candidate Genes Underlying Yield-determining Traits in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 206.	3.6	70
1320	Population Structure and Phylogenetic Relationships in a Diverse Panel of <i>Brassica rapa</i> L.. <i>Frontiers in Plant Science</i> , 2017, 8, 321.	3.6	53
1321	New Hypervariable SSR Markers for Diversity Analysis, Hybrid Purity Testing and Trait Mapping in Pigeonpea [ <i>Cajanus cajan</i> (L.) Millspaugh]. <i>Frontiers in Plant Science</i> , 2017, 8, 377.	3.6	59

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1322	Genome-Wide Association Study for Pre-harvest Sprouting Resistance in a Large Germplasm Collection of Chinese Wheat Landraces. <i>Frontiers in Plant Science</i> , 2017, 08, 401.	3.6	98
1323	Deciphering Genomic Regions for High Grain Iron and Zinc Content Using Association Mapping in Pearl Millet. <i>Frontiers in Plant Science</i> , 2017, 8, 412.	3.6	72
1324	Comparative Analysis of Expression Profiles of Panicle Development among Tolerant and Sensitive Rice in Response to Drought Stress. <i>Frontiers in Plant Science</i> , 2017, 08, 437.	3.6	19
1325	Genome-Wide Association Mapping Reveals Multiple QTLs Governing Tolerance Response for Seedling Stage Chilling Stress in Indica Rice. <i>Frontiers in Plant Science</i> , 2017, 8, 552.	3.6	49
1326	Genome-Wide Association Study Reveals the Genetic Architecture Underlying Salt Tolerance-Related Traits in Rapeseed ( <i>Brassica napus</i> L.). <i>Frontiers in Plant Science</i> , 2017, 8, 593.	3.6	89
1327	Investigation of the Genetic Diversity and Quantitative Trait Loci Accounting for Important Agronomic and Seed Quality Traits in <i>Brassica carinata</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 615.	3.6	23
1328	Genome-Wide SNP Markers Based on SLAF-Seq Uncover Breeding Traces in Rapeseed ( <i>Brassica napus</i> L.). <i>Frontiers in Plant Science</i> , 2017, 8, 648.	3.6	68
1329	Characterization of Insect Resistance Loci in the USDA Soybean Germplasm Collection Using Genome-Wide Association Studies. <i>Frontiers in Plant Science</i> , 2017, 8, 670.	3.6	53
1330	Association Mapping Reveals Novel Genetic Loci Contributing to Flooding Tolerance during Germination in Indica Rice. <i>Frontiers in Plant Science</i> , 2017, 8, 678.	3.6	53
1331	Genetic Architecture of Anther Extrusion in Spring and Winter Wheat. <i>Frontiers in Plant Science</i> , 2017, 8, 754.	3.6	53
1332	Sorghum Landrace Collections from Cooler Regions of the World Exhibit Magnificent Genetic Differentiation and Early Season Cold Tolerance. <i>Frontiers in Plant Science</i> , 2017, 8, 756.	3.6	20
1333	Association of Candidate Genes With Submergence Response in Perennial Ryegrass. <i>Frontiers in Plant Science</i> , 2017, 8, 791.	3.6	8
1334	Development of SSR Markers Based on Transcriptome Sequencing and Association Analysis with Drought Tolerance in Perennial Grass <i>Miscanthus</i> from China. <i>Frontiers in Plant Science</i> , 2017, 8, 801.	3.6	19
1335	Assessment of Five Chilling Tolerance Traits and GWAS Mapping in Rice Using the USDA Mini-Core Collection. <i>Frontiers in Plant Science</i> , 2017, 8, 957.	3.6	88
1336	Evolutionary Insights Based on SNP Haplotypes of Red Pericarp, Grain Size and Starch Synthase Genes in Wild and Cultivated Rice. <i>Frontiers in Plant Science</i> , 2017, 8, 972.	3.6	21
1337	The Interactions between the Long Non-coding RNA NERDL and Its Target Gene Affect Wood Formation in <i>Populus tomentosa</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 1035.	3.6	12
1338	Gibberellins Promote Brassinosteroids Action and Both Increase Heterosis for Plant Height in Maize ( <i>Zea mays</i> L.). <i>Frontiers in Plant Science</i> , 2017, 8, 1039.	3.6	32
1339	Identification of Novel Associations of Candidate Genes with Resistance to Late Blight in <i>Solanum tuberosum</i> Group Phureja. <i>Frontiers in Plant Science</i> , 2017, 8, 1040.	3.6	26

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1340	Genome-Wide Association Mapping Reveals the Genetic Control Underlying Branch Angle in Rapeseed ( <i>Brassica napus</i> L.). <i>Frontiers in Plant Science</i> , 2017, 8, 1054.	3.6	68
1341	Identification of Single-Nucleotide Polymorphic Loci Associated with Biomass Yield under Water Deficit in Alfalfa ( <i>Medicago sativa</i> L.) Using Genome-Wide Sequencing and Association Mapping. <i>Frontiers in Plant Science</i> , 2017, 8, 1152.	3.6	30
1342	Genome-Wide Linkage and Association Mapping of Halo Blight Resistance in Common Bean to Race 6 of the Globally Important Bacterial Pathogen. <i>Frontiers in Plant Science</i> , 2017, 8, 1170.	3.6	57
1343	Identification of Major Quantitative Trait Loci for Seed Oil Content in Soybeans by Combining Linkage and Genome-Wide Association Mapping. <i>Frontiers in Plant Science</i> , 2017, 8, 1222.	3.6	101
1344	Genome-Wide Association Study Reveals Candidate Genes for Control of Plant Height, Branch Initiation Height and Branch Number in Rapeseed ( <i>Brassica napus</i> L.). <i>Frontiers in Plant Science</i> , 2017, 8, 1246.	3.6	63
1345	Association and Genetic Identification of Loci for Four Fruit Traits in Tomato Using InDel Markers. <i>Frontiers in Plant Science</i> , 2017, 8, 1269.	3.6	23
1346	Genotyping-by-Sequencing (GBS) Revealed Molecular Genetic Diversity of Iranian Wheat Landraces and Cultivars. <i>Frontiers in Plant Science</i> , 2017, 8, 1293.	3.6	125
1347	Genome-Wide Association Study Identifies NBS-LRR-Encoding Genes Related with Anthracnose and Common Bacterial Blight in the Common Bean. <i>Frontiers in Plant Science</i> , 2017, 8, 1398.	3.6	56
1348	A Combined Association Mapping and Linkage Analysis of Kernel Number Per Spike in Common Wheat ( <i>Triticum aestivum</i> L.). <i>Frontiers in Plant Science</i> , 2017, 8, 1412.	3.6	72
1349	Genetic Mapping of the Leaf Number above the Primary Ear and Its Relationship with Plant Height and Flowering Time in Maize. <i>Frontiers in Plant Science</i> , 2017, 8, 1437.	3.6	17
1350	Climate Clever Clovers: New Paradigm to Reduce the Environmental Footprint of Ruminants by Breeding Low Methanogenic Forages Utilizing Haplotype Variation. <i>Frontiers in Plant Science</i> , 2017, 8, 1463.	3.6	21
1351	Diverse Rice Landraces of North-East India Enables the Identification of Novel Genetic Resources for Magnaporthe Resistance. <i>Frontiers in Plant Science</i> , 2017, 8, 1500.	3.6	30
1352	Comparative Mapping and Candidate Gene Analysis of SSIIa Associated with Grain Amylopectin Content in Barley ( <i>Hordeum vulgare</i> L.). <i>Frontiers in Plant Science</i> , 2017, 8, 1531.	3.6	7
1353	Genetic Tracing of <i>Jatropha curcas</i> L. from Its Mesoamerican Origin to the World. <i>Frontiers in Plant Science</i> , 2017, 8, 1539.	3.6	19
1354	Testing Domestication Scenarios of Lima Bean ( <i>Phaseolus lunatus</i> L.) in Mesoamerica: Insights from Genome-Wide Genetic Markers. <i>Frontiers in Plant Science</i> , 2017, 8, 1551.	3.6	37
1355	Genome-Wide Association Study of Major Agronomic Traits Related to Domestication in Peanut. <i>Frontiers in Plant Science</i> , 2017, 8, 1611.	3.6	87
1356	Genetic Variation and Population Structure of <i>Oryza glaberrima</i> and Development of a Mini-Core Collection Using DArTseq. <i>Frontiers in Plant Science</i> , 2017, 8, 1748.	3.6	71
1357	Genome-Wide Association Study Reveals Novel Loci for SC7 Resistance in a Soybean Mutant Panel. <i>Frontiers in Plant Science</i> , 2017, 8, 1771.	3.6	21

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1358	Global DNA Methylation Patterns Can Play a Role in Defining Terroir in Grapevine ( <i>Vitis vinifera</i> cv.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	3.6	58
1359	Genome-Wide Analysis of japonica Rice Performance under Limited Water and Permanent Flooding Conditions. <i>Frontiers in Plant Science</i> , 2017, 8, 1862.	3.6	38
1360	Application of Genome Wide Association and Genomic Prediction for Improvement of Cacao Productivity and Resistance to Black and Frosty Pod Diseases. <i>Frontiers in Plant Science</i> , 2017, 8, 1905.	3.6	50
1361	A Novel QTL for Powdery Mildew Resistance in Nordic Spring Barley ( <i>Hordeum vulgare</i> L. ssp. <i>vulgare</i> ) Revealed by Genome-Wide Association Study. <i>Frontiers in Plant Science</i> , 2017, 8, 1954.	3.6	16
1362	Comparison of Genetic Diversity between Chinese and American Soybean ( <i>Glycine max</i> (L.)) Accessions Revealed by High-Density SNPs. <i>Frontiers in Plant Science</i> , 2017, 8, 2014.	3.6	45
1363	Genetic Variation and Association Mapping of Seed-Related Traits in Cultivated Peanut ( <i>Arachis</i> Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50) 2105.	3.6	27
1364	Favorable Marker Alleles for Panicle Exsertion Length in Rice ( <i>Oryza sativa</i> L.) Mined by Association Mapping and the RSTEP-LRT Method. <i>Frontiers in Plant Science</i> , 2017, 8, 2112.	3.6	10
1365	Ten Years of Landscape Genomics: Challenges and Opportunities. <i>Frontiers in Plant Science</i> , 2017, 8, 2136.	3.6	62
1366	High-density 80ÅK SNP array is a powerful tool for genotyping <i>G. hirsutum</i> accessions and genome analysis. <i>BMC Genomics</i> , 2017, 18, 654.	2.8	122
1367	Genomewide association mapping and pathway analysis of meat tenderness in Polled Nellore cattle1. <i>Journal of Animal Science</i> , 2017, 95, 1945-1956.	0.5	6
1368	Genome-Wide Association Mapping of Correlated Traits in Cassava: Dry Matter and Total Carotenoid Content. <i>Plant Genome</i> , 2017, 10, plantgenome2016.09.0094.	2.8	63
1369	Genome-Wide Association and Prediction of Grain and Semolina Quality Traits in Durum Wheat Breeding Populations. <i>Plant Genome</i> , 2017, 10, plantgenome2017.05.0038.	2.8	75
1370	High-Density Linkage Map Construction and Mapping of Salt-Tolerant QTLs at Seedling Stage in Upland Cotton Using Genotyping by Sequencing (GBS). <i>International Journal of Molecular Sciences</i> , 2017, 18, 2622.	4.1	42
1371	Association Mapping Reveals Genetic Loci Associated with Important Agronomic Traits in <i>Lentinula edodes</i> , Shiitake Mushroom. <i>Frontiers in Microbiology</i> , 2017, 8, 237.	3.5	13
1372	Plant Phylogeny and Life History Shape Rhizosphere Bacterial Microbiome of Summer Annuals in an Agricultural Field. <i>Frontiers in Microbiology</i> , 2017, 8, 2414.	3.5	56
1373	A Multidisciplinary Phenotyping and Genotyping Analysis of a Mapping Population Enables Quality to Be Combined with Yield in Rice. <i>Frontiers in Molecular Biosciences</i> , 2017, 4, 32.	3.5	8
1374	Linkage disequilibrium and association mapping of fibre quality traits in elite Asiatic cotton ( <i>Gossypium arboreum</i> ) germplasm populations. <i>Czech Journal of Genetics and Plant Breeding</i> , 2017, 53, 159-167.	0.8	19
1375	Genetic Diversity and Association Analysis for Solvent Retention Capacity in the Accessions Derived from Soft Wheat Ningmai 9. <i>International Journal of Genomics</i> , 2017, 2017, 1-8.	1.6	3



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1376	Increasing Genomicâ€Enabled Prediction Accuracy by Modeling Genotype Ã— Environment Interactions in Kansas Wheat. <i>Plant Genome</i> , 2017, 10, plantgenome2016.12.0130.	2.8	107
1377	Genomeâ€Wide Association Mapping of Carbon Isotope and Oxygen Isotope Ratios in Diverse Soybean Genotypes. <i>Crop Science</i> , 2017, 57, 3085-3100.	1.8	63
1378	Genetic diversity and structure of Iberian Peninsula cowpeas compared to world-wide cowpea accessions using high density SNP markers. <i>BMC Genomics</i> , 2017, 18, 891.	2.8	50
1379	Markerâ€Trait Association Analysis of Iron and Zinc Concentration in Lentil ( <i>Lens culinaris</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 97	2.8	97
1380	Genomeâ€Wide Association Study of Developing Leaves' Heat Tolerance during Vegetative Growth Stages in a Sorghum Association Panel. <i>Plant Genome</i> , 2017, 10, plantgenome2016.09.0091.	2.8	54
1381	Meta-QTL for resistance to white mold in common bean. <i>PLoS ONE</i> , 2017, 12, e0171685.	2.5	52
1382	Genome-wide association analysis of agronomic traits in wheat under drought-stressed and non-stressed conditions. <i>PLoS ONE</i> , 2017, 12, e0171692.	2.5	138
1383	A high-density intraspecific SNP linkage map of pigeonpea ( <i>Cajanas cajan</i> L. Millsp.). <i>PLoS ONE</i> , 2017, 12, e0179747.	2.5	18
1384	Genome wide association analysis of cold tolerance at germination in temperate japonica rice ( <i>Oryza</i> ) Tj ETQq0 0 0.0 rgBT /Overlock 10 TF	2.5	39
1385	Global genotype flow in <i>Cercospora beticola</i> populations confirmed through genotyping-by-sequencing. <i>PLoS ONE</i> , 2017, 12, e0186488.	2.5	19
1386	A nested association mapping population identifies multiple small effect QTL conferring resistance against net blotch ( <i>Pyrenophora teres</i> f. <i>teres</i> ) in wild barley. <i>PLoS ONE</i> , 2017, 12, e0186803.	2.5	42
1387	Genetic relatedness of previously Plant-Variety-Protected commercial maize inbreds. <i>PLoS ONE</i> , 2017, 12, e0189277.	2.5	34
1388	Use of molecular markers in identification and characterization of resistance to rice blast in India. <i>PLoS ONE</i> , 2017, 12, e0176236.	2.5	26
1389	Association mapping unveils favorable alleles for grain iron and zinc concentrations in lentil ( <i>Lens</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 32	2.5	32
1390	An R2R3-type MYB transcription factor, GmMYB29, regulates isoflavone biosynthesis in soybean. <i>PLoS Genetics</i> , 2017, 13, e1006770.	3.5	128
1391	Genetic control of the root system in rice under normal and drought stress conditions by genome-wide association study. <i>PLoS Genetics</i> , 2017, 13, e1006889.	3.5	107
1392	Fruit weight is controlled by Cell Size Regulator encoding a novel protein that is expressed in maturing tomato fruits. <i>PLoS Genetics</i> , 2017, 13, e1006930.	3.5	129
1393	Identification of putative markers linked to grain plumpness in rice ( <i>Oryza sativa</i> L.) via association mapping. <i>BMC Genetics</i> , 2017, 18, 89.	2.7	9



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1394	Genetic diversity, population structure and marker-trait associations for agronomic and grain traits in wild diploid wheat <i>Triticum urartu</i> . <i>BMC Plant Biology</i> , 2017, 17, 112.	3.6	32
1395	Genome-wide association mapping for root cone angle in rice. <i>Rice</i> , 2017, 10, 45.	4.0	25
1396	Association mapping of starch chain length distribution and amylose content in pea ( <i>Pisum sativum</i> L.) using carbohydrate metabolism candidate genes. <i>BMC Plant Biology</i> , 2017, 17, 132.	3.6	17
1397	Genetic dissection of Sharka disease tolerance in peach ( <i>P. persica</i> L. Batsch). <i>BMC Plant Biology</i> , 2017, 17, 192.	3.6	19
1398	GWAS of agronomic traits in soybean collection included in breeding pool in Kazakhstan. <i>BMC Plant Biology</i> , 2017, 17, 179.	3.6	19
1399	Assessment of genetic diversity and yield performance in Jordanian barley ( <i>Hordeum vulgare</i> L.) landraces grown under Rainfed conditions. <i>BMC Plant Biology</i> , 2017, 17, 191.	3.6	45
1400	Genome-wide association mapping of black point reaction in common wheat ( <i>Triticum aestivum</i> L.). <i>BMC Plant Biology</i> , 2017, 17, 220.	3.6	141
1401	Identification of 50K Illumina-chip SNPs associated with resistance to spot blotch in barley. <i>BMC Plant Biology</i> , 2017, 17, 250.	3.6	16
1402	GWAS for plant growth stages and yield components in spring wheat ( <i>Triticum aestivum</i> L.) harvested in three regions of Kazakhstan. <i>BMC Plant Biology</i> , 2017, 17, 190.	3.6	51
1403	A comparison of genotyping-by-sequencing analysis methods on low-coverage crop datasets shows advantages of a new workflow, GB-eaSy. <i>BMC Bioinformatics</i> , 2017, 18, 586.	2.6	80
1404	Unravelling the Genetic Diversity among Cassava <i>Bemisia tabaci</i> Whiteflies Using NextRAD Sequencing. <i>Genome Biology and Evolution</i> , 2017, 9, 2958-2973.	2.5	57
1405	Evaluation of Genetic Diversity and Host Resistance to Stem Rust in USDA NSGC Durum Wheat Accessions. <i>Plant Genome</i> , 2017, 10, plantgenome2016.07.0071.	2.8	55
1406	Genetic Dissection of Stem Water-Soluble Carbohydrates and Agronomic Traits in Wheat under Different Water Regimes. <i>Journal of Agricultural Science</i> , 2017, 9, 42.	0.2	6
1407	Genome-wide association mapping for flowering and maturity in tropical soybean: implications for breeding strategies. <i>Breeding Science</i> , 2017, 67, 435-449.	1.9	14
1408	Genetic Characterization of Stem Rust Resistance in a Global Spring Wheat Germplasm Collection. <i>Crop Science</i> , 2017, 57, 2575-2589.	1.8	63
1409	Genetic Diversity among Selected Elite CIMMYT Maize Hybrids in East and Southern Africa. <i>Crop Science</i> , 2017, 57, 2395-2404.	1.8	10
1410	Genetic variation and population structure of maize inbred lines adapted to the mid-altitude sub-humid maize agro-ecology of Ethiopia using single nucleotide polymorphic (SNP) markers. <i>BMC Genomics</i> , 2017, 18, 777.	2.8	36
1411	Genome-wide characterization of non-reference transposable element insertion polymorphisms reveals genetic diversity in tropical and temperate maize. <i>BMC Genomics</i> , 2017, 18, 702.	2.8	18

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1412	Genome-wide Association Mapping of Crown Rust Resistance in Oat Elite Germplasm. Plant Genome, 2017, 10, plantgenome2016.10.0107.	2.8	29
1413	Association Mapping of Ferrous, Zinc, and Aluminum Tolerance at the Seedling Stage in Indica Rice using MAGIC Populations. Frontiers in Plant Science, 2017, 8, 1822.	3.6	42
1414	Introgressed Genomic Regions in a Set of Near-Isogenic Lines of Common Bean Revealed by Genotyping-by-Sequencing. Plant Genome, 2017, 10, plantgenome2016.08.0081.	2.8	12
1415	Identification of QTL with large effect on seed weight in a selective population of soybean with genome-wide association and fixation index analyses. BMC Genomics, 2017, 18, 529.	2.8	87
1416	Non-Mendelian Single-Nucleotide Polymorphism Inheritance and Atypical Meiotic Configurations are Prevalent in Hop. Plant Genome, 2017, 10, plantgenome2017.04.0032.	2.8	20
1417	Regional association analysis-based fine mapping of three clustered QTL for verticillium wilt resistance in cotton ( <i>G. hirsutum</i> L). BMC Genomics, 2017, 18, 661.	2.8	12
1418	Genetic diversity and association mapping of mineral element concentrations in spinach leaves. BMC Genomics, 2017, 18, 941.	2.8	39
1419	A Distinct Genetic Cluster in Cultivated Chickpea as Revealed by Genome-wide Marker Discovery and Genotyping. Plant Genome, 2017, 10, plantgenome2016.11.0115.	2.8	54
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1421	Identification of QTL underlying agronomic, morphological and physiological traits in barley under rainfed conditions using SNP markers. Acta Scientiarum - Agronomy, 2017, 39, 321.	0.6	10
1422	Markers Associated with Culm Length and Elongated Internode Length in Japonica Rice. Crop Science, 2017, 57, 2329-2344.	1.8	4
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1425	Fine mapping and candidate gene prediction of a major QTL for kernel number per ear in maize. Molecular Breeding, 2018, 38, 1.	2.1	9
1426	High-density linkage mapping of vitamin E content in maize grain. Molecular Breeding, 2018, 38, 1.	2.1	10
1427	Simultaneous improvement of grain yield and protein content in durum wheat by different phenotypic indices and genomic selection. Theoretical and Applied Genetics, 2018, 131, 1315-1329.	3.6	87
1428	The analysis of candidate genes and loci involved with carotenoid metabolism in cassava ( <i>Manihot</i> spp.). Frontiers in Plant Science, 2018, 9, 1352.	2.1	6
1429	Linkage and association mapping reveals the genetic basis of brown fibre ( <i>Gossypium hirsutum</i> ). Plant Biotechnology Journal, 2018, 16, 1654-1666.	8.3	41

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1432	Genotyping-by-sequencing reveals the origin of the Tunisian relatives of cultivated carrot ( <i>Daucus</i> ) Tj ETQq1 1 0.784314 rgBT / Overlook	1.6	8
1433	Genome-wide signatures of flowering adaptation to climate temperature: Regional analyses in a highly diverse native range of <i>Arabidopsis thaliana</i> . <i>Plant, Cell and Environment</i> , 2018, 41, 1806-1820.	5.7	49
1434	The search for loci under selection: trends, biases and progress. <i>Molecular Ecology</i> , 2018, 27, 1342-1356.	3.9	171
1435	Genetic risk factors for osteochondrosis in various horse breeds. <i>Equine Veterinary Journal</i> , 2018, 50, 556-563.	1.7	27
1436	Mapping quantitative trait loci for important agronomic traits in finger millet ( <i>Eleusine coracana</i> ) mini core collection with genomic and genic SSR markers. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2018, 27, 401-414.	1.7	4
1437	Genomics of habitat choice and adaptive evolution in a deep-sea fish. <i>Nature Ecology and Evolution</i> , 2018, 2, 680-687.	7.8	41
1438	Novel microsatellite markers reveal multiple origins of <i>Botryosphaeria dothidea</i> causing the Chinese grapevine trunk disease. <i>Fungal Ecology</i> , 2018, 33, 134-142.	1.6	9
1439	Potential SNPs related to microspore culture in <i>Raphanus sativus</i> based on a single-marker analysis. <i>Canadian Journal of Plant Science</i> , 2018, 98, 1072-1083.	0.9	5
1440	Detection of favorable alleles for yield and yield components by association mapping in upland cotton. <i>Genes and Genomics</i> , 2018, 40, 725-734.	1.4	8
1441	Breeding of Lignocellulosic Bioethanol Feedstock. <i>Journal of Crop Science and Biotechnology</i> , 2018, 21, 1-12.	1.5	1
1442	Mining of favorable alleles for lodging resistance traits in rice ( <i>Oryza sativa</i> ) through association mapping. <i>Planta</i> , 2018, 248, 155-169.	3.2	19
1443	Accounting for Errors in Low Coverage High-Throughput Sequencing Data When Constructing Genetic Maps Using Biparental Outcrossed Populations. <i>Genetics</i> , 2018, 209, 65-76.	2.9	36
1444	Linking dendroecology and association genetics in natural populations: Stress responses archived in tree rings associate with SNP genotypes in silver fir ( <i>Abies alba</i> Mill.). <i>Molecular Ecology</i> , 2018, 27, 1428-1438.	3.9	56
1445	Application of Statistical Tools for Data Analysis and Interpretation in Rice Plant Pathology. <i>Rice Science</i> , 2018, 25, 1-18.	3.9	16
1446	SSR-based association mapping of fiber quality in upland cotton using an eight-way MAGIC population. <i>Molecular Genetics and Genomics</i> , 2018, 293, 793-805.	2.1	21
1447	msgbsR: An R package for analysing methylation-sensitive restriction enzyme sequencing data. <i>Scientific Reports</i> , 2018, 8, 2190.	3.3	11
1448	SCoT marker diversity among Iranian <i>Plantago</i> ecotypes and their possible association with agronomic traits. <i>Scientia Horticulturae</i> , 2018, 233, 302-309.	3.6	23

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1450	Current Status and Future Prospects of Next-Generation Data Management and Analytical Decision Support Tools for Enhancing Genetic Gains in Crops. Advances in Biochemical Engineering/Biotechnology, 2018, 164, 277-292.	1.1	4
1451	Genetic variation and association mapping of aphid ( <i>Macrosiphoniella sanbourni</i> ) resistance in chrysanthemum ( <i>Chrysanthemum morifolium</i> Ramat.). Euphytica, 2018, 214, 1.	1.2	9
1452	Population Genetics of <i>Verticillium dahliae</i> in Iran Based on Microsatellite and Single Nucleotide Polymorphism Markers. Phytopathology, 2018, 108, 780-788.	2.2	9
1453	Allelic variation for broadâ€spectrum resistance and susceptibility to bacterial pathogens identified in a rice <scp>MAGIC</scp> population. Plant Biotechnology Journal, 2018, 16, 1559-1568.	8.3	35
1454	The first identification of genomic loci in plants associated with resistance to galling insects: a case study in Eucalyptus L'HÃ©r. (Myrtaceae). Scientific Reports, 2018, 8, 2319.	3.3	11
1455	Efficient genome-wide genotyping strategies and data integration in crop plants. Theoretical and Applied Genetics, 2018, 131, 499-511.	3.6	62
1456	Pleiotropic effects of the wheat domestication gene Q on yield and grain morphology. Planta, 2018, 247, 1089-1098.	3.2	40
1457	Candidate genes involved in the evolution of viviparity: a RAD sequencing experiment in the lizard <i>Zootoca vivipara</i> (Squamata: Lacertidae). Zoological Journal of the Linnean Society, 2018, 183, 196-207.	2.3	11
1458	Beyond pathways: genetic dissection of tocopherol content in maize kernels by combining linkage and association analyses. Plant Biotechnology Journal, 2018, 16, 1464-1475.	8.3	70
1459	Genome scan identifies flowering-independent effects of barley HsDry2.2 locus on yield traits under water deficit. Journal of Experimental Botany, 2018, 69, 1765-1779.	4.8	18
1460	Genome-wide association analysis of lead accumulation in maize. Molecular Genetics and Genomics, 2018, 293, 615-622.	2.1	8
1461	Genome-wide association studies of doubled haploid exotic introgression lines for root system architecture traits in maize ( <i>Zea mays</i> L.). Plant Science, 2018, 268, 30-38.	3.6	55
1462	Diverse Chromosomal Locations of Quantitative Trait Loci for Tolerance to <i>Maize chlorotic mottle virus</i> in Five Maize Populations. Phytopathology, 2018, 108, 748-758.	2.2	26
1463	Elevation of soybean seed oil content through selection for seed coat shininess. Nature Plants, 2018, 4, 30-35.	9.3	75
1464	Population structure and association analysis of heat stress relevant traits in chickpea ( <i>Cicer</i> ) Tj ETQq1 1 0.784314,rgBT /Overclock 10 TF	2.2	17
1465	<i>ZmCOL3</i>, a CCT gene represses flowering in maize by interfering with the circadian clock and activating expression of <i>ZmCCT</i>. Journal of Integrative Plant Biology, 2018, 60, 465-480.	8.5	43
1466	iPat: intelligent prediction and association tool for genomic research. Bioinformatics, 2018, 34, 1925-1927.	4.1	31

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1467	Genome-wide association study reveals candidate genes influencing lipids and diterpenes contents in <i>Coffea arabica</i> L. Scientific Reports, 2018, 8, 465.	3.3	53
1468	A genome-wide association study for left-sided displacement of the abomasum using a high-density single nucleotide polymorphism array. Journal of Dairy Science, 2018, 101, 1258-1266.	3.4	7
1469	Earliness traits in rapeseed ( <i>Brassica napus</i> ): SNP loci and candidate genes identified by genome-wide association analysis. DNA Research, 2018, 25, 229-244.	3.4	41
1470	A Phi-Class Glutathione S-Transferase Gene for Verticillium Wilt Resistance in <i>Gossypium arboreum</i> Identified in a Genome-Wide Association Study. Plant and Cell Physiology, 2018, 59, 275-289.	3.1	87
1471	Detection of QTLs controlling alpha-amylase activity in a diversity panel of 343 barley accessions. Molecular Breeding, 2018, 38, 1.	2.1	6
1472	Loci That Control Nonlinear, Interdependent Responses to Combinations of Drought and Nitrogen Limitation. G3: Genes, Genomes, Genetics, 2018, 8, 1481-1496.	1.8	1
1473	Evolution of Darwin's Peloric Gloxinia ( <i>Sinningia speciosa</i> ) Is Caused by a Null Mutation in a Pleiotropic TCP Gene. Molecular Biology and Evolution, 2018, 35, 1901-1915.	8.9	24
1474	Identification of natural variants affecting chlorophyll content dynamics during rice seedling development. Plant Breeding, 2018, 137, 355-363.	1.9	7
1475	Genomic prediction of the general combining ability of maize lines ( <i>Zea mays</i> L.) and the performance of their single crosses. Plant Breeding, 2018, 137, 379-387.	1.9	14
1476	Identification of novel loci associated with maturity and yield traits in early maturity soybean plant introduction lines. BMC Genomics, 2018, 19, 167.	2.8	34
1477	Genome-wide association study reveals candidate genes related to low temperature tolerance in rice ( <i>Oryza sativa</i> ) during germination. 3 Biotech, 2018, 8, 235.	2.2	15
1478	Genome-wide evidence for divergent selection between populations of a major agricultural pathogen. Molecular Ecology, 2018, 27, 2725-2741.	3.9	74
1479	Increased experimental conditions and marker densities identified more genetic loci associated with southern and northern leaf blight resistance in maize. Scientific Reports, 2018, 8, 6848.	3.3	16
1480	Genome wide association studies (GWAS) of spot blotch resistance at the seedling and the adult plant stages in a collection of spring barley. Molecular Breeding, 2018, 38, 1.	2.1	24
1481	Genome-wide association studies of net form of net blotch resistance at seedling and adult plant stages in spring barley collection. Molecular Breeding, 2018, 38, 1.	2.1	23
1482	Association analysis of drought tolerance in cut chrysanthemum ( <i>Chrysanthemum morifolium</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5	2.2	6
1483	Association mapping and favourable QTL alleles for fibre quality traits in Upland cotton ( <i>Gossypium</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	6.7	6
1484	Mapping association of molecular markers and sheath blight ( <i>Rhizoctonia solani</i> ) disease resistance and identification of novel resistance sources and loci in rice. Euphytica, 2018, 214, 1.	1.2	5

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1486	Dysregulation of expression correlates with rare-allele burden and fitness loss in maize. <i>Nature</i> , 2018, 555, 520-523.	27.8	211
1487	Proteome analysis of <i>Aspergillus flavus</i> isolate-specific responses to oxidative stress in relationship to aflatoxin production capability. <i>Scientific Reports</i> , 2018, 8, 3430.	3.3	45
1488	Genome-wide association mapping for resistance to leaf rust, stripe rust and tan spot in wheat reveals potential candidate genes. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1405-1422.	3.6	101
1489	Genome-Wide Association Studies and Heritability Estimation in the Functional Genomics Era. <i>Population Genomics</i> , 2018, , 361-425.	0.5	6
1490	Genetic diversity, population structure and genetic parameters of fruit traits in <i>Capsicum chinense</i> . <i>Scientia Horticulturae</i> , 2018, 236, 1-9.	3.6	36
1491	The <i>Microtus</i> voles: Resolving the phylogeny of one of the most speciose mammalian genera using genomics. <i>Molecular Phylogenetics and Evolution</i> , 2018, 125, 85-92.	2.7	28
1492	Population genomic analysis of the rice blast fungus reveals specific events associated with expansion of three main clades. <i>ISME Journal</i> , 2018, 12, 1867-1878.	9.8	63
1493	Genetic Loci Controlling Carotenoid Biosynthesis in Diverse Tropical Maize Lines. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1049-1065.	1.8	26
1494	Dissecting the complex regulation of lodging resistance in <i>Brassica napus</i> . <i>Molecular Breeding</i> , 2018, 38, 30.	2.1	28
1495	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.	1.6	27
1496	Recent progress in alfalfa ( <i>Medicago sativa</i> L.) genomics and genomic selection. <i>Crop Journal</i> , 2018, 6, 565-575.	5.2	46
1497	Integrating GWAS and gene expression data for functional characterization of resistance to white mould in soya bean. <i>Plant Biotechnology Journal</i> , 2018, 16, 1825-1835.	8.3	60
1498	Linkage Disequilibrium Based Association and Inheritance of Blast Resistance in Improved Varieties and Landraces of Aromatic Rice. <i>Proceedings of the National Academy of Sciences India Section B - Biological Sciences</i> , 2018, 88, 363-372.	1.0	0
1499	Allelic variations and differential expressions detected at quantitative trait loci for salt stress tolerance in wheat. <i>Plant, Cell and Environment</i> , 2018, 41, 919-935.	5.7	100
1500	Genetic diversity, population structure and association analysis in coconut ( <i>Cocos nucifera</i> L.) germplasm using SSR markers. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2018, 16, 156-168.	0.8	23
1501	Molecular and phenotypic diversity of ICARDA spring barley ( <i>Hordeum vulgare</i> L.) collection. <i>Genetic Resources and Crop Evolution</i> , 2018, 65, 255-269.	1.6	25
1502	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.	1.5	6



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1503	Genetic changes in a novel breeding population of <i>Brassica napus</i> synthesized from hundreds of crosses between <i>B.Ârapa</i> and <i>B.Âcarinata</i> . Plant Biotechnology Journal, 2018, 16, 507-519.	8.3	39
1504	Whole genome re-sequencing reveals evolutionary patterns of sacred lotus ( <i>Nelumbo</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	8.5	37
1505	Geneticâ€based dissection of arsenic accumulation in maize using a genomeâ€wide association analysis method. Plant Biotechnology Journal, 2018, 16, 1085-1093.	8.3	20
1506	Genomic population structure and conservation of the red listed <i>Carabus arcensis</i> (Coleoptera: Carabidae) in islandâ€mainland habitats of Northern Europe. Insect Conservation and Diversity, 2018, 11, 255-266.	3.0	8
1507	Genome-wide association study of heat stress-tolerance traits in spring-type <i>Brassica napus</i> L. under controlled conditions. Crop Journal, 2018, 6, 115-125.	5.2	45
1508	Determinants of Virulence and In Vitro Development Colocalize on a Genetic Map of <i>Setosphaeria turcica</i> . Phytopathology, 2018, 108, 254-263.	2.2	34
1509	Discovery of a seventh Rpp soybean rust resistance locus in soybean accession PI 605823. Theoretical and Applied Genetics, 2018, 131, 27-41.	3.6	51
1510	Identification of genetic loci conferring partial resistance to southern corn rust through a genome-wide association study. European Journal of Plant Pathology, 2018, 150, 1083-1090.	1.7	12
1511	Establishment and evaluation of a peanut association panel and analysis of key nutritional traits. Journal of Integrative Plant Biology, 2018, 60, 195-215.	8.5	11
1512	Association analysis of salt tolerance in cowpea ( <i>Vigna unguiculata</i> (L.) Walp) at germination and seedling stages. Theoretical and Applied Genetics, 2018, 131, 79-91.	3.6	41
1513	Comprehensive description of genomewide nucleotide and structural variation in shortâ€season soya bean. Plant Biotechnology Journal, 2018, 16, 749-759.	8.3	46
1514	Phylogenetic Relationships, Breeding Implications, and Cultivation History of Hawaiian Taro ( <i>Colocasia Esculenta</i> ) Through Genome-Wide SNP Genotyping. Journal of Heredity, 2018, 109, 272-282.	2.4	19
1515	Breeding for Biomass Yield in Switchgrass Using Surrogate Measures of Yield. Bioenergy Research, 2018, 11, 1-12.	3.9	15
1516	Genome-wide association study of stem rust resistance in a world collection of cultivated barley. Theoretical and Applied Genetics, 2018, 131, 107-126.	3.6	7
1517	Comparative Analysis of SSR Markers Developed in Exon, Intron, and Intergenic Regions and Distributed in Regions Controlling Fruit Quality Traits in <i>Prunus</i> Species: Genetic Diversity and Association Studies. Plant Molecular Biology Reporter, 2018, 36, 23-35.	1.8	37
1518	Evolutionary conservation and functional divergence of the LFK gene family play important roles in the photoperiodic flowering pathway of land plants. Heredity, 2018, 120, 310-328.	2.6	13
1519	Nature's genetic screens: using genomeâ€wide association studies for effector discovery. Molecular Plant Pathology, 2018, 19, 3-6.	4.2	34
1520	Coding single nucleotide polymorphisms and SmCPS1 and SmKSL1 subcellular localization are associated with tanshinone biosynthesis in <i>Salvia miltiorrhiza</i> Bunge roots. Acta Physiologiae Plantarum, 2018, 40, 1.	2.1	5



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1521	Genetic analysis of multi-environmental spring wheat trials identifies genomic regions for locus-specific trade-offs for grain weight and grain number. <i>Theoretical and Applied Genetics</i> , 2018, 131, 985-998.	3.6	127
1522	Genetic differentiation and diversity upon genotype and phenotype in cowpea ( <i>Vigna unguiculata</i> L.) Tj ETQq1 1 0.784314 rgBT /Overdo	1.2	13
1523	Combination of Acylglucose QTL reveals additive and epistatic genetic interactions and impacts insect oviposition and virus infection. <i>Molecular Breeding</i> , 2018, 38, 1.	2.1	31
1524	Spatial patterns of genetic diversity among Australian alpine flora communities revealed by comparative phylogenomics. <i>Journal of Biogeography</i> , 2018, 45, 177-189.	3.0	8
1525	Genetic mapping reveals a dominant awn-inhibiting gene related to differentiation of the variety anathera in the wild diploid wheat <i>Aegilops tauschii</i> . <i>Genetica</i> , 2018, 146, 75-84.	1.1	16
1526	Genotyping by Sequencing in Almond: SNP Discovery, Linkage Mapping, and Marker Design. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 161-172.	1.8	28
1527	Mating Design and Genetic Structure of a Multi-Parent Advanced Generation Intercross (MAGIC) Population of Sorghum ( <i>Sorghum bicolor</i> (L.) Moench). <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 331-341.	1.8	69
1528	Association mapping of drought tolerance-related traits in barley to complement a traditional biparental QTL mapping study. <i>Theoretical and Applied Genetics</i> , 2018, 131, 167-181.	3.6	36
1529	Isolation by distance, not incipient ecological speciation, explains genetic differentiation in an Andean songbird (Aves: Furnariidae: <i>Cranioleuca antisensis</i> , Linea€cheeked Spinetail) despite near threefold body size change across an environmental gradient. <i>Molecular Ecology</i> , 2018, 27, 279-296.	3.9	44
1530	DNA molecular markers in plant breeding: current status and recent advancements in genomic selection and genome editing. <i>Biotechnology and Biotechnological Equipment</i> , 2018, 32, 261-285.	1.3	487
1531	Genetic mapping of biomass yield in three interconnected <i>Miscanthus</i> populations. <i>GCB Bioenergy</i> , 2018, 10, 165-185.	5.6	29
1532	Analysis of Environment-Marker Associations in American Chestnut. <i>Forests</i> , 2018, 9, 695.	2.1	10
1533	Genetic variability of Brazilian wheat germplasm obtained by high-density SNP genotyping. <i>Crop Breeding and Applied Biotechnology</i> , 2018, 18, 399-408.	0.4	10
1534	Quantitative Genetics of the Maize Leaf Microbiome. <i>Phytobiomes Journal</i> , 2018, 2, 208-224.	2.7	110
1535	Genetic variation of dynamic fiber elongation and developmental quantitative trait locus mapping of fiber length in upland cotton ( <i>Gossypium hirsutum</i> L.). <i>BMC Genomics</i> , 2018, 19, 882.	2.8	33
1536	Combined linkage and association mapping reveal QTL for host plant resistance to common rust ( <i>Puccinia sorghi</i> ) in tropical maize. <i>BMC Plant Biology</i> , 2018, 18, 310.	3.6	14
1537	Genome-wide association study of rice genes and loci conferring resistance to <i>Magnaporthe oryzae</i> isolates from Taiwan. , 2018, 59, 32.		15
1538	Combining Three Mapping Strategies to Reveal Quantitative Trait Loci and Candidate Genes for Maize Ear Length. <i>Plant Genome</i> , 2018, 11, 170107.	2.8	6

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1539	Comparing Four Genome-Wide Association Study (GWAS) Programs with Varied Input Data Quantity. , 2018, , .		3
1540	Exploring SNP diversity in wheat landraces germplasm and setting of a molecular barcode for fingerprinting. Cereal Research Communications, 2018, 46, 377-387.	1.6	11
1541	Genetic Properties of a Nested Association Mapping Population Constructed With Semi-Winter and Spring Oilseed Rapeseeds. Frontiers in Plant Science, 2018, 9, 1740.	3.6	29
1542	Selection Signatures Underlying Dramatic Male Inflorescence Transformation During Modern Hybrid Maize Breeding. Genetics, 2018, 210, 1125-1138.	2.9	45
1543	Partitioning genetic and species diversity refines our understanding of speciesâ€“genetic diversity relationships. Ecology and Evolution, 2018, 8, 12351-12364.	1.9	16
1544	Genome Scans Reveal Homogenization and Local Adaptations in Populations of the Soybean Cyst Nematode. Frontiers in Plant Science, 2018, 9, 987.	3.6	6
1545	Lessons from Common Bean on How Wild Relatives and Landraces Can Make Tropical Crops More Resistant to Climate Change. , 2018, , .		10
1546	Genome-wide scan using DArT markers for selection footprints in six-rowed naked barley from the Tibetan Plateau. Cereal Research Communications, 2018, 46, 591-603.	1.6	1
1547	Analysis of Radar Backscattering from First-Year Sea Ice With C-Shaped Profiles. , 2018, , .		0
1548	Genome-wide association analysis of kernel morphology in breeding lines derived from synthetic hexaploid wheat in Qinghai Province, China. Cereal Research Communications, 2018, 46, 399-411.	1.6	0
1549	TCAP FACâ€“WIN6 Elite Barley GWAS Panel QTL. II. Malting Quality QTL in Elite North American Facultative and Winter Sixâ€“Rowed Barley Identified via GWAS. Crop Science, 2018, 58, 120-132.	1.8	4
1550	A genome-wide data assessment of the African lion (Panthera leo) population genetic structure and diversity in Tanzania. PLoS ONE, 2018, 13, e0205395.	2.5	16
1551	Integrating Coexpression Networks with GWAS to Prioritize Causal Genes in Maize. Plant Cell, 2018, 30, 2922-2942.	6.6	137
1552	Genetic Characterization of Maximilian Sunflower for the Development of a Locally Adapted Perennial Grain Oilseed. Crop Science, 2018, 58, 2241-2260.	1.8	8
1553	A genome-wide association study using a Vietnamese landrace panel of rice (Oryza sativa) reveals new QTLs controlling panicle morphological traits. BMC Plant Biology, 2018, 18, 282.	3.6	36
1554	Exploring the genetic basis of gene transcript abundance and metabolite levels in loblolly pine (Pinus) Tj ETQq1 1 0,784314 rgBT /Overl	2.7	10
1555	Resistance to Multiple Temperate and Tropical Stem and Sheath Diseases of Rice. Plant Genome, 2018, 11, 170029.	2.8	11
1556	A genome-wide associate study reveals favorable alleles conferring apical and basal spikelet fertility in wheat (Triticum aestivum L.). Molecular Breeding, 2018, 38, 1.	2.1	2

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1557	Pasta-Making Quality QTLome From Mediterranean Durum Wheat Landraces. <i>Frontiers in Plant Science</i> , 2018, 9, 1512.	3.6	30
1558	Genome-Wide Association Studies Reveal Genomic Regions Associated With the Response of Wheat ( <i>Triticum aestivum</i> L.) to Mycorrhizae Under Drought Stress Conditions. <i>Frontiers in Plant Science</i> , 2018, 9, 1728.	3.6	48
1559	Discovery of Anthocyanin Acyltransferase1 (AAT1) in Maize Using Genotyping-by-Sequencing (GBS). <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3669-3678.	1.8	22
1560	Genetic architecture of common bunt resistance in winter wheat using genome-wide association study. <i>BMC Plant Biology</i> , 2018, 18, 280.	3.6	37
1561	Computational Tools for Population Genomics. <i>Population Genomics</i> , 2018, , 127-160.	0.5	2
1562	Screening of diverse tall fescue population for salinity tolerance based on SSR marker-physiological trait association. <i>Euphytica</i> , 2018, 214, 1.	1.2	6
1563	Association Mapping of Flowering and Height Traits in Germplasm Enhancement of Maize Doubled Haploid (GEMâ€DH) Lines. <i>Plant Genome</i> , 2018, 11, 170083.	2.8	33
1564	Development of species diagnostic SNP markers for quality control genotyping in four rice ( <i>Oryza</i> L.) species. <i>Molecular Breeding</i> , 2018, 38, 131.	2.1	22
1565	Association mapping of quantitative resistance to charcoal root rot in mulberry germplasm. <i>PLoS ONE</i> , 2018, 13, e0200099.	2.5	18
1566	Genetic Diversity and Resistance to Fusarium Head Blight in Synthetic Hexaploid Wheat Derived From <i>Aegilops tauschii</i> and Diverse <i>Triticum turgidum</i> Subspecies. <i>Frontiers in Plant Science</i> , 2018, 9, 1829.	3.6	20
1567	SNPiversity: a web-based tool for visualizing diversity. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	9
1568	Genome-Wide Association Mapping of Major Root Length QTLs Under PEG Induced Water Stress in Wheat. <i>Frontiers in Plant Science</i> , 2018, 9, 1759.	3.6	34
1569	Naturally Available Genetic Adaptation in Common Bean and Its Response to Climate Change. , 2018, , .		9
1570	Accuracy of genomic selection for growth and wood quality traits in two control-pollinated progeny trials using exome capture as the genotyping platform in Norway spruce. <i>BMC Genomics</i> , 2018, 19, 946.	2.8	75
1571	Population structure and association analyses of the core collection of hexaploid accessions conserved &lt;i>ex situ&/i> in the Japanese gene bank NBRP-Wheat. <i>Genes and Genetic Systems</i> , 2018, 93, 237-254.	0.7	13
1572	Genome-wide association mapping of spot blotch resistance in wheat association mapping initiative (WAMI) panel of spring wheat ( <i>Triticum aestivum</i> L.). <i>PLoS ONE</i> , 2018, 13, e0208196.	2.5	17
1573	Genomic Selection for Ascochyta Blight Resistance in Pea. <i>Frontiers in Plant Science</i> , 2018, 9, 1878.	3.6	18
1574	Genome-wide functional analyses of plant coiledâ€coil NLR-type pathogen receptors reveal essential roles of their N-terminal domain in oligomerization, networking, and immunity. <i>PLoS Biology</i> , 2018, 16, e2005821.	5.6	52

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1575	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.	3.6	29
1576	Identification of Novel Quantitative Trait Loci Linked to Crown Rot Resistance in Spring Wheat. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2666.	4.1	22
1577	Identification of QTNs Controlling Seed Protein Content in Soybean Using Multi-Locus Genome-Wide Association Studies. <i>Frontiers in Plant Science</i> , 2018, 9, 1690.	3.6	40
1578	Genome-Wide Association Study Using Historical Breeding Populations Discovers Genomic Regions Involved in High-Quality Rice. <i>Plant Genome</i> , 2018, 11, 170076.	2.8	26
1579	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.	2.5	20
1580	Molecular identification of blast resistance genes in rice landraces from northeastern India. <i>Plant Pathology</i> , 2019, 68, 537-546.	2.4	7
1581	Population genomics and climate adaptation of a C4 perennial grass, <i>Panicum hallii</i> (Poaceae). <i>BMC Genomics</i> , 2018, 19, 792.	2.8	9
1582	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.	3.6	56
1583	Identification of genomic loci associated with 21chlorophyll fluorescence phenotypes by genome-wide association analysis in soybean. <i>BMC Plant Biology</i> , 2018, 18, 312.	3.6	19
1584	Genome-wide association study of kernel moisture content at harvest stage in maize. <i>Breeding Science</i> , 2018, 68, 622-628.	1.9	24
1585	On the Causes of Rapid Diversification in the Páramos: Isolation by Ecology and Genomic Divergence in Espeletia. <i>Frontiers in Plant Science</i> , 2018, 9, 1700.	3.6	58
1586	Detecting the QTL-Allele System of Seed Oil Traits Using Multi-Locus Genome-Wide Association Analysis for Population Characterization and Optimal Cross Prediction in Soybean. <i>Frontiers in Plant Science</i> , 2018, 9, 1793.	3.6	19
1587	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.	2.8	65
1588	Genome-Wide Association and Metabolic Pathway Analysis of Corn Earworm Resistance in Maize. <i>Plant Genome</i> , 2018, 11, 170069.	2.8	20
1589	Genome-Wide Association Study Reveals Novel Genomic Regions for Grain Yield and Yield-Related Traits in Drought-Stressed Synthetic Hexaploid Wheat. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3011.	4.1	90
1590	Genome-Wide Association Analysis of Mucilage and Hull Content in Flax ( <i>Linum usitatissimum</i> L.) Seeds. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2870.	4.1	42
1591	2D association and integrative omics analysis in rice provides systems biology view in trait analysis. <i>Communications Biology</i> , 2018, 1, 153.	4.4	4
1592	CWAS analysis in spring barley ( <i>Hordeum vulgare</i> L.) for morphological traits exposed to drought. <i>PLoS ONE</i> , 2018, 13, e0204952.	2.5	55

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1593	Genome-Wide Association Study in Pseudo-F2 Populations of Switchgrass Identifies Genetic Loci Affecting Heading and Anthesis Dates. <i>Frontiers in Plant Science</i> , 2018, 9, 1250.	3.6	22
1594	<b>Linkage disequilibrium and population structure in <i>Fragaria chiloensis</i> revealed by SSR markers transferred from commercial strawberry. <i>Acta Scientiarum - Agronomy</i> , 2018, 40, 34966.	0.6	5
1595	Evaluation of Soybean Germplasm for Resistance to Multiple Nematode Species: <i>Heterodera glycines</i> , <i>Meloidogyne incognita</i> , and <i>Rotylenchulus reniformis</i> . <i>Crop Science</i> , 2018, 58, 2511-2522.	1.8	21
1596	Genome-wide SNP-based association mapping of resistance to <i>Phytophthora sojae</i> in soybean ( <i>Glycine</i> ) Tj ETQq1 1,0,784314,rgBT /Ove	1.2	9
1597	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.	1.5	3
1598	Genetic diversity of <sc><i>Manihot esculenta</i></sc> Crantz germplasm based on singleâ€nucleotide polymorphism markers. <i>Annals of Applied Biology</i> , 2018, 173, 271-284.	2.5	18
1599	Association mapping of salt tolerance traits at germination stage of rapeseed ( <i>Brassica napus</i> L.). <i>Euphytica</i> , 2018, 214, 1.	1.2	14
1600	Reliability of genomic predictions of complex human phenotypes. <i>BMC Proceedings</i> , 2018, 12, 51.	1.6	7
1601	Association of SSR and Candidate Gene Markers with Genetic Variations in Summer Heat and Drought Performance for Creeping Bentgrass. <i>Crop Science</i> , 2018, 58, 2644-2656.	1.8	10
1602	Genome-wide association analysis of quantitative trait loci for salinity-tolerance related morphological indices in bread wheat. <i>Euphytica</i> , 2018, 214, 1.	1.2	15
1603	Natural variation at XND1 impacts root hydraulics and trade-off for stress responses in <i>Arabidopsis</i> . <i>Nature Communications</i> , 2018, 9, 3884.	12.8	67
1604	Identification of Quantitative Trait Loci and Candidate Genes for Maize Starch Granule Size through Association Mapping. <i>Scientific Reports</i> , 2018, 8, 14236.	3.3	11
1605	Genetic Diversity, Population Structure, and Botanical Variety of 320 Global Peanut Accessions Revealed Through Tunable Genotyping-by-Sequencing. <i>Scientific Reports</i> , 2018, 8, 14500.	3.3	33
1606	Genetic Diversity, Population Structure, and Linkage Disequilibrium in a Spanish Common Bean Diversity Panel Revealed through Genotyping-by-Sequencing. <i>Genes</i> , 2018, 9, 518.	2.4	32
1607	Genome-wide generation and genotyping of informative SNPs to scan molecular signatures for seed yield in chickpea. <i>Scientific Reports</i> , 2018, 8, 13240.	3.3	27
1608	Genotyping-by-sequencing highlights patterns of genetic structure and domestication in artichoke and cardoon. <i>PLoS ONE</i> , 2018, 13, e0205988.	2.5	43
1609	Association Analysis and Identification of ZmHKT1;5 Variation With Salt-Stress Tolerance. <i>Frontiers in Plant Science</i> , 2018, 9, 1485.	3.6	51
1610	Thirteen years under arid conditions: exploring marker-trait associations in <i>Eucalyptus cladocalyx</i> for complex traits related to flowering, stem form and growth. <i>Breeding Science</i> , 2018, 68, 367-374.	1.9	13

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1611	Multi-Environmental Trials Reveal Genetic Plasticity of Oat Agronomic Traits Associated With Climate Variable Changes. <i>Frontiers in Plant Science</i> , 2018, 9, 1358.	3.6	12
1612	Agro-morphological description, genetic diversity and population structure of sugarcane varieties from sub-tropical India. <i>3 Biotech</i> , 2018, 8, 469.	2.2	2
1613	Genetic insight and mapping of the pod constriction trait in Virginia-type peanut. <i>BMC Genetics</i> , 2018, 19, 93.	2.7	9
1614	Single-nucleotide polymorphisms(SNPs) in a sucrose synthase gene are associated with wood properties in <i>Catalpa fargesii</i> bur. <i>BMC Genetics</i> , 2018, 19, 99.	2.7	5
1615	Integration of conventional and advanced molecular tools to track footprints of heterosis in cotton. <i>BMC Genomics</i> , 2018, 19, 776.	2.8	14
1616	Genome-wide association study for electrolyte leakage in rapeseed/canola ( <i>Brassica napus</i> L.). <i>Molecular Breeding</i> , 2018, 38, 1.	2.1	9
1617	Polygenic Basis and Variable Genetic Architectures Contribute to the Complex Nature of Body Weight â€”A Genome-Wide Study in Four Chinese Indigenous Chicken Breeds. <i>Frontiers in Genetics</i> , 2018, 9, 229.	2.3	7
1618	Abiotic Stress Tolerance in Rice ( <i>Oryza sativa</i> L.): A Genomics Perspective of Salinity Tolerance. , 0, , .		3
1619	Carotenoid Presence Is Associated with the Or Gene in Domesticated Carrot. <i>Genetics</i> , 2018, 210, 1497-1508.	2.9	75
1620	Genetic Diversity Patterns and Heterosis Prediction Based on SSRs and SNPs in Hybrid Parents of Pearl Millet. <i>Crop Science</i> , 2018, 58, 2379-2390.	1.8	15
1621	Association analysis for seed yield, forage yield and traits related to drought tolerance in orchardgrass ( <i>Dactylis glomerata</i> ). <i>Crop and Pasture Science</i> , 2018, 69, 1150.	1.5	7
1622	Genetic diversity assessed by genotyping by sequencing (GBS) and for phenological traits in blueberry cultivars. <i>PLoS ONE</i> , 2018, 13, e0206361.	2.5	21
1623	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.	4.1	72
1624	Construction of a high-density genetic map and fine QTL mapping for growth and nutritional traits of <i>Crassostrea gigas</i> . <i>BMC Genomics</i> , 2018, 19, 626.	2.8	39
1625	Genome-wide association study of agronomic traits in rice cultivated in temperate regions. <i>BMC Genomics</i> , 2018, 19, 706.	2.8	18
1626	Association genetics of acetophenone defence against spruce budworm in mature white spruce. <i>BMC Plant Biology</i> , 2018, 18, 231.	3.6	18
1627	Marker-trait associations in two-rowed spring barley accessions from Kazakhstan and the USA. <i>PLoS ONE</i> , 2018, 13, e0205421.	2.5	14
1628	Heat Stress Tolerance in Rice ( <i>Oryza sativa</i> L.): Identification of Quantitative Trait Loci and Candidate Genes for Seedling Growth Under Heat Stress. <i>Frontiers in Plant Science</i> , 2018, 9, 1578.	3.6	98



#	ARTICLE	IF	CITATIONS
1629	Understanding the Complexity of Cold Tolerance in White Clover using Temperature Gradient Locations and a GWAS Approach. <i>Plant Genome</i> , 2018, 11, 170096.	2.8	23
1630	Haplotype Loci Under Selection in Canadian Durum Wheat Germplasm Over 60 Years of Breeding: Association With Grain Yield, Quality Traits, Protein Loss, and Plant Height. <i>Frontiers in Plant Science</i> , 2018, 9, 1589.	3.6	29
1631	Dissecting the Genetic Architecture of Melon Chilling Tolerance at the Seedling Stage by Association Mapping and Identification of the Elite Alleles. <i>Frontiers in Plant Science</i> , 2018, 9, 1577.	3.6	14
1632	A Genome-Wide Association Study Reveals Candidate Genes Related to Salt Tolerance in Rice ( <i>Oryza</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 42	4.1	59
1633	Identification of the Genomic Region Underlying Seed Weight per Plant in Soybean ( <i>Glycine max</i> L.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 42 <i>Frontiers in Plant Science</i> , 2018, 9, 1392.	3.6	20
1634	Genome-wide association study reveals favorable alleles associated with common bunt resistance in synthetic hexaploid wheat. <i>Euphytica</i> , 2018, 214, 1.	1.2	23
1635	Identification of a major QTL affecting resistance to brown spot in tobacco ( <i>Nicotiana tabacum</i> L.) via linkage and association mapping methods. <i>Euphytica</i> , 2018, 214, 1.	1.2	8
1636	Genome-Wide Association Studies Reveal the Genetic Basis of Ionomic Variation in Rice. <i>Plant Cell</i> , 2018, 30, 2720-2740.	6.6	164
1637	Genetic diversity and population structure of a mini-core subset from the world cowpea ( <i>Vigna</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 42	3.3	63
1638	DNA fingerprinting at farm level maps rice biodiversity across Bangladesh and reveals regional varietal preferences. <i>Scientific Reports</i> , 2018, 8, 14920.	3.3	20
1639	Single-Locus and Multi-Locus Genome-Wide Association Studies in the Genetic Dissection of Fiber Quality Traits in Upland Cotton ( <i>Gossypium hirsutum</i> L.). <i>Frontiers in Plant Science</i> , 2018, 9, 1083.	3.6	74
1640	Genome-Wide Association Mapping of Seedling Heat Tolerance in Winter Wheat. <i>Frontiers in Plant Science</i> , 2018, 9, 1272.	3.6	103
1641	Single Nucleotide Polymorphism Markers Associated with Seed Quality Characteristics of Cultivated Lentil. <i>Plant Genome</i> , 2018, 11, 170051.	2.8	45
1642	Identification of a locus in maize controlling response to a host-selective toxin derived from <i>Cochliobolus heterostrophus</i> , causal agent of southern leaf blight. <i>Theoretical and Applied Genetics</i> , 2018, 131, 2601-2612.	3.6	3
1643	Population genomics and morphometric assignment of western honey bees ( <i>Apis mellifera</i> L.) in the Republic of South Africa. <i>BMC Genomics</i> , 2018, 19, 615.	2.8	18
1644	Validation of QTLs for plant ideotype, earliness and growth habit traits in pigeonpea ( <i>Cajanus cajan</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 42	3.1	3
1645	Plant Genetics and Molecular Biology. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2018, , .	1.1	6
1646	Genome-Wide Association Mapping in a Rice MAGIC Plus Population Detects QTLs and Genes Useful for Biofortification. <i>Frontiers in Plant Science</i> , 2018, 9, 1347.	3.6	103



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1647	Genetic analysis of resistance to stripe rust in durum wheat ( <i>Triticum turgidum</i> L. var. durum). PLoS ONE, 2018, 13, e0203283.	2.5	17
1648	Genetic dissection of grain zinc concentration in spring wheat for mainstreaming biofortification in CIMMYT wheat breeding. Scientific Reports, 2018, 8, 13526.	3.3	109
1649	Genomic selection in soybean: accuracy and time gain in relation to phenotypic selection. Molecular Breeding, 2018, 38, 1.	2.1	38
1650	Stepwise cis-Regulatory Changes in ZCN8 Contribute to Maize Flowering-Time Adaptation. Current Biology, 2018, 28, 3005-3015.e4.	3.9	116
1651	Conservation Genetics of the Endangered Del Mar Manzanita ( <i>Arctostaphylos</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582 Td (glandul	0.4	3
1652	A PECTIN METHYLESTERASE gene at the maize Ga1 locus confers male function in unilateral cross-incompatibility. Nature Communications, 2018, 9, 3678.	12.8	54
1653	Identification of SNPs and Candidate Genes Associated With Salt Tolerance at the Seedling Stage in Cotton ( <i>Gossypium hirsutum</i> L.). Frontiers in Plant Science, 2018, 9, 1011.	3.6	50
1654	Multi-Locus Genome-Wide Association Studies of Fiber-Quality Related Traits in Chinese Early-Maturity Upland Cotton. Frontiers in Plant Science, 2018, 9, 1169.	3.6	54
1655	Survey of Candidate Genes for Maize Resistance to Infection by <i>Aspergillus flavus</i> and/or Aflatoxin Contamination. Toxins, 2018, 10, 61.	3.4	15
1656	Genomic Signatures of Adaptation to a Precipitation Gradient in Nigerian Sorghum. G3: Genes, Genomes, Genetics, 2018, 8, 3269-3281.	1.8	23
1657	Enhancement of Glen Moy x Latham raspberry linkage map using GbS to further understand control of developmental processes leading to fruit ripening. BMC Genetics, 2018, 19, 59.	2.7	31
1658	Genome-wide association analysis and QTL mapping reveal the genetic control of cadmium accumulation in maize leaf. BMC Genomics, 2018, 19, 91.	2.8	60
1659	Genome-Wide Association Study of Resistance to Ear Rot by <i>Fusarium verticillioides</i> in a Tropical Field Maize and Popcorn Core Collection. Crop Science, 2018, 58, 564-578.	1.8	32
1660	Efficient QTL detection of flowering date in a soybean RIL population using the novel restricted two-stage multi-locus GWAS procedure. Theoretical and Applied Genetics, 2018, 131, 2581-2599.	3.6	31
1661	Harnessing genetic potential of wheat germplasm banks through impact-oriented-prebreeding for future food and nutritional security. Scientific Reports, 2018, 8, 12527.	3.3	113
1662	Coregulation of ribosomal RNA with hundreds of genes contributes to phenotypic variation. Genome Research, 2018, 28, 1555-1565.	5.5	16
1663	High-resolution genetic linkage map of European pear ( <i>Pyrus communis</i> ) and QTL fine-mapping of vegetative budbreak time. BMC Plant Biology, 2018, 18, 175.	3.6	26
1664	Genome-wide association mapping of yield components and drought tolerance-related traits in cotton. Molecular Breeding, 2018, 38, 1.	2.1	13

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1665	Identification of Genes Related to Cold Tolerance and a Functional Allele That Confers Cold Tolerance. <i>Plant Physiology</i> , 2018, 177, 1108-1123.	4.8	68
1666	Identification and validation of QTL for grain yield and plant water status under contrasting water treatments in fall-sown spring wheats. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1741-1759.	3.6	90
1667	RADseq approaches and applications for forest tree genetics. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	1.6	58
1668	Population structure analysis and association mapping for iron deficiency chlorosis in worldwide cowpea ( <i>Vigna unguiculata</i> (L.) Walp) germplasm. <i>Euphytica</i> , 2018, 214, 1.	1.2	3
1669	When less can be better: How can we make genomic selection more cost-effective and accurate in barley?. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1873-1890.	3.6	45
1670	Identification of candidate genes for blood metabolites in Iranian chickens using a genome-wide association study. <i>British Poultry Science</i> , 2018, 59, 381-388.	1.7	5
1671	Genomic signatures of different adaptations to environmental stimuli between wild and cultivated <i>Vitis vinifera</i> L. <i>Horticulture Research</i> , 2018, 5, 34.	6.3	42
1672	Genome wide association study for gray leaf spot resistance in tropical maize core. <i>PLoS ONE</i> , 2018, 13, e0199539.	2.5	27
1673	Genomic Selection in Preliminary Yield Trials in a Winter Wheat Breeding Program. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2735-2747.	1.8	74
1674	Association mapping in rice: basic concepts and perspectives for molecular breeding. <i>Plant Production Science</i> , 2018, 21, 159-176.	2.0	28
1675	Genome-Wide Association Analyses Reveal the Importance of Alternative Splicing in Diversifying Gene Function and Regulating Phenotypic Variation in Maize. <i>Plant Cell</i> , 2018, 30, 1404-1423.	6.6	66
1676	Diversity analysis and genome-wide association studies of grain shape and eating quality traits in rice ( <i>Oryza sativa</i> L.) using DArT markers. <i>PLoS ONE</i> , 2018, 13, e0198012.	2.5	33
1677	Population structure and association mapping to detect QTL controlling tomato spotted wilt virus resistance in cultivated peanuts. <i>Crop Journal</i> , 2018, 6, 516-526.	5.2	7
1678	Diallel genetic analysis for multiple traits in eggplant and assessment of genetic distances for predicting hybrids performance. <i>PLoS ONE</i> , 2018, 13, e0199943.	2.5	43
1679	Genetic Differentiation and Adaptability of Teak ( <i>Tectona grandis</i> L.f.) Meta-Population in India. <i>Plant Molecular Biology Reporter</i> , 2018, 36, 564-575.	1.8	7
1680	Genotyping-by-sequencing of Brassica oleracea vegetables reveals unique phylogenetic patterns, population structure and domestication footprints. <i>Horticulture Research</i> , 2018, 5, 38.	6.3	37
1681	TCAP FACâ€šWIN6 Elite Barley GWAS Panel QTL. I. Barley Stripe Rust Resistance QTL in Facultative and Winter Sixâ€šRowed Malt Barley Breeding Programs Identified via GWAS. <i>Crop Science</i> , 2018, 58, 103-119.	1.8	12
1682	Multienvironment Models Increase Prediction Accuracy of Complex Traits in Advanced Breeding Lines of Rice. <i>Crop Science</i> , 2018, 58, 1519-1530.	1.8	41

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1683	Genome-Wide Association Study of Resistance to Cassava Green Mite Pest and Related Traits in Cassava. <i>Crop Science</i> , 2018, 58, 1907-1918.	1.8	28
1684	Genetic Diversity and Genome-Wide Association Study of Major Ear Quantitative Traits Using High-Density SNPs in Maize. <i>Frontiers in Plant Science</i> , 2018, 9, 966.	3.6	46
1685	Stable predictive markers for <i>Phytophthora sojae</i> avirulence genes that impair infection of soybean uncovered by whole genome sequencing of 31 isolates. <i>BMC Biology</i> , 2018, 16, 80.	3.8	40
1686	Genome-wide identification of single nucleotide polymorphisms (SNPs) and molecular characterization of <i>Prunus</i> rootstock germplasm using a genotyping-by-sequencing (GBS) approach. <i>Acta Horticulturae</i> , 2018, , 27-34.	0.2	1
1687	Genome-Wide Association Study Reveals Both Overlapping and Independent Genetic Loci to Control Seed Weight and Silique Length in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 921.	3.6	37
1688	Association genetics studies on frost tolerance in wheat ( <i>Triticum aestivum</i> L.) reveal new highly conserved amino acid substitutions in CBF-A3, CBF-A15, VRN3 and PPD1 genes. <i>BMC Genomics</i> , 2018, 19, 409.	2.8	31
1689	Characterization of Linkage Disequilibrium and Population Structure in a Mungbean Diversity Panel. <i>Frontiers in Plant Science</i> , 2017, 8, 2102.	3.6	71
1690	Morphometrics Reveals Complex and Heritable Apple Leaf Shapes. <i>Frontiers in Plant Science</i> , 2017, 8, 2185.	3.6	46
1691	Genome-Wide Association Study of Seed Dormancy and the Genomic Consequences of Improvement Footprints in Rice ( <i>Oryza sativa</i> L.). <i>Frontiers in Plant Science</i> , 2017, 8, 2213.	3.6	25
1692	Genome-Wide Association Study Identifying Candidate Genes Influencing Important Agronomic Traits of Flax ( <i>Linum usitatissimum</i> L.) Using SLAF-seq. <i>Frontiers in Plant Science</i> , 2017, 8, 2232.	3.6	62
1693	Population Genetic Structure in Glyphosate-Resistant and -Susceptible Palmer Amaranth ( <i>Amaranthus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T	3.6	31
1694	Divergent Hd1, Ghd7, and DTH7 Alleles Control Heading Date and Yield Potential of Japonica Rice in Northeast China. <i>Frontiers in Plant Science</i> , 2018, 9, 35.	3.6	42
1695	Epigenetic Variance, Performing Cooperative Structure with Genetics, Is Associated with Leaf Shape Traits in Widely Distributed Populations of Ornamental Tree <i>Prunus mume</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 41.	3.6	31
1696	A Genome-Wide Association Study of Field and Seedling Response to Individual Stem Rust Pathogen Races Reveals Combinations of Race-Specific Genes in North American Spring Wheat. <i>Frontiers in Plant Science</i> , 2018, 9, 52.	3.6	66
1697	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.	3.6	129
1698	Prediction of Cacao ( <i>Theobroma cacao</i> ) Resistance to <i>Moniliophthora</i> spp. Diseases via Genome-Wide Association Analysis and Genomic Selection. <i>Frontiers in Plant Science</i> , 2018, 9, 343.	3.6	43
1699	Association Study Reveals Novel Genes Related to Yield and Quality of Fruit in Cape Gooseberry ( <i>Physalis peruviana</i> L.). <i>Frontiers in Plant Science</i> , 2018, 9, 362.	3.6	12
1700	Genome-Wide Association Study of Cadmium Accumulation at the Seedling Stage in Rapeseed ( <i>Brassica</i> ) Tj ETQq1 1 0.784314 rgBT /Ov	3.6	44

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1701	Genome-Wide Association Study for Identification and Validation of Novel SNP Markers for Sr6 Stem Rust Resistance Gene in Bread Wheat. <i>Frontiers in Plant Science</i> , 2018, 9, 380.	3.6	68
1702	Association Mapping for Important Agronomic Traits in Safflower ( <i>Carthamus tinctorius</i> L.) Core Collection Using Microsatellite Markers. <i>Frontiers in Plant Science</i> , 2018, 9, 402.	3.6	45
1703	Assessment of Genetic Variation and Population Structure of Diverse Rice Genotypes Adapted to Lowland and Upland Ecologies in Africa Using SNPs. <i>Frontiers in Plant Science</i> , 2018, 9, 446.	3.6	27
1704	Genome-Wide Association Studies of 11 Agronomic Traits in Cassava ( <i>Manihot esculenta</i> Crantz). <i>Frontiers in Plant Science</i> , 2018, 9, 503.	3.6	43
1705	Tools for Genetic Studies in Experimental Populations of Polyploids. <i>Frontiers in Plant Science</i> , 2018, 9, 513.	3.6	175
1706	Genome Wide Association Mapping of Seedling and Adult Plant Resistance to Barley Stripe Rust ( <i>Puccinia striiformis</i> f. sp. <i>hordei</i> ) in India. <i>Frontiers in Plant Science</i> , 2018, 9, 520.	3.6	47
1707	Genetic Dissection of Maize Embryonic Callus Regenerative Capacity Using Multi-Locus Genome-Wide Association Studies. <i>Frontiers in Plant Science</i> , 2018, 9, 561.	3.6	99
1708	Genotyping of Soybean Cultivars With Medium-Density Array Reveals the Population Structure and QTNs Underlying Maturity and Seed Traits. <i>Frontiers in Plant Science</i> , 2018, 9, 610.	3.6	34
1709	An Immortalized Genetic Mapping Population for Perennial Ryegrass: A Resource for Phenotyping and Complex Trait Mapping. <i>Frontiers in Plant Science</i> , 2018, 9, 717.	3.6	5
1710	Association Genetics in Populus Reveal the Allelic Interactions of Pto-MIR167a and Its Targets in Wood Formation. <i>Frontiers in Plant Science</i> , 2018, 9, 744.	3.6	14
1711	An Integration of Genome-Wide Association Study and Gene Co-expression Network Analysis Identifies Candidate Genes of Stem Lodging-Related Traits in Brassica napus. <i>Frontiers in Plant Science</i> , 2018, 9, 796.	3.6	36
1712	Comparative Aerial and Ground Based High Throughput Phenotyping for the Genetic Dissection of NDVI as a Proxy for Drought Adaptive Traits in Durum Wheat. <i>Frontiers in Plant Science</i> , 2018, 9, 893.	3.6	117
1713	Mining of favorable marker alleles for flag leaf inclination in some rice ( <i>Oryza sativa</i> L.) accessions by association mapping. <i>Euphytica</i> , 2018, 214, 1.	1.2	7
1714	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.	4.1	37
1715	Linkage mapping combined with association analysis reveals QTL and candidate genes for three husk traits in maize. <i>Theoretical and Applied Genetics</i> , 2018, 131, 2131-2144.	3.6	19
1716	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.	3.6	54
1717	Identification of quantitative trait loci associated with soyasaponin I concentration in soybean seed. <i>Theoretical and Applied Genetics</i> , 2018, 131, 2157-2165.	3.6	3
1718	Genome-Wide Association Study for Spot Blotch Resistance in Hard Winter Wheat. <i>Frontiers in Plant Science</i> , 2018, 9, 926.	3.6	77

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1719	Association mapping of cadmium-tolerant QTLs in <i>Brassica napus</i> L. and insight into their contributions to phytoremediation. <i>Environmental and Experimental Botany</i> , 2018, 155, 420-428.	4.2	26
1720	SNP â€˜skimming: A fast approach to map loci generating quantitative variation in natural populations. <i>Molecular Ecology Resources</i> , 2018, 18, 1402-1414.	4.8	10
1721	Identification of Novel Genomic Loci Associated with Soybean Shoot Tissue Macro and Micronutrient Concentrations. <i>Plant Genome</i> , 2018, 11, 170066.	2.8	17
1722	Genome-Wide Association Study of Haploid Male Fertility in Maize ( <i>Zea Mays</i> L.). <i>Frontiers in Plant Science</i> , 2018, 9, 974.	3.6	27
1723	QTL Identification for Cooking and Eating Quality in indica Rice Using Multi-Parent Advanced Generation Intercross (MAGIC) Population. <i>Frontiers in Plant Science</i> , 2018, 9, 868.	3.6	37
1724	Genetic Diversity and Population Structure of F3:6 Nebraska Winter Wheat Genotypes Using Genotyping-By-Sequencing. <i>Frontiers in Genetics</i> , 2018, 9, 76.	2.3	183
1725	Inferring Variation in Copy Number Using High Throughput Sequencing Data in R. <i>Frontiers in Genetics</i> , 2018, 9, 123.	2.3	16
1726	Nitrogen Use Efficiency and the Genetic Variation of Maize Expired Plant Variety Protection Germplasm. <i>Agriculture (Switzerland)</i> , 2018, 8, 3.	3.1	16
1727	Advances in Integrating Genomics and Bioinformatics in the Plant Breeding Pipeline. <i>Agriculture (Switzerland)</i> , 2018, 8, 75.	3.1	55
1728	Genomeâ€‘wide association and gene validation studies for early root vigour to improve direct seeding of rice. <i>Plant, Cell and Environment</i> , 2018, 41, 2731-2743.	5.7	35
1729	<i>Hair</i>, encoding a single C2H2 zincâ€‘finger protein, regulates multicellular trichome formation in tomato. <i>Plant Journal</i> , 2018, 96, 90-102.	5.7	97
1730	Physiological and Proteomics Analyses Reveal Low-Phosphorus Stress Affected the Regulation of Photosynthesis in Soybean. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1688.	4.1	32
1731	An intercross population study reveals genes associated with body size and plumage color in ducks. <i>Nature Communications</i> , 2018, 9, 2648.	12.8	167
1732	Identification of candidate genes for gelatinization temperature, gel consistency and pericarp color by GWAS in rice based on SLAF-sequencing. <i>PLoS ONE</i> , 2018, 13, e0196690.	2.5	25
1733	The Maize ABA Receptors ZmPYL8, 9, and 12 Facilitate Plant Drought Resistance. <i>Frontiers in Plant Science</i> , 2018, 9, 422.	3.6	69
1734	Tolerance traits related to climate change resilience are independent and polygenic. <i>Global Change Biology</i> , 2018, 24, 5348-5360.	9.5	38
1735	Natural variation in <i>Gm<sc>GBP</sc>1</i> promoter affects photoperiod control of flowering time and maturity in soybean. <i>Plant Journal</i> , 2018, 96, 147-162.	5.7	45
1736	Association mapping for total polyphenol content, total flavonoid content and antioxidant activity in barley. <i>BMC Genomics</i> , 2018, 19, 81.	2.8	45

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1737	Genetic diversity near the DGAT1-2 gene for high oleic acid content and kernel trait variation in a maize breeding collection. <i>Molecular Breeding</i> , 2018, 38, 1.	2.1	3
1738	Superior adaptation of aerobic rice under drought stress in Iran and validation test of linked SSR markers to major QTLs by MLM analysis across two years. <i>Molecular Biology Reports</i> , 2018, 45, 1037-1053.	2.3	11
1739	Genomic variations and association study of agronomic traits in flax. <i>BMC Genomics</i> , 2018, 19, 512.	2.8	46
1740	Maize Genomes to Fields: 2014 and 2015 field season genotype, phenotype, environment, and inbred ear image datasets. <i>BMC Research Notes</i> , 2018, 11, 452.	1.4	25
1741	Dissection of complicate genetic architecture and breeding perspective of cottonseed traits by genome-wide association study. <i>BMC Genomics</i> , 2018, 19, 451.	2.8	22
1742	Genetic variation in transcription factors and photosynthesis light-reaction genes regulates photosynthetic traits. <i>Tree Physiology</i> , 2018, 38, 1871-1885.	3.1	6
1743	Low pyrrolizidine alkaloid levels in perennial ryegrass is associated with the absence of a homospermidine synthase gene. <i>BMC Plant Biology</i> , 2018, 18, 56.	3.6	6
1744	Insights into teleost sex determination from the <i>Seriola dorsalis</i> genome assembly. <i>BMC Genomics</i> , 2018, 19, 31.	2.8	44
1745	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.	1.9	17
1746	Genome-wide association study of seedling stage salinity tolerance in temperate japonica rice germplasm. <i>BMC Genetics</i> , 2018, 19, 2.	2.7	39
1747	Association between sequence variants in panicle development genes and the number of spikelets per panicle in rice. <i>BMC Genetics</i> , 2018, 19, 5.	2.7	11
1748	Association of yield-related traits in founder genotypes and derivatives of common wheat ( <i>Triticum</i> ) Tj ETQq1 1 0.784314 rgBT /Overl	3.6	28
1749	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.	1.4	8
1750	Genome-wide association study dissects yield components associated with low-phosphorus stress tolerance in maize. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1699-1714.	3.6	53
1751	Apple fruit acidity is genetically diversified by natural variations in three hierarchical epistatic genes: <i>MdSAUR37</i> , <i>MdPP2CH</i> and <i>MdALMTII</i> . <i>Plant Journal</i> , 2018, 95, 427-443.	5.7	71
1752	Discovery and validation of genomic regions associated with resistance to maize lethal necrosis in four biparental populations. <i>Molecular Breeding</i> , 2018, 38, 66.	2.1	29
1753	Genetic homogeneity of the invasive lionfish across the Northwestern Atlantic and the Gulf of Mexico based on Single Nucleotide Polymorphisms. <i>Scientific Reports</i> , 2018, 8, 5062.	3.3	23
1754	Root plasticity under fluctuating soil moisture stress exhibited by backcross inbred line of a rice variety, Nipponbare carrying introgressed segments from KDML105 and detection of the associated QTLs. <i>Plant Production Science</i> , 2018, 21, 106-122.	2.0	8



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1755	Genome-Wide Detection of Genes Under Positive Selection in Worldwide Populations of the Barley Scald Pathogen. <i>Genome Biology and Evolution</i> , 2018, 10, 1315-1332.	2.5	28
1756	Genomewide association analysis of salt tolerance in soybean [ <i>Glycine max</i> (L.) Merr.]. <i>Plant Breeding</i> , 2018, 137, 714-720.	1.9	9
1757	Validation of Grain Yield QTLs from Soft Winter Wheat Using a CIMMYT Spring Wheat Panel. <i>Crop Science</i> , 2018, 58, 1964-1971.	1.8	12
1758	Genome-Wide Association Study and Selection Signatures Detect Genomic Regions Associated with Seed Yield and Oil Quality in Flax. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2303.	4.1	49
1759	A genome-wide association study uncovers novel genomic regions and candidate genes of yield-related traits in upland cotton. <i>Theoretical and Applied Genetics</i> , 2018, 131, 2413-2425.	3.6	31
1760	Genome-Wide Association Studies to Identify Loci and Candidate Genes Controlling Kernel Weight and Length in a Historical United States Wheat Population. <i>Frontiers in Plant Science</i> , 2018, 9, 1045.	3.6	39
1761	Genetic characterization of inbred lines from Shaan A and B groups for identifying loci associated with maize grain yield. <i>BMC Genetics</i> , 2018, 19, 63.	2.7	28
1762	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.	2.1	17
1763	High-Resolution Genetic Map and QTL Analysis of Growth-Related Traits of <i>Hevea brasiliensis</i> Cultivated Under Suboptimal Temperature and Humidity Conditions. <i>Frontiers in Plant Science</i> , 2018, 9, 1255.	3.6	27
1764	Genome-Wide Association Studies for Dynamic Plant Height and Number of Nodes on the Main Stem in Summer Sowing Soybeans. <i>Frontiers in Plant Science</i> , 2018, 9, 1184.	3.6	67
1765	Analysis of Genetic Variation and Enhancement of Salt Tolerance in French Pea ( <i>Pisum Sativum</i> L.). <i>International Journal of Molecular Sciences</i> , 2018, 19, 2433.	4.1	45
1766	Identification of stable QTLs for fiber quality and plant structure in Upland cotton ( <i>G. hirsutum</i> L.) under drought stress. <i>Industrial Crops and Products</i> , 2018, 124, 776-786.	5.2	16
1767	A Genome-Wide Association Study of Apple Quality and Scab Resistance. <i>Plant Genome</i> , 2018, 11, 170075.	2.8	61
1768	Mapping adult plant stem rust resistance in barley accessions Hietpas-5 and GAW-79. <i>Theoretical and Applied Genetics</i> , 2018, 131, 2245-2266.	3.6	9
1769	Unlocking the novel genetic diversity and population structure of synthetic Hexaploid wheat. <i>BMC Genomics</i> , 2018, 19, 591.	2.8	76
1770	Connectivity in riparian plants: influence of vegetation type and habitat fragmentation overrides water flow. <i>Oecologia</i> , 2018, 188, 465-478.	2.0	12
1771	Genomic-enabled prediction models using multi-environment trials to estimate the effect of genotype×environment interaction on prediction accuracy in chickpea. <i>Scientific Reports</i> , 2018, 8, 11701.	3.3	61
1772	A Genome-Wide Association Study Reveals a Rich Genetic Architecture of Flour Color-Related Traits in Bread Wheat. <i>Frontiers in Plant Science</i> , 2018, 9, 1136.	3.6	34



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1774	A genome-wide association study of early-maturation traits in upland cotton based on the CottonSNP80K array. Journal of Integrative Plant Biology, 2018, 60, 970-985.	8.5	28
1775	Drought Sensitivity of Norway Spruce at the Species' Warmest Fringe: Quantitative and Molecular Analysis Reveals High Genetic Variation Among and Within Provenances. G3: Genes, Genomes, Genetics, 2018, 8, 1225-1245.	1.8	58
1776	Uneven recombination rate and linkage disequilibrium across a reference SNP map for common bean ( <i>Phaseolus vulgaris</i> L.). PLoS ONE, 2018, 13, e0189597.	2.5	108
1777	Effect of multiple allelic combinations of genes on regulating grain size in rice. PLoS ONE, 2018, 13, e0190684.	2.5	29
1778	Tolerance to mild salinity stress in japonica rice: A genome-wide association mapping study highlights calcium signaling and metabolism genes. PLoS ONE, 2018, 13, e0190964.	2.5	57
1779	Genome-Scale Association Study of Abnormal Scale Pattern in Yellow River Carp Identified Previously Known Causative Gene in European Mirror Carp. Marine Biotechnology, 2018, 20, 573-583.	2.4	24
1780	A high-quality genome sequence of <i>Rosa chinensis</i> to elucidate ornamental traits. Nature Plants, 2018, 4, 473-484.	9.3	224
1781	Genome-wide association study to identify candidate loci and genes for Mn toxicity tolerance in rice. PLoS ONE, 2018, 13, e0192116.	2.5	21
1782	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. PLoS ONE, 2018, 13, e0193121.	2.5	17
1783	Genetic Diversity and Molecular Characterization of Iranian Durum Wheat Landraces ( <i>Triticum</i> ) Tj ETQq0 0 0 rgBT /Oyerlock 10 Tf 50 34	1.7	26
1784	Detection of QTL (quantitative trait loci) associated with wood density by evaluating genetic structure and linkage disequilibrium of teak. Journal of Forestry Research, 2019, 30, 2247-2258.	3.6	6
1785	Genome-wide association mapping of virulence gene in rice blast fungus <i>Magnaporthe oryzae</i> using a genotyping by sequencing approach. Genomics, 2019, 111, 661-668.	2.9	25
1786	Genetic architecture underlying the lignin biosynthesis pathway involves noncoding <i>scRNA</i> s and transcription factors for growth and wood properties in <i>Populus</i> . Plant Biotechnology Journal, 2019, 17, 302-315.	8.3	54
1787	Candidate gene based association analysis of salt tolerance in traditional and improved varieties of rice ( <i>Oryza sativa</i> L.). Journal of Plant Biochemistry and Biotechnology, 2019, 28, 76-83.	1.7	3
1788	Genome-wide association study for frost tolerance in canola ( <i>Brassica napus</i> L.) under field conditions. Journal of Plant Biochemistry and Biotechnology, 2019, 28, 211-222.	1.7	7
1789	Genome-wide marker-trait association analysis in a core set of <i>Dolichos</i> bean germplasm. Plant Genetic Resources: Characterisation and Utilisation, 2019, 17, 1-11.	0.8	9
1790	Environmental drivers and genomic architecture of trait differentiation in fire-adapted <i>Banksia attenuata</i> ecotypes. Journal of Integrative Plant Biology, 2019, 61, 417-432.	8.5	10

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1792	Agronomic Performance and Nitrogen Fixation of Heirloom and Conventional Dry Bean Varieties Under Low-Nitrogen Field Conditions. <i>Frontiers in Plant Science</i> , 2019, 10, 952.	3.6	39
1793	Loci Controlling Adaptation to Heat Stress Occurring at the Reproductive Stage in Durum Wheat. <i>Agronomy</i> , 2019, 9, 414.	3.0	31
1794	Development of molecular markers associated with resistance to <i>Meloidogyne incognita</i> by performing quantitative trait locus analysis and genome-wide association study in sweetpotato. <i>DNA Research</i> , 2019, 26, 399-409.	3.4	17
1795	First Genome-wide Association Analysis for Growth Traits in the Largest Coral Reef-Dwelling Bony Fishes, the Giant Grouper ( <i>Epinephelus lanceolatus</i> ). <i>Marine Biotechnology</i> , 2019, 21, 707-717.	2.4	29
1796	Genome-wide association study reveals new loci for yield-related traits in Sichuan wheat germplasm under stripe rust stress. <i>BMC Genomics</i> , 2019, 20, 640.	2.8	19
1797	Genome-wide association study for leaf area, rachis length and total dry weight in oil palm ( <i>Eleaegisguineensis</i> ) using genotyping by sequencing. <i>PLoS ONE</i> , 2019, 14, e0220626.	2.5	13
1798	Dissecting genetic loci affecting grain morphological traits to improve grain weight via nested association mapping. <i>Theoretical and Applied Genetics</i> , 2019, 132, 3115-3128.	3.6	28
1799	Whole-genome resequencing of <i>Cucurbita pepo</i> morphotypes to discover genomic variants associated with morphology and horticulturally valuable traits. <i>Horticulture Research</i> , 2019, 6, 94.	6.3	34
1800	Adaptive phenotypic divergence in an annual grass differs across biotic contexts*. <i>Evolution; International Journal of Organic Evolution</i> , 2019, 73, 2230-2246.	2.3	22
1801	Advanced software programs for the analysis of genetic diversity in livestock genomics: a mini review. <i>Biological Rhythm Research</i> , 2019, , 1-11.	0.9	6
1802	Molecular marker dissection of stem rust resistance in Nebraska bread wheat germplasm. <i>Scientific Reports</i> , 2019, 9, 11694.	3.3	14
1803	Association mapping for agronomic traits in six-rowed spring barley from the USA harvested in Kazakhstan. <i>PLoS ONE</i> , 2019, 14, e0221064.	2.5	14
1804	Genetic determinants controlling maize rubisco activase gene expression and a comparison with rice counterparts. <i>BMC Plant Biology</i> , 2019, 19, 351.	3.6	9
1805	Genome wide association mapping and candidate gene analysis for hundred seed weight in soybean [ <i>Glycine max</i> (L.) Merrill]. <i>BMC Genomics</i> , 2019, 20, 648.	2.8	21
1806	Challenges in funding and developing genomic software: roots and remedies. <i>Genome Biology</i> , 2019, 20, 147.	8.8	21
1807	Detection of First Marker Trait Associations for Resistance Against <i>Sclerotinia sclerotiorum</i> in <i>Brassica juncea</i> "Erucastrum cardaminoides Introgression Lines. <i>Frontiers in Plant Science</i> , 2019, 10, 1015.	3.6	43
1808	Dissection of loci conferring resistance to stripe rust in Chinese wheat landraces from the middle and lower reaches of the Yangtze River via genome-wide association study. <i>Plant Science</i> , 2019, 287, 110204.	3.6	22

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1809	Small RNAs from the plant pathogenic fungus <i>Sclerotinia sclerotiorum</i> highlight host candidate genes associated with quantitative disease resistance. <i>Molecular Plant Pathology</i> , 2019, 20, 1279-1297.	4.2	78
1810	Genomic-Wide Association Study of Popping Expansion in Tropical Popcorn and Field Corn Germplasm. <i>Crop Science</i> , 2019, 59, 2007-2019.	1.8	23
1811	Genetic Detection of Lint Percentage Applying Single-Locus and Multi-Locus Genome-Wide Association Studies in Chinese Early-Maturity Upland Cotton. <i>Frontiers in Plant Science</i> , 2019, 10, 964.	3.6	11
1812	A Genome-Wide Association Study of Highly Heritable Agronomic Traits in Durum Wheat. <i>Frontiers in Plant Science</i> , 2019, 10, 919.	3.6	30
1813	Association Analysis of Charcoal Rot Disease Resistance in Soybean. <i>Plant Pathology Journal</i> , 2019, 35, 189-199.	1.7	8
1814	1k-RiCA (1K-Rice Custom Amplicon) a novel genotyping amplicon-based SNP assay for genetics and breeding applications in rice. <i>Rice</i> , 2019, 12, 55.	4.0	46
1815	Association between sequence variants in cadmium-related genes and the cadmium accumulation trait in thermo-sensitive genic male sterile rice. <i>Breeding Science</i> , 2019, 69, 455-463.	1.9	3
1816	Genome-Wide Association Study Reveals Candidate Genes for Flowering Time Variation in Common Bean ( <i>Phaseolus vulgaris</i> L.). <i>Frontiers in Plant Science</i> , 2019, 10, 962.	3.6	61
1817	Exploring the genetic diversity within traditional Philippine pigmented Rice. <i>Rice</i> , 2019, 12, 27.	4.0	12
1818	Genetic Dissection of the Seminal Root System Architecture in Mediterranean Durum Wheat Landraces by Genome-Wide Association Study. <i>Agronomy</i> , 2019, 9, 364.	3.0	35
1819	Identification of favorable alleles for rice seedling anoxic tolerance using natural and bi-parental populations. <i>Euphytica</i> , 2019, 215, 1.	1.2	2
1820	Sex-specific markers for waterhemp ( <i>Amaranthus tuberculatus</i> ) and Palmer amaranth ( <i>Amaranthus palmeri</i> ). <i>Weed Science</i> , 2019, 67, 412-418.	1.5	25
1821	Genetic Diversity of Field Pennycress ( <i>Thlaspi arvense</i> ) Reveals Untapped Variability and Paths Toward Selection for Domestication. <i>Agronomy</i> , 2019, 9, 302.	3.0	21
1822	Genetic Analysis for Fruit Phenolics Content, Flesh Color, and Browning Related Traits in Eggplant ( <i>Solanum melongena</i> ). <i>International Journal of Molecular Sciences</i> , 2019, 20, 2990.	4.1	16
1823	From landraces to improved cultivars: Assessment of genetic diversity and population structure of Mediterranean wheat using SNP markers. <i>PLoS ONE</i> , 2019, 14, e0219867.	2.5	66
1824	Genome-wide SNP-based diversity analysis and association mapping in linseed ( <i>Linum usitatissimum</i> L.). <i>Euphytica</i> , 2019, 215, 1.	1.2	16
1825	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.	2.3	27
1826	Phenotypic and Genomic Local Adaptation across Latitude and Altitude in <i>Populus trichocarpa</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 2256-2272.	2.5	46

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1827	Genome-wide association study to identify genomic regions influencing spontaneous fertility in maize haploids. <i>Euphytica</i> , 2019, 215, 138.	1.2	29
1828	Combination of multi-locus genome-wide association study and QTL mapping reveals genetic basis of tassel architecture in maize. <i>Molecular Genetics and Genomics</i> , 2019, 294, 1421-1440.	2.1	12
1829	Artificial selection on GmOLEO1 contributes to the increase in seed oil during soybean domestication. <i>PLoS Genetics</i> , 2019, 15, e1008267.	3.5	75
1830	Detecting the genetic basis of local adaptation in loblolly pine ( <i>Pinus taeda</i> L.) using whole exome-wide genotyping and an integrative landscape genomics analysis approach. <i>Ecology and Evolution</i> , 2019, 9, 6798-6809.	1.9	25
1831	Genetic diversity assessment of sorghum ( <i>Sorghum bicolor</i> (L.) Moench) accessions using single nucleotide polymorphism markers. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2019, 17, 412-420.	0.8	17
1832	Genome-wide association study and candidate gene analysis of alkalinity tolerance in japonica rice germplasm at the seedling stage. <i>Rice</i> , 2019, 12, 24.	4.0	57
1833	Genome-wide association study of pre-harvest sprouting tolerance using a 90K SNP array in common wheat ( <i>Triticum aestivum</i> L.). <i>Theoretical and Applied Genetics</i> , 2019, 132, 2947-2963.	3.6	48
1834	Genome resequencing of the orange-spotted grouper ( <i>Epinephelus coioides</i> ) for a genome-wide association study on ammonia tolerance. <i>Aquaculture</i> , 2019, 512, 734332.	3.5	24
1835	Genome-wide association study and genomic prediction analyses of drought stress tolerance in China in a collection of off-PVP maize inbred lines. <i>Molecular Breeding</i> , 2019, 39, 1.	2.1	17
1836	Identification of genomewide single-nucleotide polymorphisms associated with presummer, summer and autumn bolls in upland cotton. <i>Journal of Genetics</i> , 2019, 98, 1.	0.7	1
1837	Phased genome sequence of an interspecific hybrid flowering cherry, 'Somei-Yoshino'™ ( <i>Cerasus</i> 'Somei-Yoshino'™) Tj ETQq0.0 0.0 rgBT /Overlock 1	3.4	59
1838	Genetic diversity, linkage disequilibrium, and population structure analysis of the tea plant ( <i>Camellia</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 1 genotyping-by-sequencing. <i>BMC Plant Biology</i> , 2019, 19, 328.	3.6	65
1839	The Maize Clade A PP2C Phosphatases Play Critical Roles in Multiple Abiotic Stress Responses. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3573.	4.1	57
1840	Integrative system genetic analysis reveals mRNA-lncRNA network associated with mouse spontaneous lung cancer susceptibility. <i>Oncotarget</i> , 2019, 10, 339-351.	1.8	2
1841	Candidate screening of blast resistance donors for rice breeding. <i>Journal of Genetics</i> , 2019, 98, 1.	0.7	10
1842	SNP haplotypes for soybean resistance to SCN race 1 and 3. <i>Euphytica</i> , 2019, 215, 1.	1.2	1
1843	Genome-Wide Association Study for Multiple Biotic Stress Resistance in Synthetic Hexaploid Wheat. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3667.	4.1	31
1844	Identification of loci and candidate genes for plant height in soybean ( <i>Glycine max</i> ) via genome-wide association study. <i>Plant Breeding</i> , 2019, 138, 721-732.	1.9	8

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1845	Genome-wide association analysis of salt tolerance QTLs with SNP markers in maize ( <i>Zea mays</i> L.). <i>Genes and Genomics</i> , 2019, 41, 1135-1145.	1.4	11
1846	Identification of Loci and Candidate Genes Responsible for Pod Dehiscence in Soybean via Genome-Wide Association Analysis Across Multiple Environments. <i>Frontiers in Plant Science</i> , 2019, 10, 811.	3.6	26
1847	Genetic dissection of grain iron and zinc concentrations in lentil ( <i>Lens culinaris</i> Medik.). <i>Journal of Genetics</i> , 2019, 98, 1.	0.7	32
1848	Deciphering the genetic basis of root morphology, nutrient uptake, yield, and yield-related traits in rice under dry direct-seeded cultivation systems. <i>Scientific Reports</i> , 2019, 9, 9334.	3.3	37
1849	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.	2.5	31
1850	Genetic diversity and linkage disequilibrium using SNP (KASP) and AFLP markers in a worldwide durum wheat ( <i>Triticum turgidum</i> L. var <i>durum</i> ) collection. <i>PLoS ONE</i> , 2019, 14, e0218562.	2.5	28
1851	Combined linkage and association mapping reveal candidate loci for kernel size and weight in maize. <i>Breeding Science</i> , 2019, 69, 420-428.	1.9	9
1852	Mapping quantitative traits for grain physical and textural quality in Cambodian Jasmine rice PRD. <i>Euphytica</i> , 2019, 215, 1.	1.2	2
1853	Genetic Diversity of <i>Verticillium dahliae</i> Isolates From Mint Detected with Genotyping by Sequencing. <i>Phytopathology</i> , 2019, 109, 1966-1974.	2.2	5
1854	Darwin's finches: a model of landscape effects on metacommunity dynamics in the Galápagos Archipelago. <i>Ecography</i> , 2019, 42, 1636-1647.	4.5	3
1855	Efficiency of Genomic Prediction of Nonassessed Testcrosses. <i>Crop Science</i> , 2019, 59, 2020-2027.	1.8	8
1856	Genome-wide association study overcomes the genome complexity in autohexaploid chrysanthemum and tags SNP markers onto the flower color genes. <i>Scientific Reports</i> , 2019, 9, 13947.	3.3	23
1857	Carotenoid pigmentation in salmon: variation in expression at <i>BCO2-1</i> locus controls a key fitness trait affecting red coloration. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20191588.	2.6	31
1858	Local adaptation drives the diversification of effectors in the fungal wheat pathogen <i>Parastagonospora nodorum</i> in the United States. <i>PLoS Genetics</i> , 2019, 15, e1008223.	3.5	66
1859	Population genetic analysis of two species of <i>Distylium</i> : <i>D. racemosum</i> growing in East Asian evergreen broad-leaved forests and <i>D. lepidotum</i> endemic to the Ogasawara (Bonin) Islands. <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	1.6	3
1860	Expression regulation of myo-inositol 3-phosphate synthase 1 (INO1) in determination of phytic acid accumulation in rice grain. <i>Scientific Reports</i> , 2019, 9, 14866.	3.3	12
1861	Identification and Validation of Candidate Genes Involved in Fatty Acid Content in Oil Palm by Genome-Wide Association Analysis. <i>Frontiers in Plant Science</i> , 2019, 10, 1263.	3.6	24
1862	GWAS and Coexpression Network Reveal Ionomic Variation in Cultivated Peanut. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 12026-12036.	5.2	20

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1863	Association mapping for grain diameter and weight in lentil using SSR markers. <i>Plant Gene</i> , 2019, 20, 100204.	2.3	18
1864	Genetic relationships and population structure of pears ( <i>Pyrus</i> spp.) assessed with genome-wide SNPs detected by genotyping-by-sequencing. <i>Horticulture Environment and Biotechnology</i> , 2019, 60, 945-953.	2.1	5
1865	Whole genome resequencing of watermelons to identify single nucleotide polymorphisms related to flesh color and lycopene content. <i>PLoS ONE</i> , 2019, 14, e0223441.	2.5	15
1866	Characterization and Application of EST-SSR Markers Developed From the Transcriptome of <i>Amentotaxus argotaenia</i> (Taxaceae), a Relict Vulnerable Conifer. <i>Frontiers in Genetics</i> , 2019, 10, 1014.	2.3	11
1867	Distinct patterns of natural selection determine sub-population structure in the fire blight pathogen, <i>Erwinia amylovora</i> . <i>Scientific Reports</i> , 2019, 9, 14017.	3.3	18
1868	Last-Generation Genome-Environment Associations Reveal the Genetic Basis of Heat Tolerance in Common Bean ( <i>Phaseolus vulgaris</i> L.). <i>Frontiers in Genetics</i> , 2019, 10, 954.	2.3	73
1870	Extensive phenotypic diversity in the cultivated Florist <sup>™</sup> s Gloxinia, <i>Sinningia speciosa</i> (Lodd.) Hiern, is derived from the domestication of a single founder population. <i>Plants People Planet</i> , 2019, 1, 363-374.	3.3	4
1871	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.	2.3	35
1872	Multi-environments and multi-models association mapping identified candidate genes of lint percentage and seed index in <i>Gossypium hirsutum</i> L.. <i>Molecular Breeding</i> , 2019, 39, 1.	2.1	7
1873	Haplotype Networking of GWAS Hits for Citrulline Variation Associated with the Domestication of Watermelon. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5392.	4.1	8
1874	Impact of fruit shape selection on genetic structure and diversity uncovered from genome-wide perfect SNPs genotyping in eggplant. <i>Molecular Breeding</i> , 2019, 39, 1.	2.1	16
1875	Genetic Variation, Population Structure and the Possibility of Association Mapping of Biochemical and Agronomic Traits Using Dominant Molecular Markers in Iranian Tea Accessions. <i>Iranian Journal of Science and Technology, Transaction A: Science</i> , 2019, 43, 2769-2780.	1.5	4
1876	Identification of Superior Alleles for Seedling Stage Salt Tolerance in the USDA Rice Mini-Core Collection. <i>Plants</i> , 2019, 8, 472.	3.5	23
1877	In-Depth Characterisation of Common Bean Diversity Discloses Its Breeding Potential for Sustainable Agriculture. <i>Sustainability</i> , 2019, 11, 5443.	3.2	11
1878	Genome-wide association study for starch content and constitution in sorghum ( <i>Sorghum bicolor</i> ) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	3.5	26
1879	Genotyping-by-Sequencing Reveals Fine-Scale Differentiation in Populations of <i>Pseudoperonospora humuli</i> . <i>Phytopathology</i> , 2019, 109, 1801-1810.	2.2	14
1880	Population genomics and morphological features underlying the adaptive evolution of the eastern honey bee ( <i>Apis cerana</i> ). <i>BMC Genomics</i> , 2019, 20, 869.	2.8	12
1881	Bread Wheat With High Salinity and Sodicity Tolerance. <i>Frontiers in Plant Science</i> , 2019, 10, 1280.	3.6	74



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1882	Comparison of Weighted and Unweighted Stageâ€Wise Analysis for Genomeâ€Wide Association Studies and Genomic Selection. <i>Crop Science</i> , 2019, 59, 2572-2584.	1.8	9
1883	Genome Wide Association Study and Genomic Selection of Amino Acid Concentrations in Soybean Seeds. <i>Frontiers in Plant Science</i> , 2019, 10, 1445.	3.6	31
1884	GWAS Discovery Of Candidate Genes for Yield-Related Traits in Peanut and Support from Earlier QTL Mapping Studies. <i>Genes</i> , 2019, 10, 803.	2.4	25
1885	Chronic radiation exposure at Chernobyl shows no effect on genetic diversity in the freshwater crustacean, <i>Asellus aquaticus</i> thirty years on. <i>Ecology and Evolution</i> , 2019, 9, 10135-10144.	1.9	22
1886	Linkage disequilibrium mapping of high-throughput image-derived descriptors of plant architecture traits under field conditions. <i>Field Crops Research</i> , 2019, 244, 107619.	5.1	8
1887	Population structure and linkage disequilibrium in a large collection of <i>Fusarium oxysporum</i> strains analysed through iPBS markers. <i>Journal of Phytopathology</i> , 2019, 167, 576-590.	1.0	7
1888	Genomeâ€Wide Population Structure Analyses of Three Minor Millets: Kodo Millet, Little Millet, and Proso Millet. <i>Plant Genome</i> , 2019, 12, 1-9.	2.8	35
1889	GWAS for <i>Fusarium</i> Head Blight Traits in a Soft Red Winter Wheat Mapping Panel. <i>Crop Science</i> , 2019, 59, 1823-1837.	1.8	23
1890	Mapping of resistance to corn borers in a MAGIC population of maize. <i>BMC Plant Biology</i> , 2019, 19, 431.	3.6	37
1891	GWAS for Starch-Related Parameters in Japonica Rice ( <i>Oryza sativa</i> L.). <i>Plants</i> , 2019, 8, 292.	3.5	30
1892	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.	1.6	22
1893	Genome-Wide Association Study to Identify Favorable SNP Allelic Variations and Candidate Genes That Control the Timing of Spring Bud Flush of Tea ( <i>Camellia sinensis</i> ) Using SLAF-seq. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 10380-10391.	5.2	24
1894	Genetic loci and candidate genes of symbiotic nitrogen fixationâ€related characteristics revealed by a genome-wide association study in soybean. <i>Molecular Breeding</i> , 2019, 39, 1.	2.1	10
1895	Comprehensive evaluation of resistance effects of pyramiding lines with different broad-spectrum resistance genes against <i>Magnaporthe oryzae</i> in rice ( <i>Oryza sativa</i> L.). <i>Rice</i> , 2019, 12, 11.	4.0	38
1896	Identification of new rice cultivars and resistance loci against rice black-streaked dwarf virus disease through genome-wide association study. <i>Rice</i> , 2019, 12, 49.	4.0	26
1897	Estimation of a significance threshold for genome-wide association studies. <i>BMC Genomics</i> , 2019, 20, 618.	2.8	100
1898	Identification of SNP loci and candidate genes related to four important fatty acid composition in <i>Brassica napus</i> using genome wide association study. <i>PLoS ONE</i> , 2019, 14, e0221578.	2.5	20
1899	Epistasis Detection and Modeling for Genomic Selection in Cowpea ( <i>Vigna unguiculata</i> L. Walp.). <i>Frontiers in Genetics</i> , 2019, 10, 677.	2.3	19



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1900	Genetic Mapping and Prediction Analysis of FHB Resistance in a Hard Red Spring Wheat Breeding Population. <i>Frontiers in Plant Science</i> , 2019, 10, 1007.	3.6	24
1901	Identification of Maize CC-Type Glutaredoxins That Are Associated with Response to Drought Stress. <i>Genes</i> , 2019, 10, 610.	2.4	17
1902	Identifying markers for resistance to sugarcane orange rust ( <i>Puccinia kuehnii</i> ) via selective genotyping and capture sequencing. <i>Euphytica</i> , 2019, 215, 1.	1.2	10
1903	Whole Genome Diversity, Population Structure, and Linkage Disequilibrium Analysis of Chickpea ( <i>Cicer</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	2.4	25
1904	Genome-wide association analysis of 1-octen-3-ol content related to soymilk off-flavor in soybean seed. <i>Crop and Pasture Science</i> , 2019, 70, 133.	1.5	11
1905	Genome-wide association mapping and candidate gene analysis for seed shape in soybean ( <i>Glycine max</i> ). <i>Crop and Pasture Science</i> , 2019, 70, 684.	1.5	7
1906	High-throughput identification of SNPs reveals extensive heterosis with intra-group hybridization and genetic characteristics in a large rapeseed ( <i>Brassica napus</i> L.) panel. <i>Euphytica</i> , 2019, 215, 1.	1.2	3
1907	Identification of candidate genes controlling oil content by combination of genome-wide association and transcriptome analysis in the oilseed crop <i>Brassica napus</i> . <i>Biotechnology for Biofuels</i> , 2019, 12, 216.	6.2	40
1908	Whole-Genome Resequencing of Seven Eggplant ( <i>Solanum melongena</i> ) and One Wild Relative ( <i>S.</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	3.6	46
1909	Genotyping-by-Sequencing Reveals Molecular Genetic Diversity in Italian Common Bean Landraces. <i>Diversity</i> , 2019, 11, 154.	1.7	12
1910	Genetic analysis of Taishu horses on and off Tsushima Island: Implications for conservation. <i>Journal of Equine Science</i> , 2019, 30, 33-40.	0.8	2
1911	Genetic dissection of hexanol content in soybean seed through genome-wide association analysis. <i>Journal of Integrative Agriculture</i> , 2019, 18, 1222-1229.	3.5	6
1912	A large-scale chromosomal inversion is not associated with life history development in rainbow trout from Southeast Alaska. <i>PLoS ONE</i> , 2019, 14, e0223018.	2.5	15
1913	Whole-genome resequencing of <i>Trichophyton rubrum</i> provides insights into population differentiation and drug resistance. <i>Mycopathologia</i> , 2020, 185, 103-112.	3.1	11
1914	Characterization of Selected Maize Inbred Lines Adapted to Highland Agro-Ecologies of Ethiopia Using Morphological and Molecular Genetic Distances. <i>Advances in Crop Science and Technology</i> , 2019, 07, .	0.4	1
1915	Association genetics of bunch weight and its component traits in East African highland banana ( <i>Musa</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	3.6	17
1916	Core set construction and association analysis of <i>Pinus massoniana</i> from Guangdong province in southern China using SLAF-seq. <i>Scientific Reports</i> , 2019, 9, 13157.	3.3	12
1917	Using genome conservation between <i>Lotus japonicus</i> and agronomically important <i>Lotus</i> species for discovering drought tolerance QTLs. <i>Euphytica</i> , 2019, 215, 1.	1.2	1

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1918	Combined linkage and association mapping of putative QTLs controlling black tea quality and drought tolerance traits. <i>Euphytica</i> , 2019, 215, 1.	1.2	5
1919	Genetic dissection of winter barley seedling response to salt and osmotic stress. <i>Molecular Breeding</i> , 2019, 39, 1.	2.1	11
1920	Chlorophyll fluorescence analysis in diverse rice varieties reveals the positive correlation between the seedlings salt tolerance and photosynthetic efficiency. <i>BMC Plant Biology</i> , 2019, 19, 403.	3.6	93
1921	Genetic Identity Based on Whole-Genome SNP Array Data of Weedy Rice in Nagano, Japan. <i>Agronomy</i> , 2019, 9, 472.	3.0	1
1922	Population genomics reveals possible genetic evidence for parallel evolution of <i>Sebastiscus marmoratus</i> in the northwestern Pacific Ocean. <i>Open Biology</i> , 2019, 9, 190028.	3.6	8
1923	Variations in straw fodder quality and grainâ€“Straw relationships in a mapping population of 287 diverse spring wheat lines. <i>Field Crops Research</i> , 2019, 243, 107627.	5.1	9
1924	Haplotypes at the Phg-2 Locus Are Determining Pathotype-Specificity of Angular Leaf Spot Resistance in Common Bean. <i>Frontiers in Plant Science</i> , 2019, 10, 1126.	3.6	15
1925	Comparing Singleâ€“SNP, Multiâ€“SNP, and Haplotypeâ€“Based Approaches in Association Studies for Major Traits in Barley. <i>Plant Genome</i> , 2019, 12, 1-14.	2.8	48
1926	Sorghum as a Novel Crop for Central Europe: Using a Broad Diversity Set to Dissect Temperate-Adaptation. <i>Agronomy</i> , 2019, 9, 535.	3.0	14
1927	Assessing the genetic diversity and characterizing genomic regions conferring Tan Spot resistance in cultivated rye. <i>PLoS ONE</i> , 2019, 14, e0214519.	2.5	23
1928	Characterization and fine mapping of qkrnw4, a major QTL controlling kernel row number in maize. <i>Theoretical and Applied Genetics</i> , 2019, 132, 3321-3331.	3.6	11
1929	Population Genomic Approaches for Weed Science. <i>Plants</i> , 2019, 8, 354.	3.5	14
1930	Contemporary evolution of maize landraces and their wild relatives influenced by gene flow with modern maize varieties. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 21302-21311.	7.1	25
1931	SRG extractor: a skinny reference genome approach for reduced-representation sequencing. <i>Bioinformatics</i> , 2019, 35, 3160-3162.	4.1	1
1932	Genetic dissection of root architectural traits by QTL and genome-wide association mapping in rapeseed ( <i>Brassica napus</i> ). <i>Plant Breeding</i> , 2019, 138, 184-192.	1.9	13
1933	Association Mapping of Fertility Restorer Gene for CMS PET1 in Sunflower. <i>Agronomy</i> , 2019, 9, 49.	3.0	19
1934	Phenotypic and molecular dissection of grain quality using the USDA rice mini-core collection. <i>Food Chemistry</i> , 2019, 284, 312-322.	8.2	11
1935	Development of an integrated 200K <sc>SNP</sc> genotyping array and application for genetic mapping, genome assembly improvement and genome wide association studies in pear ( <i>Pyrus</i> ). <i>Plant Biotechnology Journal</i> , 2019, 17, 1582-1594.	8.3	46

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1936	GWAS analysis of sorghum association panel lines identifies SNPs associated with disease response to Texas isolates of <i>Colletotrichum sublineola</i> . <i>Theoretical and Applied Genetics</i> , 2019, 132, 1389-1396.	3.6	32
1937	Genome-wide association study reveals the genetic control underlying node of the first fruiting branch and its height in upland cotton ( <i>Gossypium hirsutum</i> L.). <i>Euphytica</i> , 2019, 215, 1.	1.2	8
1938	Identification of Loci and Candidate Genes Responsible for Fiber Length in Upland Cotton ( <i>Gossypium</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T	3.6	20
1939	Identification of favorable SNP alleles and candidate genes responsible for inflorescence-related traits via GWAS in chrysanthemum. <i>Plant Molecular Biology</i> , 2019, 99, 407-420.	3.9	27
1940	Genome-wide association study identifies favorable SNP alleles and candidate genes for waterlogging tolerance in chrysanthemums. <i>Horticulture Research</i> , 2019, 6, 21.	6.3	40
1941	Blast resistance in Indian rice landraces: Genetic dissection by gene specific markers. <i>PLoS ONE</i> , 2019, 14, e0211061.	2.5	33
1942	polyRAD: Genotype Calling with Uncertainty from Sequencing Data in Polyploids and Diploids. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 663-673.	1.8	76
1943	Heatâ€Tolerant QTLs Associated with Grain Yield and Its Components in Spring Bread Wheat under Heatâ€Stressed Environments of Sudan and Egypt. <i>Crop Science</i> , 2019, 59, 199-211.	1.8	39
1944	Predicting contemporary rangeâ€wide genomic variation using climatic, phylogeographic and morphological knowledge in an ancient, unglaciated landscape. <i>Journal of Biogeography</i> , 2019, 46, 503-514.	3.0	12
1945	Genome-Wide Associations of Chlorophyll Fluorescence OJIP Transient Parameters Connected With Soil Drought Response in Barley. <i>Frontiers in Plant Science</i> , 2019, 10, 78.	3.6	43
1946	Tantalizing dilemma in risk prediction from disease scoring statistics. <i>Briefings in Functional Genomics</i> , 2019, 18, 211-219.	2.7	1
1947	A largeâ€scale circular <scp>RNA</scp> profiling reveals universal molecular mechanisms responsive to drought stress in maize and <i>Arabidopsis</i> . <i>Plant Journal</i> , 2019, 98, 697-713.	5.7	99
1948	Edit at will: Genotype independent plant transformation in the era of advanced genomics and genome editing. <i>Plant Science</i> , 2019, 281, 186-205.	3.6	57
1949	Genetic characterization of maize germplasm derived from Suwan population and temperate resources. <i>Hereditas</i> , 2019, 156, 2.	1.4	14
1950	Quantitative trait loci controlling <i>Phytophthora cactorum</i> resistance in the cultivated octoploid strawberry ( <i>Fragaria</i> â€%Ã—â€%ananassa). <i>Horticulture Research</i> , 2019, 6, 60.	6.3	27
1951	Refining the Genomic Region Containing a Major Locus Controlling Fruit Maturity in Peach. <i>Scientific Reports</i> , 2019, 9, 7522.	3.3	30
1952	Candidate loci for the kernel row number in maize revealed by a combination of transcriptome analysis and regional association mapping. <i>BMC Plant Biology</i> , 2019, 19, 201.	3.6	10
1953	Novel Polymorphisms in RAPGEF6 Gene Associated with Egg-Laying Rate in Chinese Jing Hong Chicken using Genome-Wide SNP Scan. <i>Genes</i> , 2019, 10, 384.	2.4	7

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1954	Evidence for the genetic basis and epistatic interactions underlying oceanâ€•and riverâ€•maturing ecotypes of Pacific Lamprey ( <i>Entosphenus tridentatus</i> ) returning to the Klamath River, California. Molecular Ecology, 2019, 28, 3171-3185.	3.9	15
1955	QTL-seq reveals a major root-knot nematode resistance locus on chromosome 11 in rice ( <i>Oryza sativa</i> ) Tj ETQq1 1 0.784314 rgBT /Overl	1.2	25
1956	Genome-wide association study reveals E2F3 as the candidate gene for scallop growth. Aquaculture, 2019, 511, 734216.	3.5	22
1957	Introgression of novel genetic diversity to improve soybean yield. Theoretical and Applied Genetics, 2019, 132, 2541-2552.	3.6	17
1958	Consequences of PCA graphs, SNP codings, and PCA variants for elucidating population structure. PLoS ONE, 2019, 14, e0218306.	2.5	26
1959	Analysis of Hematological Traits in Polled Yak by Genome-Wide Association Studies Using Individual SNPs and Haplotypes. Genes, 2019, 10, 463.	2.4	17
1960	Whole genome resequencing data for three rockfish species of Sebastes. Scientific Data, 2019, 6, 97.	5.3	12
1961	A genomeâ€•wide association study for partial resistance to southern corn rust in tropical maize. Plant Breeding, 2019, 138, 770-780.	1.9	11
1962	Genome-wide association mapping of root system architecture traits in common wheat ( <i>Triticum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.2	19
1963	Allele Frequency Changes Provide Evidence for Selection and Identification of Candidate Loci for Survival in Red Clover ( <i>Trifolium pratense</i> L.). Frontiers in Plant Science, 2019, 10, 718.	3.6	23
1964	Influence of a climatic gradient on genetic exchange between two oak species. American Journal of Botany, 2019, 106, 864-878.	1.7	7
1965	Re-evaluation of the role of Indian germplasm as center of melon diversification based on genotyping-by-sequencing analysis. BMC Genomics, 2019, 20, 448.	2.8	35
1966	Genetic variation of biomass recalcitrance in a natural <i>Salix viminalis</i> (L.) population. Biotechnology for Biofuels, 2019, 12, 135.	6.2	17
1967	The search for candidate genes associated with natural variation of grain Zn accumulation in barley. Biochemical Journal, 2019, 476, 1889-1909.	3.7	12
1968	An allele of <i>ZmPORB2</i> encoding a protochlorophyllide oxidoreductase promotes tocopherol accumulation in both leaves and kernels of maize. Plant Journal, 2019, 100, 114-127.	5.7	21
1969	Population Structure and Genomeâ€•Wide Association Analysis of Bruchid Resistance in Ethiopian Common Bean Genotypes. Crop Science, 2019, 59, 1504-1515.	1.8	24
1970	Late Pleistocene range expansion of North American topminnows accompanied by admixture and introgression. Journal of Biogeography, 2019, 46, 2126-2140.	3.0	10
1971	Genome-wide cis-regulatory signatures for modulation of agronomic traits as exemplified by drought yield index (DYI) in chickpea. Functional and Integrative Genomics, 2019, 19, 973-992.	3.5	1

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1972	Mutation of a histidine-rich calcium-binding-protein gene in wheat confers resistance to Fusarium head blight. <i>Nature Genetics</i> , 2019, 51, 1106-1112.	21.4	200
1973	Genome-Wide Association Mapping of Seedling Net Form Net Blotch Resistance in an Ethiopian and Eritrean Barley Collection. <i>Crop Science</i> , 2019, 59, 1625-1638.	1.8	11
1974	Genome-wide variation patterns between landraces and cultivars uncover divergent selection during modern wheat breeding. <i>Theoretical and Applied Genetics</i> , 2019, 132, 2509-2523.	3.6	56
1975	Detecting novel loci underlying rice blast resistance by integrating a genome-wide association study and RNA sequencing. <i>Molecular Breeding</i> , 2019, 39, 1.	2.1	10
1976	A local score approach improves GWAS resolution and detects minor QTL: application to <i>Medicago truncatula</i> quantitative disease resistance to multiple <i>Aphanomyces euteiches</i> isolates. <i>Heredity</i> , 2019, 123, 517-531.	2.6	36
1977	Genome-Wide Association Studies in Apple Reveal Loci for Aroma Volatiles, Sugar Composition, and Harvest Date. <i>Plant Genome</i> , 2019, 12, 180104.	2.8	70
1978	Identification of Ideal Allele Combinations for the Adaptation of Spring Barley to Northern Latitudes. <i>Frontiers in Plant Science</i> , 2019, 10, 542.	3.6	10
1979	Molecular Characterization of 87 Functional Genes in Wheat Diversity Panel and Their Association With Phenotypes Under Well-Watered and Water-Limited Conditions. <i>Frontiers in Plant Science</i> , 2019, 10, 717.	3.6	43
1980	Genomic signatures of adaptation to Sahelian and Soudanian climates in sorghum landraces of Senegal. <i>Ecology and Evolution</i> , 2019, 9, 6038-6051.	1.9	30
1981	Genetic diversity and population structure of native, naturalized, and cultivated <i>Salix purpurea</i> . <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	1.6	13
1982	Marker-trait association analysis for postharvest needle retention/abscission in balsam fir ( <i>Abies</i> ). <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	1.9	2
1983	Genome-Wide Association Study of Yield Component Traits in Intermediate Wheatgrass and Implications in Genomic Selection and Breeding. <i>C3: Genes, Genomes, Genetics</i> , 2019, 9, 2429-2439.	1.8	34
1984	Uncovering of natural allelic variants of key yield contributing genes by targeted resequencing in rice ( <i>Oryza sativa</i> L.). <i>Scientific Reports</i> , 2019, 9, 8192.	3.3	5
1985	The genetics of resistance to lettuce drop ( <i>Sclerotinia</i> spp.) in lettuce in a recombinant inbred line population from Reine des Glaces—Eruption. <i>Theoretical and Applied Genetics</i> , 2019, 132, 2439-2460.	3.6	25
1986	Identification of powdery mildew resistance loci in wheat by integrating genome-wide association study (GWAS) and linkage mapping. <i>Crop Journal</i> , 2019, 7, 294-306.	5.2	23
1987	The multi-allelic APRR2 gene is associated with fruit pigment accumulation in melon and watermelon. <i>Journal of Experimental Botany</i> , 2019, 70, 3781-3794.	4.8	84
1988	Genome-wide association study reveals significant genomic regions for improving yield, adaptability of rice under dry direct seeded cultivation condition. <i>BMC Genomics</i> , 2019, 20, 471.	2.8	26
1989	Reimagining Maize Inbred Potential: Identifying Breeding Crosses Using Genetic Variance of Simulated Progeny. <i>Crop Science</i> , 2019, 59, 1457-1468.	1.8	6

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1990	Insights into the Population Structure and Association Mapping in Globe Artichoke. Compendium of Plant Genomes, 2019, , 129-143.	0.5	0
1991	Evaluation of linkage disequilibrium, population structure, and genetic diversity in the U.S. peanut mini core collection. BMC Genomics, 2019, 20, 481.	2.8	39
1992	Genome-Wide Analysis of TCP Family Genes in Zea mays L. Identified a Role for ZmTCP42 in Drought Tolerance. International Journal of Molecular Sciences, 2019, 20, 2762.	4.1	58
1993	Variation in seed longevity among diverse Indica rice varieties. Annals of Botany, 2019, 124, 447-460.	2.9	45
1994	Genome-wide Association Study of a Panel of Vietnamese Rice Landraces Reveals New QTLs for Tolerance to Water Deficit During the Vegetative Phase. Rice, 2019, 12, 4.	4.0	45
1995	Genetic analyses of nitrogen assimilation enzymes in Brassica juncea (L.) Czern & Coss. Molecular Biology Reports, 2019, 46, 4235-4244.	2.3	6
1996	Genome-Wide Association Study Reveals Novel Genomic Regions Associated With High Grain Protein Content in Wheat Lines Derived From Wild Emmer Wheat. Frontiers in Plant Science, 2019, 10, 464.	3.6	29
1997	Genome-wide association mapping and candidate gene analysis for saturated fatty acid content in soybean seed. Plant Breeding, 2019, 138, 588-598.	1.9	8
1998	SNPs associated with barley resistance to isolates of Pyrenophora teres f. teres. BMC Genomics, 2019, 20, 292.	2.8	13
1999	Genetic diversity, population structure, and relationships in a collection of pepper (Capsicum spp.) landraces from the Spanish centre of diversity revealed by genotyping-by-sequencing (GBS). Horticulture Research, 2019, 6, 54.	6.3	61
2000	Genome-wide association study (GWAS) of leaf cuticular wax components in Camelina sativa identifies genetic loci related to intracellular wax transport. BMC Plant Biology, 2019, 19, 187.	3.6	22
2001	Genome-wide association analysis identifies a natural variation in basic helix-loop-helix transcription factor regulating ascorbate biosynthesis via D-mannose/L-galactose pathway in tomato. PLoS Genetics, 2019, 15, e1008149.	3.5	66
2002	Genetic architecture of maize chlorotic mottle virus and maize lethal necrosis through GWAS, linkage analysis and genomic prediction in tropical maize germplasm. Theoretical and Applied Genetics, 2019, 132, 2381-2399.	3.6	53
2003	Rice Galaxy: an open resource for plant science. GigaScience, 2019, 8, .	6.4	11
2004	Gradual evolution towards flightlessness in steamer ducks*. Evolution; International Journal of Organic Evolution, 2019, 73, 1916-1926.	2.3	21
2005	Genome-wide association study and linkage analysis on resistance to rice black-streaked dwarf virus disease. Molecular Breeding, 2019, 39, 1.	2.1	11
2006	Genome of the African cassava whitefly Bemisia tabaci and distribution and genetic diversity of cassava-colonizing whiteflies in Africa. Insect Biochemistry and Molecular Biology, 2019, 110, 112-120.	2.7	47
2007	Development of a core set of KASP markers for assaying genetic diversity in Brassica rapa subsp. chinensis Makino. Plant Breeding, 2019, 138, 309-324.	1.9	9



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2008	Development of a core SNP arrays based on the KASP method for molecular breeding of rice. Rice, 2019, 12, 21.	4.0	60
2009	The tomato pan-genome uncovers new genes and a rare allele regulating fruit flavor. Nature Genetics, 2019, 51, 1044-1051.	21.4	441
2010	Computational Analysis of AmpSeq Data for Targeted, High-Throughput Genotyping of Amplicons. Frontiers in Plant Science, 2019, 10, 599.	3.6	115
2011	Identification of candidate genes associated with resistance to bruchid ( <i>Callosobruchus maculatus</i> ) in cowpea. Plant Breeding, 2019, 138, 605-613.	1.9	14
2012	Identification and development of a core set of informative genic SNP markers for assaying genetic diversity in Chinese cabbage. Horticulture Environment and Biotechnology, 2019, 60, 411-425.	2.1	7
2013	Utilization of Molecular Marker Based Genetic Diversity Patterns in Hybrid Parents to Develop Better Forage Quality Multi-Cut Hybrids in Pearl Millet. Agriculture (Switzerland), 2019, 9, 97.	3.1	9
2014	Validation of Yield Component Traits Identified by Genome-Wide Association Mapping in a tropical japonica – tropical japonica Rice Biparental Mapping Population. Plant Genome, 2019, 12, 180021.	2.8	13
2015	Association mapping of agro-morphological traits in European hazelnut ( <i>Corylus avellana</i> ). Euphytica, 2019, 215, 1.	1.2	6
2016	Winter hardiness of <i>Miscanthus</i> (II): Genetic mapping for overwintering ability and adaptation traits in three interconnected <i>Miscanthus</i> populations. GCB Bioenergy, 2019, 11, 706-726.	5.6	7
2017	Genome-wide association studies of seven agronomic traits under two sowing conditions in bread wheat. BMC Plant Biology, 2019, 19, 149.	3.6	68
2018	Association Analysis of Baking and Milling Quality Traits in an Elite Soft Red Winter Wheat Population. Crop Science, 2019, 59, 1085-1094.	1.8	9
2019	Development and Validation of Markers for the Fertility Restorer Gene Rf1 in Sunflower. International Journal of Molecular Sciences, 2019, 20, 1260.	4.1	15
2020	Favorable alleles mining for gelatinization temperature, gel consistency and amylose content in <i>Oryza sativa</i> by association mapping. BMC Genetics, 2019, 20, 34.	2.7	16
2021	Candidate quantitative trait loci and genes for fiber quality in <i>Gossypium hirsutum</i> L. detected using single- and multi-locus association mapping. Industrial Crops and Products, 2019, 134, 356-369.	5.2	12
2022	Population genomics reveals a fine-scale recombination landscape for genetic improvement of cotton. Plant Journal, 2019, 99, 494-505.	5.7	31
2023	Genome-wide diversity and demographic dynamics of Cameroon goats and their divergence from east African, north African, and Asian conspecifics. PLoS ONE, 2019, 14, e0214843.	2.5	6
2024	Bayesian Mapping Reveals Large-Effect Pleiotropic QTLs for Wood Density and Slenderness Index in 17-Year-Old Trees of <i>Eucalyptus cladocalyx</i> . Forests, 2019, 10, 241.	2.1	11
2025	Genome-wide association study (GWAS) for stem height increment in oil palm ( <i>Elaeis guineensis</i> ) germplasm using SNP markers. Tree Genetics and Genomes, 2019, 15, 1.	1.6	20



#	ARTICLE	IF	CITATIONS
2026	A novel quantitative trait locus on chromosome A9 controlling oleic acid content in <i>Brassica napus</i> . Plant Biotechnology Journal, 2019, 17, 2313-2324.	8.3	34
2027	Genome-Wide Association Study for Adult-Plant Resistance to Stripe Rust in Chinese Wheat Landraces ( <i>Triticum aestivum</i> L.) From the Yellow and Huai River Valleys. Frontiers in Plant Science, 2019, 10, 596.	3.6	41
2028	A Novel QTL for Root-Knot Nematode Resistance is Identified from a South African Sweet Sorghum Line. Phytopathology, 2019, 109, 1011-1017.	2.2	1
2029	Genetic variation of HvXYN1 associated with endoxylanase activity and TAX content in barley ( <i>Hordeum vulgare</i> L.). BMC Plant Biology, 2019, 19, 170.	3.6	5
2030	A group VII ethylene response factor gene, <i>ZmEREB180</i> , coordinates waterlogging tolerance in maize seedlings. Plant Biotechnology Journal, 2019, 17, 2286-2298.	8.3	91
2031	Genome-wide association analysis for fumonisin content in maize kernels. BMC Plant Biology, 2019, 19, 166.	3.6	21
2032	Genetic Dissection of Root System Architectural Traits in Spring Barley. Frontiers in Plant Science, 2019, 10, 400.	3.6	58
2033	Multiple interacting QTLs affect disease challenge survival in common carp ( <i>Cyprinus carpio</i> ). Heredity, 2019, 123, 565-578.	2.6	20
2034	Association mapping reveals multiple QTLs for grain protein content in rice useful for biofortification. Molecular Genetics and Genomics, 2019, 294, 963-983.	2.1	31
2035	A discriminatory test for the wheat B and G genomes reveals misclassified accessions of <i>Triticum timopheevii</i> and <i>Triticum turgidum</i> . PLoS ONE, 2019, 14, e0215175.	2.5	11
2036	Stability Analysis of Kernel Quality Traits in Exotic-Derived Doubled Haploid Maize Lines. Plant Genome, 2019, 12, 170114.	2.8	12
2037	Gene flow signature in the S-allele region of cultivated buckwheat. BMC Plant Biology, 2019, 19, 125.	3.6	26
2038	Genome-wide association study of resistance to stripe rust ( <i>Puccinia striiformis</i> f. sp. <i>tritici</i> ) in Sichuan wheat. BMC Plant Biology, 2019, 19, 147.	3.6	39
2039	Association of candidate genes with drought tolerance traits in zoysiagrass germplasm. Journal of Plant Physiology, 2019, 237, 61-71.	3.5	6
2040	Effects of input data quantity on genome-wide association studies (GWAS). International Journal of Data Mining and Bioinformatics, 2019, 22, 19.	0.1	5
2041	Development of Single Nucleotide Polymorphism Markers for the Wheat Curl Mite Resistance Gene <i>Cmc4</i> . Crop Science, 2019, 59, 1567-1575.	1.8	23
2042	Joint linkage and association mapping of complex traits in shrub willow ( <i>Salix purpurea</i> L.). Annals of Botany, 2019, 124, 701-715.	2.9	37
2043	Identification of new loci for salt tolerance in soybean by high-resolution genome-wide association mapping. BMC Genomics, 2019, 20, 318.	2.8	46

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2044	Transgenerational response to early spring warming in <i>Daphnia</i> . <i>Scientific Reports</i> , 2019, 9, 4449.	3.3	21
2045	Starch phosphorylation associated SNPs found by genome-wide association studies in the potato ( <i>Solanum tuberosum</i> L.). <i>BMC Genetics</i> , 2019, 20, 29.	2.7	20
2046	Haplotype analysis of a major and stable QTL underlying soybean ( <i>Glycine max</i> ) seed oil content reveals footprint of artificial selection. <i>Molecular Breeding</i> , 2019, 39, 1.	2.1	5
2047	A fruit firmness QTL identified on linkage group 4 in sweet cherry ( <i>Prunus avium</i> L.) is associated with domesticated and bred germplasm. <i>Scientific Reports</i> , 2019, 9, 5008.	3.3	29
2048	QTL mapping for maize starch content and candidate gene prediction combined with co-expression network analysis. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1931-1941.	3.6	31
2049	Genome-wide haplotype analysis improves trait predictions in <i>Brassica napus</i> hybrids. <i>Plant Science</i> , 2019, 283, 157-164.	3.6	26
2050	Integrating Molecular Markers and Environmental Covariates To Interpret Genotype by Environment Interaction in Rice ( <i>Oryza sativa</i> L.) Grown in Subtropical Areas. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1519-1531.	1.8	59
2051	Genetic diversity among tropical provitamin a maize inbred lines and implications for a biofortification program. <i>Cereal Research Communications</i> , 2019, 47, 134-144.	1.6	9
2052	The genetic architecture of phosphorus efficiency in sorghum involves pleiotropic QTL for root morphology and grain yield under low phosphorus availability in the soil. <i>BMC Plant Biology</i> , 2019, 19, 87.	3.6	51
2053	Genome-wide haplotype-based association analysis of key traits of plant lodging and architecture of maize identifies major determinants for leaf angle: hapLA4. <i>PLoS ONE</i> , 2019, 14, e0212925.	2.5	37
2054	The genetic architecture of teosinte catalyzed and constrained maize domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 5643-5652.	7.1	59
2055	High SNP diversity in the non-toxic indigenous <i>Jatropha curcas</i> germplasm widens the potential of this upcoming major biofuel crop species. <i>Annals of Botany</i> , 2019, 124, 645-652.	2.9	8
2056	Population genomics of rapid evolution in natural populations: polygenic selection in response to power station thermal effluents. <i>BMC Evolutionary Biology</i> , 2019, 19, 61.	3.2	67
2057	Association between seed yield-related traits and cDNA-AFLP markers in cumin ( <i>Cuminum cyminum</i> ) under drought and irrigation regimes. <i>Industrial Crops and Products</i> , 2019, 133, 276-283.	5.2	15
2058	Natural variations of FT family genes in soybean varieties covering a wide range of maturity groups. <i>BMC Genomics</i> , 2019, 20, 230.	2.8	33
2059	Phylogenomics shows lignotuber state is taxonomically informative in closely related eucalypts. <i>Molecular Phylogenetics and Evolution</i> , 2019, 135, 236-248.	2.7	14
2060	Metabolome-Scale Genome-Wide Association Studies Reveal Chemical Diversity and Genetic Control of Maize Specialized Metabolites. <i>Plant Cell</i> , 2019, 31, 937-955.	6.6	75
2061	Characterization of molecular diversity and genome-wide association study of stripe rust resistance at the adult plant stage in Northern Chinese wheat landraces. <i>BMC Genetics</i> , 2019, 20, 38.	2.7	56

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2062	Identification of duplicates in cassava germplasm banks based on single-nucleotide polymorphisms (SNPs). <i>Scientia Agricola</i> , 2019, 76, 328-336.	1.2	18
2063	Genome-Wide Association Analysis Pinpoints Additional Major Genomic Regions Conferring Resistance to Soybean Cyst Nematode ( <i>Heterodera glycines</i> Ichinohe). <i>Frontiers in Plant Science</i> , 2019, 10, 401.	3.6	32
2064	Fine-mapping and validation of the genomic region underpinning pear red skin colour. <i>Horticulture Research</i> , 2019, 6, 29.	6.3	31
2065	Genetic Diversity and Population Structure of a <i>Camelina sativa</i> Spring Panel. <i>Frontiers in Plant Science</i> , 2019, 10, 184.	3.6	118
2066	Genetic diversity of 324 cultivated tomato germplasm resources using agronomic traits and InDel markers. <i>Euphytica</i> , 2019, 215, 1.	1.2	17
2067	Genetic architecture of yellow and stem rust resistance in a durum wheat diversity panel. <i>Euphytica</i> , 2019, 215, 1.	1.2	17
2068	New Deep Learning Genomic-Based Prediction Model for Multiple Traits with Binary, Ordinal, and Continuous Phenotypes. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1545-1556.	1.8	81
2069	â€˜apparentâ€™™: a simple and flexible R package for accurate SNP-based parentage analysis in the absence of guiding information. <i>BMC Bioinformatics</i> , 2019, 20, 108.	2.6	8
2070	Introgression and monitoring of wild <i>Helianthus praecox</i> alien segments associated with <i>Sclerotinia</i> basal stalk rot resistance in sunflower using genotyping-by-sequencing. <i>PLoS ONE</i> , 2019, 14, e0213065.	2.5	7
2071	Assessment of Genetic Differentiation and Linkage Disequilibrium in <i>Solanum pimpinellifolium</i> Using Genome-Wide High-Density SNP Markers. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1497-1505.	1.8	12
2072	Evolutionary Toxicogenomics of the Striped Killifish ( <i>Fundulus majalis</i> ) in the New Bedford Harbor (Massachusetts, USA). <i>International Journal of Molecular Sciences</i> , 2019, 20, 1129.	4.1	7
2073	Genetic variation and development of a SCAR marker of anemone-type flower in chrysanthemum. <i>Molecular Breeding</i> , 2019, 39, 1.	2.1	9
2074	Genomics overrules mitochondrial DNA, siding with morphology on a controversial case of species delimitation. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20182924.	2.6	40
2075	Linkage mapping and genome-wide association reveal candidate genes conferring thermotolerance of seed-set in maize. <i>Journal of Experimental Botany</i> , 2019, 70, 4849-4864.	4.8	38
2076	The genetic structure of flax illustrates environmental and anthropogenic selections that gave rise to its eco-geographical adaptation. <i>Molecular Phylogenetics and Evolution</i> , 2019, 137, 22-32.	2.7	22
2077	Evaluation of genotyping by sequencing for population genetics of sibling and hybridizing birds: an example using Syrian and Great Spotted Woodpeckers. <i>Journal of Ornithology</i> , 2019, 160, 287-294.	1.1	5
2078	Non-linear regression models for time to flowering in wild chickpea combine genetic and climatic factors. <i>BMC Plant Biology</i> , 2019, 19, 94.	3.6	21
2079	Transcription factors involved in the regulatory networks governing the Calvinâ€“Bensonâ€“Bassham cycle. <i>Tree Physiology</i> , 2019, 39, 1159-1172.	3.1	3

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2080	Comparison of Representative and Custom Methods of Generating Core Subsets of a Carrot Germplasm Collection. <i>Crop Science</i> , 2019, 59, 1107-1121.	1.8	13
2081	Linkage Mapping and Genome-Wide Association Studies of the Rf Gene Cluster in Sunflower ( <i>Helianthus annuus</i> L.) and Their Distribution in World Sunflower Collections. <i>Frontiers in Genetics</i> , 2019, 10, 216.	2.3	34
2082	Genomic, Transcriptomic, and Epigenomic Features Differentiate Genes That Are Relevant for Muscular Polyunsaturated Fatty Acids in the Common Carp. <i>Frontiers in Genetics</i> , 2019, 10, 217.	2.3	20
2083	New candidate loci and marker genes on chromosome 7 for improved chilling tolerance in sorghum. <i>Journal of Experimental Botany</i> , 2019, 70, 3357-3371.	4.8	31
2084	Genetic Loci Associated with Salt Tolerance in Advanced Breeding Populations of Tetraploid Alfalfa Using Genome-Wide Association Studies. <i>Plant Genome</i> , 2019, 12, 180026.	2.8	15
2085	A novel QTL QTrl.saw-2D.2 associated with the total root length identified by linkage and association analyses in wheat ( <i>Triticum aestivum</i> L.). <i>Planta</i> , 2019, 250, 129-143.	3.2	30
2086	Towards high-biomass yielding bioenergy crop <i>Silphium perfoliatum</i> L.: phenotypic and genotypic evaluation of five cultivated populations. <i>Biomass and Bioenergy</i> , 2019, 124, 102-113.	5.7	25
2087	A Very Oil Yellow1 Modifier of the Oil Yellow1-N1989 Allele Uncovers a Cryptic Phenotypic Impact of Cis-regulatory Variation in Maize. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 375-390.	1.8	9
2088	Genome-wide association studies for yield-related traits in soft red winter wheat grown in Virginia. <i>PLoS ONE</i> , 2019, 14, e0208217.	2.5	84
2089	New alleles for chlorophyll content and stay-green traits revealed by a genome wide association study in rice ( <i>Oryza sativa</i> ). <i>Scientific Reports</i> , 2019, 9, 2541.	3.3	34
2090	Identification of a novel seed size associated locus SW9-1 in soybean. <i>Crop Journal</i> , 2019, 7, 548-559.	5.2	19
2091	Genetic variations in plant architecture traits in cotton ( <i>Gossypium hirsutum</i> ) revealed by a genome-wide association study. <i>Crop Journal</i> , 2019, 7, 209-216.	5.2	16
2092	Diverse Components of Resistance to <i>Fusarium verticillioides</i> Infection and Fumonisin Contamination in Four Maize Recombinant Inbred Families. <i>Toxins</i> , 2019, 11, 86.	3.4	18
2093	Integrating a newly developed BAC-based physical mapping resource for <i>Lolium perenne</i> with a genome-wide association study across a <i>L. perenne</i> European ecotype collection identifies genomic contexts associated with agriculturally important traits. <i>Annals of Botany</i> , 2019, 123, 977-992.	2.9	6
2094	Genome-wide association mapping of grain yield in a diverse collection of spring wheat ( <i>Triticum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.5	108
2095	The distribution pattern of endopolyploidy in maize. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1487-1503.	3.6	6
2096	Genome-wide association study of inflorescence length of cultivated soybean based on the high-throughout single-nucleotide markers. <i>Molecular Genetics and Genomics</i> , 2019, 294, 607-620.	2.1	6
2097	ABC Transporter-Mediated Transport of Glutathione Conjugates Enhances Seed Yield and Quality in Chickpea. <i>Plant Physiology</i> , 2019, 180, 253-275.	4.8	21

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2098	Integrating genetic and physical positions of the anthracnose resistance genes described in bean chromosomes Pv01 and Pv04. PLoS ONE, 2019, 14, e0212298.	2.5	28
2099	Development of High-Density SNP Markers and Their Application in Evaluating Genetic Diversity and Population Structure in <i>Elaeis guineensis</i> . Frontiers in Plant Science, 2019, 10, 130.	3.6	49
2100	Response of Tibetan Wild Barley Genotypes to Drought Stress and Identification of Quantitative Trait Loci by Genome-Wide Association Analysis. International Journal of Molecular Sciences, 2019, 20, 791.	4.1	15
2101	Transcriptional signatures modulating shoot apical meristem morphometric and plant architectural traits enhance yield and productivity in chickpea. Plant Journal, 2019, 98, 864-883.	5.7	6
2102	Exploiting Genetic and Genomic Resources to Enhance Heat-Tolerance in Tomatoes. Agronomy, 2019, 9, 22.	3.0	45
2103	Impact of Genomics on Capsicum Breeding. Compendium of Plant Genomes, 2019, , 209-219.	0.5	2
2104	Molecular tools for detecting Pdh1 can improve soybean breeding efficiency by reducing yield losses due to pod shatter. Molecular Breeding, 2019, 39, 1.	2.1	19
2105	QTL mapping of Fusarium head blight resistance and deoxynivalenol accumulation in the Kansas wheat variety 'Everest'. Molecular Breeding, 2019, 39, 1.	2.1	15
2106	Phenotypic and genetic introgression across a moving woodpecker hybrid zone. Molecular Ecology, 2019, 28, 1692-1708.	3.9	22
2107	Genome-wide association and transcriptional studies reveal novel genes for unsaturated fatty acid synthesis in a panel of soybean accessions. BMC Genomics, 2019, 20, 68.	2.8	31
2108	Diversification of seed carotenoid content and profile in wild barley ( <i>Hordeum chilense</i> Roem. et) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3 215, 1.	1.2	13
2109	Next-Generation Sequencing Enabled Genetics in Hexaploid Wheat. , 2019, , 49-63.		4
2110	Leveraging <scp>GWAS</scp> data to identify metabolic pathways and networks involved in maize lipid biosynthesis. Plant Journal, 2019, 98, 853-863.	5.7	37
2111	The genetic basis of drought tolerance in the high oil crop <i>Sesamum indicum</i> . Plant Biotechnology Journal, 2019, 17, 1788-1803.	8.3	63
2112	Genome-wide association study of seed protein, oil and amino acid contents in soybean from maturity groups I to IV. Theoretical and Applied Genetics, 2019, 132, 1639-1659.	3.6	77
2113	Heterotic grouping based on genetic variation and population structure of maize inbred lines from current breeding program in Sichuan province, Southwest China using genotyping by sequencing (GBS). Molecular Breeding, 2019, 39, 1.	2.1	11
2114	Multienvironment and Multitrait Genomic Selection Models in Unbalanced Early-Generation Wheat Yield Trials. Crop Science, 2019, 59, 491-507.	1.8	54
2115	BnaMPK3 Is a Key Regulator of Defense Responses to the Devastating Plant Pathogen <i>Sclerotinia sclerotiorum</i> in Oilseed Rape. Frontiers in Plant Science, 2019, 10, 91.	3.6	33

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2116	Genome analysis to identify SNPs associated with oil content and fatty acid components in soybean. <i>Euphytica</i> , 2019, 215, 1.	1.2	11
2117	Genome-Wide Association Study of Resistance to <i>Xanthomonas gardneri</i> in the USDA Pepper ( <i>Capsicum</i> ) Collection. <i>Phytopathology</i> , 2019, 109, 1217-1225.	2.2	10
2118	Genome-wide analysis of Chongqing native intersexual goats using next-generation sequencing. 3 <i>Biotech</i> , 2019, 9, 99.	2.2	3
2119	Association Genetics Identifies Single Nucleotide Polymorphisms Related to Kernel Oil Content and Quality in <i>Camellia oleifera</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 2547-2562.	5.2	8
2120	Introgression of <i>rpg4</i> / <i>Rpg5</i> Into Barley Germplasm Provides Insights Into the Genetics of Resistance to <i>Puccinia graminis</i> f. sp. <i>tritici</i> Race TTKSK and Resources for Developing Resistant Cultivars. <i>Phytopathology</i> , 2019, 109, 1018-1028.	2.2	4
2121	Genetic identification of loci for Hessian fly resistance in durum wheat. <i>Molecular Breeding</i> , 2019, 39, 1.	2.1	38
2122	Assessment of genetic diversity among low-nitrogen-tolerant early generation maize inbred lines using SNP markers. <i>South African Journal of Plant and Soil</i> , 2019, 36, 181-188.	1.1	8
2123	Genetic diversity and re-classification of coffee ( <i>Coffea canephora</i> Pierre ex A. Froehner) from South Western Nigeria through genotyping-by-sequencing-single nucleotide polymorphism analysis. <i>Genetic Resources and Crop Evolution</i> , 2019, 66, 685-696.	1.6	18
2124	Transcriptome-Wide Association Supplements Genome-Wide Association in <i>Zea mays</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3023-3033.	1.8	64
2125	Genetic markers to detect introgression of cultivar genes in wild carrot populations. <i>Acta Horticulturae</i> , 2019, , 165-174.	0.2	2
2126	A Bayesian Genomic Multi-output Regressor Stacking Model for Predicting Multi-trait Multi-environment Plant Breeding Data. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3381-3393.	1.8	22
2127	An enrichment method for mapping ambiguous reads to the reference genome for NGS analysis. <i>Journal of Bioinformatics and Computational Biology</i> , 2019, 17, 1940012.	0.8	2
2128	Unraveling the Genetic Elements Involved in Shoot and Root Growth Regulation by Jasmonate in Rice Using a Genome-Wide Association Study. <i>Rice</i> , 2019, 12, 69.	4.0	31
2129	The Genomic Basis for Short-Term Evolution of Environmental Adaptation in Maize. <i>Genetics</i> , 2019, 213, 1479-1494.	2.9	23
2130	Marker-trait associations of yield related traits in bread wheat ( <i>Triticum aestivum</i> L.) under a semi-arid climate. <i>Czech Journal of Genetics and Plant Breeding</i> , 2019, 55, 138-145.	0.8	4
2131	Genome-Wide Association Study of 13 Traits in Maize Seedlings under Low Phosphorus Stress. <i>Plant Genome</i> , 2019, 12, 1-13.	2.8	36
2132	Glacial cycles drive rapid divergence of cryptic field vole species. <i>Ecology and Evolution</i> , 2019, 9, 14101-14113.	1.9	4
2133	Favorable Alleles of GRAIN-FILLING RATE1 Increase the Grain-Filling Rate and Yield of Rice. <i>Plant Physiology</i> , 2019, 181, 1207-1222.	4.8	30



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2134	Marker-Trait Associations for Enhancing Agronomic Performance, Disease Resistance, and Grain Quality in Synthetic and Bread Wheat Accessions in Western Siberia. G3: Genes, Genomes, Genetics, 2019, 9, 4209-4222.	1.8	18
2135	Development of a Multiparent Population for Genetic Mapping and Allele Discovery in Six-Row Barley. Genetics, 2019, 213, 595-613.	2.9	23
2136	Training Population Optimization for Genomic Selection. Plant Genome, 2019, 12, 1-14.	2.8	49
2137	Genome-Wide Association Study of a Worldwide Collection of Wheat Genotypes Reveals Novel Quantitative Trait Loci for Leaf Rust Resistance. Plant Genome, 2019, 12, 1-14.	2.8	23
2138	A genetic characterization of Korean waxy maize (Zea mays L.) landraces having flowering time variation by RNA sequencing. Scientific Reports, 2019, 9, 20023.	3.3	1
2139	Dissection of Phenotypic and Genetic Variation of Drought-Related Traits in Diverse Chinese Wheat Landraces. Plant Genome, 2019, 12, 1-14.	2.8	44
2140	Genetic Basis of Fiber Improvement and Decreased Stress Tolerance in Cultivated Versus Semi-Domesticated Upland Cotton. Frontiers in Plant Science, 2019, 10, 1572.	3.6	11
2141	Genetic Diversity, Population Structure, and Linkage Disequilibrium of Pearl Millet. Plant Genome, 2019, 12, 1-12.	2.8	34
2142	Cataloguing of blast resistance genes in landraces and breeding lines of rice from India. Journal of Genetics, 2019, 98, 1.	0.7	4
2143	Genome-wide associated study identifies NAC42-activated nitrate transporter conferring high nitrogen use efficiency in rice. Nature Communications, 2019, 10, 5279.	12.8	153
2144	Genetic Diversity, Population Structure, and Marker-Trait Association for Drought Tolerance in US Rice Germplasm. Plants, 2019, 8, 530.	3.5	13
2145	Genetic analysis of resistance to bacterial leaf spot in the heirloom lettuce cultivar Reine des Glaces. Molecular Breeding, 2019, 39, 1.	2.1	11
2146	Assessing the potential for assisted gene flow using past introduction of Norway spruce in southern Sweden: Local adaptation and genetic basis of quantitative traits in trees. Evolutionary Applications, 2019, 12, 1946-1959.	3.1	36
2147	Organellar Genome Variation and Genetic Diversity of Chinese Pyropia yezoensis. Frontiers in Marine Science, 2019, 6, .	2.5	10
2148	Evaluating Selection of a Quantitative Trait: Snow Mold Tolerance in Winter Wheat. , 2019, 2, 1-8.		5
2149	SNP- and Haplotype-Based GWAS of Flowering-Related Traits in Maize with Network-Assisted Gene Prioritization. Agronomy, 2019, 9, 725.	3.0	13
2150	Increased individual homozygosity is correlated with low fitness in a fragmented lizard population. Biological Journal of the Linnean Society, 2019, 128, 952-962.	1.6	5
2151	ddRAD sequencing-based identification of inter-genepool SNPs and association analysis in Brassica juncea. BMC Plant Biology, 2019, 19, 594.	3.6	25



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2152	Genome-Wide Association Study for Squalene Contents and Functional Haplotype Analysis in Rice. ACS Omega, 2019, 4, 19358-19365.	3.5	5
2153	Genetic and biophysical modelling evidence of generational connectivity in the intensively exploited, Western North Atlantic red grouper ( <i>Epinephelus morio</i> ). ICES Journal of Marine Science, 2019, , .	2.5	0
2154	Genome-wide association analysis for maize stem Cell Wall-bound Hydroxycinnamates. BMC Plant Biology, 2019, 19, 519.	3.6	13
2155	Identification of QTN and Candidate Gene for Seed-flooding Tolerance in Soybean [ <i>Glycine max</i> (L.) Merr.] using Genome-Wide Association Study (GWAS). Genes, 2019, 10, 957.	2.4	32
2156	Detection of QTLs for outcrossing-related traits in rice ( <i>Oryza sativa</i> L.) by association mapping and the RSTEP-LRT method. Euphytica, 2019, 215, 1.	1.2	3
2157	Genome-Wide Association Study of Powdery Mildew Resistance in Russian Spring Wheat ( <i>T. aestivum</i> L.) Varieties. Russian Journal of Genetics, 2019, 55, 1360-1374.	0.6	6
2158	Genome-Wide Correlation of 36 Agronomic Traits in the 287 Pepper ( <i>Capsicum</i> ) Accessions Obtained from the SLAF-seq-Based GWAS. International Journal of Molecular Sciences, 2019, 20, 5675.	4.1	40
2159	Exome resequencing and GWAS for growth, ecophysiology, and chemical and metabolomic composition of wood of <i>Populus trichocarpa</i> . BMC Genomics, 2019, 20, 875.	2.8	19
2160	Identification of quantitative trait loci for increased $\gamma$ -tocopherol biosynthesis in wild soybean using a high-density genetic map. BMC Plant Biology, 2019, 19, 510.	3.6	18
2161	Understanding the Genetic Basis of Spike Fertility to Improve Grain Number, Harvest Index, and Grain Yield in Wheat Under High Temperature Stress Environments. Frontiers in Plant Science, 2019, 10, 1481.	3.6	37
2162	Haplotype Characterization of the <i>sd1</i> Semidwarf Gene in United States Rice. Plant Genome, 2019, 12, 190010.	2.8	16
2163	Genotyping-by-Sequencing of <i>Gossypium hirsutum</i> Races and Cultivars Uncovers Novel Patterns of Genetic Relationships and Domestication Footprints. Evolutionary Bioinformatics, 2019, 15, 117693431988994.	1.2	8
2164	Genome-wide association study of agronomic traits in bread wheat reveals novel putative alleles for future breeding programs. BMC Plant Biology, 2019, 19, 541.	3.6	77
2165	Phenotypic and molecular assessment of genetic structure and diversity in a panel of winged yam ( <i>Dioscorea alata</i> ) clones and cultivars. Scientific Reports, 2019, 9, 18221.	3.3	42
2166	Characterization and quantitative trait locus mapping of late-flowering from a Thai soybean cultivar introduced into a photoperiod-insensitive genetic background. PLoS ONE, 2019, 14, e0226116.	2.5	20
2167	Genomic Selection of Forage Quality Traits in Winter Wheat. Crop Science, 2019, 59, 2473-2483.	1.8	7
2168	Identification of genetic loci and candidate genes related to soybean flowering through genome wide association study. BMC Genomics, 2019, 20, 987.	2.8	15
2169	The <i>tin1</i> gene retains the function of promoting tillering in maize. Nature Communications, 2019, 10, 5608.	12.8	44

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2170	Multiple genes recruited from hormone pathways partition maize diterpenoid defences. <i>Nature Plants</i> , 2019, 5, 1043-1056.	9.3	60
2171	Improving grain yield, stress resilience and quality of bread wheat using large-scale genomics. <i>Nature Genetics</i> , 2019, 51, 1530-1539.	21.4	216
2172	Natural variation in ZmFBL41 confers banded leaf and sheath blight resistance in maize. <i>Nature Genetics</i> , 2019, 51, 1540-1548.	21.4	138
2173	Genome-wide association study (GWAS) for morphological and yield-related traits in an oil palm hybrid ( <i>Elaeis oleifera</i> x <i>Elaeis guineensis</i> ) population. <i>BMC Plant Biology</i> , 2019, 19, 533.	3.6	33
2174	A genome-wide association study reveals a genomic region associated with the carrot root shape. <i>Acta Horticulturae</i> , 2019, , 129-134.	0.2	0
2175	Determination of genomic regions associated with carrot response to salinity stress. <i>Acta Horticulturae</i> , 2019, , 205-210.	0.2	0
2176	The Complex Genetic Architecture of Early Root and Shoot Traits in Flax Revealed by Genome-Wide Association Analyses. <i>Frontiers in Plant Science</i> , 2019, 10, 1483.	3.6	24
2177	The combined use of raw and phylogenetically independent methods of outlier detection uncovers genome-wide dynamics of local adaptation in a lizard. <i>Ecology and Evolution</i> , 2019, 9, 14356-14367.	1.9	2
2178	Genome-Wide Association Mapping of Resistance to Septoria Nodorum Leaf Blotch in a Nordic Spring Wheat Collection. <i>Plant Genome</i> , 2019, 12, 180105.	2.8	22
2179	Developing Growth-Associated Molecular Markers Via High-Throughput Phenotyping in Spinach. <i>Plant Genome</i> , 2019, 12, 190027.	2.8	15
2180	Profiling SNP and Nucleotide Diversity to Characterize Mekong Delta Rice Landraces in Southeast Asian Populations. <i>Plant Genome</i> , 2019, 12, 190042.	2.8	6
2181	Genome-Wide Association Mapping and Gene Expression Analyses Reveal Genetic Mechanisms of Disease Resistance Variations in <i>Cynoglossus semilaevis</i> . <i>Frontiers in Genetics</i> , 2019, 10, 1167.	2.3	21
2182	Deployment of Lidar from a Ground Platform: Customizing a Low-Cost, Information-Rich and User-Friendly Application for Field Phenomics Research. <i>Sensors</i> , 2019, 19, 5358.	3.8	5
2183	Genome-wide association mapping of gene loci affecting disease resistance in the rice-Fusarium fujikuroi pathosystem. <i>Rice</i> , 2019, 12, 85.	4.0	11
2184	Intraspecific Variation within the <i>Utricularia amethystina</i> Species Morphotypes Based on Chloroplast Genomes. <i>International Journal of Molecular Sciences</i> , 2019, 20, 6130.	4.1	23
2185	Genome-Wide Association Studies of Protein, Lutein, Vitamin C, and Fructose Concentration in Wild and Cultivated Chickpea Seeds. <i>Crop Science</i> , 2019, 59, 2652-2666.	1.8	7
2186	Introgression of a High Protein Allele into an Elite Soybean Cultivar Results in a High-Protein Near-Isogenic Line with Yield Parity. <i>Crop Science</i> , 2019, 59, 2498-2508.	1.8	15
2187	Functional mutation allele mining of plant architecture and yield-related agronomic traits and characterization of their effects in wheat. <i>BMC Genetics</i> , 2019, 20, 102.	2.7	2

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2189	Resequencing core accessions of a pedigree identifies derivation of genomic segments and key agronomic trait loci during cotton improvement. Plant Biotechnology Journal, 2019, 17, 762-775.	8.3	40
2190	A <i>Ma10</i> gene encoding P-type ATPase is involved in fruit organic acid accumulation in apple. Plant Biotechnology Journal, 2019, 17, 674-686.	8.3	62
2191	Allele-specific analysis of single parent backcross population identifies HOX10 transcription factor as a candidate gene regulating rice root growth. Physiologia Plantarum, 2019, 166, 596-611.	5.2	8
2192	A Genome Wide Association Study Reveals Markers and Genes Associated with Resistance to <i>Fusarium verticillioides</i> Infection of Seedlings in a Maize Diversity Panel. G3: Genes, Genomes, Genetics, 2019, 9, 571-579.	1.8	34
2193	Whole-Genome Association Mapping and Genomic Prediction for Iron Concentration in Wheat Grains. International Journal of Molecular Sciences, 2019, 20, 76.	4.1	52
2194	High-density quantitative trait locus mapping revealed genetic architecture of leaf angle and tassel size in maize. Molecular Breeding, 2019, 39, 1.	2.1	10
2195	Genome-wide association analysis of salinity responsive traits in <i>Medicago truncatula</i> . Plant, Cell and Environment, 2019, 42, 1513-1531.	5.7	26
2196	High-throughput 3D modelling to dissect the genetic control of leaf elongation in barley ( <i>Hordeum vulgare</i> ). Plant Journal, 2019, 98, 555-570.	5.7	20
2197	A Benchmarking Between Deep Learning, Support Vector Machine and Bayesian Threshold Best Linear Unbiased Prediction for Predicting Ordinal Traits in Plant Breeding. G3: Genes, Genomes, Genetics, 2019, 9, 601-618.	1.8	95
2198	Resolving population structure and genetic differentiation associated with RAD-SNP loci under selection in tossa jute ( <i>Corchorus olitorius</i> L.). Molecular Genetics and Genomics, 2019, 294, 479-492.	2.1	20
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2200	Mapping loci controlling fatty acid profiles, oil and protein content by genome-wide association study in <i>Brassica napus</i> . Crop Journal, 2019, 7, 217-226.	5.2	19
2201	Genetic analysis of cob resistance to <i>F. verticillioides</i> : another step towards the protection of maize from ear rot. Theoretical and Applied Genetics, 2019, 132, 1049-1059.	3.6	15
2202	An assessment of true and false positive detection rates of stepwise epistatic model selection as a function of sample size and number of markers. Heredity, 2019, 122, 660-671.	2.6	18
2203	Expression polymorphism at the <i>ARPC4</i> locus links the actin cytoskeleton with quantitative disease resistance to <i>Sclerotinia sclerotiorum</i> in <i>Arabidopsis thaliana</i> . New Phytologist, 2019, 222, 480-496.	7.3	30
2204	Genetic and transcriptional variations in NRAMP-2 and OPAQUE1 genes are associated with salt stress response in wheat. Theoretical and Applied Genetics, 2019, 132, 323-346.	3.6	20
2205	Association Analysis of Three Diverse Rice ( <i>Oryza sativa</i> L.) Germplasm Collections for Loci Regulating Grain Quality Traits. Plant Genome, 2019, 12, 170085.	2.8	33

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2207	Characterization of Proteome Variation During Modern Maize Breeding*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 263-276.	3.8	36
2208	Association and genome analyses to propose putative candidate genes for malt quality traits. <i>Journal of the Science of Food and Agriculture</i> , 2019, 99, 2775-2785.	3.5	8
2209	Loci and candidate genes in soybean that confer resistance to <i>Fusarium graminearum</i> . <i>Theoretical and Applied Genetics</i> , 2019, 132, 431-441.	3.6	14
2210	QTLs for Resistance to <i>Fusarium</i> Ear Rot in a Multiparent Advanced Generation Intercross (MAGIC) Maize Population. <i>Plant Disease</i> , 2019, 103, 897-904.	1.4	37
2211	Genomic dissection of pod shattering in common bean: mutations at non-orthologous loci at the basis of convergent phenotypic evolution under domestication of leguminous species. <i>Plant Journal</i> , 2019, 97, 693-714.	5.7	54
2212	Molecular characterization of a diverse Iranian table grapevine germplasm using REMAP markers: population structure, linkage disequilibrium and association mapping of berry yield and quality traits. <i>Biologia (Poland)</i> , 2019, 74, 173-185.	1.5	3
2213	Metabolite profiling and genome-wide association studies reveal response mechanisms of phosphorus deficiency in maize seedling. <i>Plant Journal</i> , 2019, 97, 947-969.	5.7	79
2214	Assessment of genetic diversity in <i>Lepidium sativum</i> L. using inter simple sequence repeat (ISSR) marker. <i>Physiology and Molecular Biology of Plants</i> , 2019, 25, 399-406.	3.1	8
2215	Nucleotide polymorphisms associated with climate and physiological traits in silver fir ( <i>Abies alba</i> ) Tj ETQq1 1 0.784314 rgBT 6/Overlook	1.2	1
2216	Association mapping of ectomycorrhizal traits in loblolly pine ( <i>Pinus taeda</i> L.). <i>Molecular Ecology</i> , 2019, 28, 2088-2099.	3.9	6
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2218	QTL Mapping Identifies Novel Source of Resistance to <i>Fusarium</i> Wilt Race 1 in <i>Citrullus amarus</i> . <i>Plant Disease</i> , 2019, 103, 984-989.	1.4	16
2219	GmBRC1 is a Candidate Gene for Branching in Soybean ( <i>Glycine max</i> (L.) Merrill). <i>International Journal of Molecular Sciences</i> , 2019, 20, 135.	4.1	23
2220	TaARF4 genes are linked to root growth and plant height in wheat. <i>Annals of Botany</i> , 2019, 124, 903-915.	2.9	38
2221	Genome-wide Association Studies and Candidate Gene Identification for Leaf Scald and Net Blotch in Barley ( <i>Hordeum vulgare</i> L.). <i>Plant Disease</i> , 2019, 103, 880-889.	1.4	25
2222	Leaf morphology, rather than plant water status, underlies genetic variation of rice leaf rolling under drought. <i>Plant, Cell and Environment</i> , 2019, 42, 1532-1544.	5.7	67
2223	A cation diffusion facilitator, GmCDF1, negatively regulates salt tolerance in soybean. <i>PLoS Genetics</i> , 2019, 15, e1007798.	3.5	70

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2224	Deleterious Mutation Burden and Its Association with Complex Traits in Sorghum ( <i>Sorghum</i> ) Tj ETQq0 0 0 rgBT /Q Overlock 10 Tf 50 7	2.9	51
2225	Single Nucleotide Polymorphism-Based Haplotypes Associated with Charcoal Rot Resistance in Brazilian Soybean Germplasm. <i>Agronomy Journal</i> , 2019, 111, 182-192.	1.8	12
2226	Genetic dissection of grain morphology in hexaploid wheat by analysis of the NBRP-Wheat core collection. <i>Genes and Genetic Systems</i> , 2019, 94, 35-49.	0.7	8
2227	Evolutionary aspects of direct or indirect selection for seed size and seed metabolites in <i>Brassica juncea</i> and diploid progenitor species. <i>Molecular Biology Reports</i> , 2019, 46, 1227-1238.	2.3	11
2228	Genome-wide association mapping of stress-tolerance traits in cotton. <i>Crop Journal</i> , 2019, 7, 77-88.	5.2	26
2229	Identification of New Resistance Loci Against Sheath Blight Disease in Rice Through Genome-Wide Association Study. <i>Rice Science</i> , 2019, 26, 21-31.	3.9	31
2230	Imputation accuracy of wheat genotyping-by-sequencing (GBS) data using barley and wheat genome references. <i>PLoS ONE</i> , 2019, 14, e0208614.	2.5	48
2231	Genomic Selection Using Maize Exâ€Plant Variety Protection Germplasm for the Prediction of Nitrogenâ€Use Traits. <i>Crop Science</i> , 2019, 59, 212-220.	1.8	19
2232	Genetic Dissection of Grain Nutritional Traits and Leaf Blight Resistance in Rice. <i>Genes</i> , 2019, 10, 30.	2.4	26
2233	Construction of a high-density linkage map and QTL detection of downy mildew resistance in <i>Vitis aestivalis</i> -derived â€Nortonâ€™. <i>Theoretical and Applied Genetics</i> , 2019, 132, 137-147.	3.6	66
2234	Integrating genomic-enabled prediction and high-throughput phenotyping in breeding for climate-resilient bread wheat. <i>Theoretical and Applied Genetics</i> , 2019, 132, 177-194.	3.6	78
2235	Genetic diversity, linkage disequilibrium, and population structure in a panel of Brazilian rice accessions. <i>Journal of Applied Genetics</i> , 2019, 60, 27-31.	1.9	4
2236	Habitat discontinuities form strong barriers to gene flow among mangrove populations, despite the capacity for longâ€distance dispersal. <i>Diversity and Distributions</i> , 2019, 25, 298-309.	4.1	52
2237	Characterization of Select Wild Soybean Accessions in the USDA Germplasm Collection for Seed Composition and Agronomic Traits. <i>Crop Science</i> , 2019, 59, 233-251.	1.8	29
2238	Patterns of mutation within an emerging endemic lineage of <scp>HEV</scp>â€™a. <i>Journal of Viral Hepatitis</i> , 2019, 26, 191-198.	2.0	5
2239	Optimising the identification of causal variants across varying genetic architectures in crops. <i>Plant Biotechnology Journal</i> , 2019, 17, 893-905.	8.3	29
2240	Genotyping-by-sequencing based genetic mapping reveals large number of epistatic interactions for stem rot resistance in groundnut. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1001-1016.	3.6	42
2241	Kernel sizeâ€related genes revealed by an integrated <scp>eQTL</scp> analysis during early maize kernel development. <i>Plant Journal</i> , 2019, 98, 19-32.	5.7	34

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2243	Genetic diversity and population structure of synthetic hexaploid-derived wheat ( <i>Triticum aestivum</i> L.) accessions. <i>Genetic Resources and Crop Evolution</i> , 2019, 66, 335-348.	1.6	10
2244	Reference genome sequences of two cultivated allotetraploid cottons, <i>Gossypium hirsutum</i> and <i>Gossypium barbadense</i> . <i>Nature Genetics</i> , 2019, 51, 224-229.	21.4	468
2245	CWASpro: a high-performance genome-wide association analysis server. <i>Bioinformatics</i> , 2019, 35, 2512-2514.	4.1	18
2246	Genome-Wide Association and Genomic Prediction Models of Tocochromanols in Fresh Sweet Corn Kernels. <i>Plant Genome</i> , 2019, 12, 180038.	2.8	37
2247	Hybrid durum wheat: heterosis of grain yield and quality traits and genetic architecture of anther extrusion. <i>Theoretical and Applied Genetics</i> , 2019, 132, 921-932.	3.6	18
2248	Computational aspects underlying genome to phenome analysis in plants. <i>Plant Journal</i> , 2019, 97, 182-198.	5.7	50
2249	Whole genome sequencing of a MAGIC population identified genomic loci and candidate genes for major fiber quality traits in upland cotton ( <i>Gossypium hirsutum</i> L.). <i>Theoretical and Applied Genetics</i> , 2019, 132, 989-999.	3.6	43
2250	Genotyping-by-sequencing performance in selected livestock species. <i>Genomics</i> , 2019, 111, 186-195.	2.9	50
2251	Call of the wild rice: <i>Oryza rufipogon</i> shapes weedy rice evolution in Southeast Asia. <i>Evolutionary Applications</i> , 2019, 12, 93-104.	3.1	45
2252	Detection and validation of EST-SSR markers associated with sugar-related traits in sugarcane using linkage and association mapping. <i>Genomics</i> , 2019, 111, 1-9.	2.9	44
2253	Multiplex restriction amplicon sequencing: a novel next-generation sequencing-based marker platform for high-throughput genotyping. <i>Plant Biotechnology Journal</i> , 2020, 18, 254-265.	8.3	18
2254	Genome wide association study (GWAS) and identification of candidate genes for yield and oil yield related traits in oil palm ( <i>Eleaéis guineensis</i> ) using SNPs by genotyping-based sequencing. <i>Genomics</i> , 2020, 112, 1011-1020.	2.9	20
2255	Analysis of the genetic architecture of maize kernel size traits by combined linkage and association mapping. <i>Plant Biotechnology Journal</i> , 2020, 18, 207-221.	8.3	64
2256	Downregulation of three novel candidate genes is important for freezing tolerance of field and laboratory cold acclimated barley. <i>Journal of Plant Physiology</i> , 2020, 244, 153049.	3.5	9
2257	GPU empowered pipelines for calculating genome-wide kinship matrices with ultra-high dimensional genetic variants and facilitating 1D and 2D GWAS. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqz009.	3.2	2
2258	Characterization of genetic diversity and population structure in wheat using array based SNP markers. <i>Molecular Biology Reports</i> , 2020, 47, 293-306.	2.3	60
2259	Natural variation and selection in <i>GmSWEET39</i> affect soybean seed oil content. <i>New Phytologist</i> , 2020, 225, 1651-1666.	7.3	73



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2260	Regulatory changes in <i>TaSNAC8A</i> are associated with drought tolerance in wheat seedlings. <i>Plant Biotechnology Journal</i> , 2020, 18, 1078-1092.	8.3	73
2261	Mapping of the stem rust resistance gene <i>Pg13</i> in cultivated oat. <i>Theoretical and Applied Genetics</i> , 2020, 133, 259-270.	3.6	11
2262	A systematic dissection of the mechanisms underlying the natural variation of silique number in rapeseed ( <i>Brassica napus</i> L.) germplasm. <i>Plant Biotechnology Journal</i> , 2020, 18, 568-580.	8.3	26
2263	Genome assembly provides insights into the genome evolution and flowering regulation of orchardgrass. <i>Plant Biotechnology Journal</i> , 2020, 18, 373-388.	8.3	51
2264	Population Structure of the World Vegetable Center Mungbean Mini Core Collection and Genome-Wide Association Mapping of Loci Associated with Variation of Seed Coat Luster. <i>Tropical Plant Biology</i> , 2020, 13, 1-12.	1.9	31
2265	Genomic signatures of seed mass adaptation to global precipitation gradients in sorghum. <i>Heredity</i> , 2020, 124, 108-121.	2.6	28
2266	Association mapping of drought tolerance indices in wheat: QTL-rich regions on chromosome 4A. <i>Scientia Agricola</i> , 2020, 77, .	1.2	40
2267	Species-diagnostic SNP markers for the black basses ( <i>Micropterus</i> spp.): a new tool for black bass conservation and management. <i>Conservation Genetics Resources</i> , 2020, 12, 319-328.	0.8	12
2268	GWAS: Fast-forwarding gene identification and characterization in temperate Cereals: lessons from Barley – A review. <i>Journal of Advanced Research</i> , 2020, 22, 119-135.	9.5	227
2269	Genetic variation in <i>ZmTIP1</i> contributes to root hair elongation and drought tolerance in maize. <i>Plant Biotechnology Journal</i> , 2020, 18, 1271-1283.	8.3	85
2270	Whole-genome resequencing identifies quantitative trait loci associated with mycorrhizal colonization of soybean. <i>Theoretical and Applied Genetics</i> , 2020, 133, 409-417.	3.6	19
2271	Vacuolar invertase genes <i>SbVIN1</i> and <i>SbVIN2</i> are differently associated with stem and grain traits in sorghum ( <i>Sorghum bicolor</i> ). <i>Crop Journal</i> , 2020, 8, 299-312.	5.2	4
2272	Genome-wide association study for frost tolerance in rapeseed/canola ( <i>Brassica napus</i> ) under simulating freezing conditions. <i>Plant Breeding</i> , 2020, 139, 356-367.	1.9	11
2273	Improving Imputation Quality in BEAGLE for Crop and Livestock Data. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 177-188.	1.8	43
2274	Characterization of a repertoire of tomato fruit genetic variants in the San marzano genetic background. <i>Scientia Horticulturae</i> , 2020, 261, 108927.	3.6	12
2275	Genome-wide association study of vitamin E in sweet corn kernels. <i>Crop Journal</i> , 2020, 8, 341-350.	5.2	20
2276	Genome-wide association analysis for lethal brachycephalic-like facial dysmorphism in Labrador Retrievers. <i>Animal Genetics</i> , 2020, 51, 122-126.	1.7	0
2277	Genome-Wide Associations and Transcriptional Profiling Reveal ROS Regulation as One Underlying Mechanism of Sheath Blight Resistance in Rice. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 212-222.	2.6	24



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2279	Dietary interference on the oxidation and hydrolysis of liposomes during in vitro digestion. <i>International Journal of Food Science and Technology</i> , 2020, 55, 729-741.	2.7	3
2280	Genome-wide association mapping of QTLs implied in potato virus Y population sizes in pepper: evidence for widespread resistance QTL pyramiding. <i>Molecular Plant Pathology</i> , 2020, 21, 3-16.	4.2	17
2281	Pod indehiscence is a domestication and aridity resilience trait in common bean. <i>New Phytologist</i> , 2020, 225, 558-570.	7.3	57
2282	Linkage disequilibrium dissection of the epigenetic quantitative trait loci (epiQTLs) underlying growth and wood properties in <i>Populus</i> . <i>New Phytologist</i> , 2020, 225, 1218-1233.	7.3	25
2283	Genome-wide association study identifies QTLs conferring salt tolerance in rice. <i>Plant Breeding</i> , 2020, 139, 73-82.	1.9	19
2284	Genetic basis of kernel nutritional traits during maize domestication and improvement. <i>Plant Journal</i> , 2020, 101, 278-292.	5.7	25
2285	Association mapping of magnesium and manganese concentrations in the seeds of <i>C. arietinum</i> and <i>C. reticulatum</i> . <i>Genomics</i> , 2020, 112, 1633-1642.	2.9	5
2286	Association mapping of wheat Fusarium head blight resistance-related regions using a candidate-gene approach and their verification in a biparental population. <i>Theoretical and Applied Genetics</i> , 2020, 133, 341-351.	3.6	3
2287	Genome-wide association study in historical and contemporary U.S. winter wheats identifies height-reducing loci. <i>Crop Journal</i> , 2020, 8, 243-251.	5.2	8
2288	Large-scale GWAS in sorghum reveals common genetic control of grain size among cereals. <i>Plant Biotechnology Journal</i> , 2020, 18, 1093-1105.	8.3	72
2290	Variation of grain quality characters and marker-trait association in rice ( <i>Oryza sativa</i> L.). <i>Journal of Genetics</i> , 2020, 99, 1.	0.7	8
2291	Genetic dissection of yield-related traits via genome-wide association analysis across multiple environments in wild soybean ( <i>Glycine soja</i> Sieb. and Zucc.). <i>Planta</i> , 2020, 251, 39.	3.2	18
2292	Genome-wide association study identifies acyl-lipid metabolism candidate genes involved in the genetic control of natural variation for seed fatty acid traits in <i>Brassica napus</i> L.. <i>Industrial Crops and Products</i> , 2020, 145, 112080.	5.2	8
2293	Genetic architecture of polyphenol oxidase activity in wheat flour by genome-wide association study. <i>Crop Science</i> , 2020, 60, 1281-1293.	1.8	18
2294	Folate profile diversity and associated SNPs using genome wide association study in pea. <i>Euphytica</i> , 2020, 216, 1.	1.2	16
2295	Genetic characterization of cassava ( <i>Manihot esculenta</i> Crantz) genotypes using agro-morphological and single nucleotide polymorphism markers. <i>Physiology and Molecular Biology of Plants</i> , 2020, 26, 317-330.	3.1	14
2296	Screening of molecular markers associated to cold tolerance-related traits in <i>Citrus</i> . <i>Scientia Horticulturae</i> , 2020, 263, 109145.	3.6	8

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2297	Reuse of voucher specimens provides insights into the genomic associations and taxonomic value of wing colour and genitalic differences in a pest group (Lepidoptera: Tortricidae: Choristoneura ). Systematic Entomology, 2020, 45, 583-593.	3.9	2
2298	PAST: The Pathway Association Studies Tool to Infer Biological Meaning from GWAS Datasets. Plants, 2020, 9, 58.	3.5	17
2299	Natural variation of an EF-hand Ca <sup>2+</sup> -binding-protein coding gene confers saline-alkaline tolerance in maize. Nature Communications, 2020, 11, 186.	12.8	72
2300	Toward validation of QTLs associated with pod and seed size in common bean using two nested recombinant inbred line populations. Molecular Breeding, 2020, 40, 1.	2.1	8
2301	Genome-wide association mapping of flooding tolerance in soybean. Molecular Breeding, 2020, 40, 1.	2.1	25
2302	Genome-wide SNP discovery through genotyping by sequencing, population structure, and linkage disequilibrium in Brazilian peach breeding germplasm. Tree Genetics and Genomes, 2020, 16, 1.	1.6	15
2303	Transcriptome and GWAS analyses reveal candidate gene for seminal root length of maize seedlings under drought stress. Plant Science, 2020, 292, 110380.	3.6	81
2304	Preliminary identification of candidate genes associated with the peach fruit sorbitol content based on comparative transcriptome analysis. Scientia Horticulturae, 2020, 263, 109151.	3.6	6
2305	Identifying Vitamin E Biosynthesis Genes in <i>Elaeis guineensis</i> by Genome-Wide Association Study. Journal of Agricultural and Food Chemistry, 2020, 68, 678-685.	5.2	7
2306	Genome-wide association study reveals new genes involved in leaf trichome formation in polyploid oilseed rape ( <i>Brassica napus</i> L.). Plant, Cell and Environment, 2020, 43, 675-691.	5.7	28
2307	Genetic Analysis of QTL for Resistance to Maize Lethal Necrosis in Multiple Mapping Populations. Genes, 2020, 11, 32.	2.4	19
2308	High-density SNP-based genetic diversity and heterotic patterns of tropical maize breeding lines. Crop Science, 2020, 60, 779-787.	1.8	9
2309	Whole genome sequencing and novel candidate genes for CAKUT and altered nephrogenesis in the HSRA rat. Physiological Genomics, 2020, 52, 56-70.	2.3	5
2311	Genome-wide association study identifies an NLR gene that confers partial resistance to <i>Magnaporthe oryzae</i> in rice. Plant Biotechnology Journal, 2020, 18, 1376-1383.	8.3	35
2312	Single-marker and haplotype-based association analysis of anthracnose ( <i>Colletotrichum</i> ) in rice. Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 18	1.9	11
2313	Genetic components of root architecture and anatomy adjustments to water deficit stress in spring barley. Plant, Cell and Environment, 2020, 43, 692-711.	5.7	37
2314	Dissecting the genetics of cold tolerance in a multiparental maize population. Theoretical and Applied Genetics, 2020, 133, 503-516.	3.6	29
2315	Genetic architecture of subspecies divergence in trace mineral accumulation and elemental correlations in the rice grain. Theoretical and Applied Genetics, 2020, 133, 529-545.	3.6	38

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2316	Comparative phylogeography of mainland and insular species of Neotropical molossid bats ( <i>Molossus</i> ). <i>Ecology and Evolution</i> , 2020, 10, 389-409.	1.9	9
2317	Isolation and functional analysis of the zmARM4 locus in a novel maize ( <i>Zea mays</i> ) grain-filling mutant. <i>Plant Breeding</i> , 2020, 139, 217-226.	1.9	3
2318	Genotyping-by-sequencing and multilocation evaluation of two interspecific backcross populations identify QTLs for yield-related traits in pigeonpea. <i>Theoretical and Applied Genetics</i> , 2020, 133, 737-749.	3.6	18
2319	Favorable haplotypes and associated genes for flowering time and photoperiod sensitivity identified by comparative selective signature analysis and GWAS in temperate and tropical maize. <i>Crop Journal</i> , 2020, 8, 227-242.	5.2	6
2320	Genome-Wide Association Study Identifies Single Nucleotide Polymorphism Markers Associated with Mycelial Growth (at 15, 20, and 25°C), Mefenoxam Resistance, and Mating Type in <i>Phytophthora infestans</i> . <i>Phytopathology</i> , 2020, 110, 822-833.	2.2	8
2321	Combined GWAS and QTL analysis for dissecting the genetic architecture of kernel test weight in maize. <i>Molecular Genetics and Genomics</i> , 2020, 295, 409-420.	2.1	31
2322	Genetic dissection of zinc, iron, copper, manganese and phosphorus in wheat ( <i>Triticum aestivum</i> L.) grain and rachis at two developmental stages. <i>Plant Science</i> , 2020, 291, 110338.	3.6	55
2323	Association mapping for root system architecture traits under two nitrogen conditions in germplasm enhancement of maize doubled haploid lines. <i>Crop Journal</i> , 2020, 8, 213-226.	5.2	18
2324	Linkage Mapping for Foliar Necrosis of Soybean Sudden Death Syndrome. <i>Phytopathology</i> , 2020, 110, 907-915.	2.2	4
2325	New North American Isolates of <i>Venturia inaequalis</i> Can Overcome Apple Scab Resistance of <i>Malus floribunda</i> . <i>Plant Disease</i> , 2020, 104, 649-655.	1.4	32
2326	Effect-directed profiling and identification of bioactive metabolites from field, in vitro-grown and acclimatized <i>Musa</i> spp. accessions using high-performance thin-layer chromatography-mass spectrometry. <i>Journal of Chromatography A</i> , 2020, 1616, 460774.	3.7	9
2327	Detection of significant SNP associated with production and oil quality traits in interspecific oil palm hybrids using RARSeq. <i>Plant Science</i> , 2020, 291, 110366.	3.6	5
2328	Mapping of QTL for partial resistance to powdery mildew in two Chinese common wheat cultivars. <i>Euphytica</i> , 2020, 216, 1.	1.2	24
2329	Dissection of genetic architecture for glucosinolate accumulations in leaves and seeds of <i>Brassica napus</i> by genome-wide association study. <i>Plant Biotechnology Journal</i> , 2020, 18, 1472-1484.	8.3	47
2330	A targeted genotyping-by-sequencing tool (Rapture) for genomics-assisted breeding in oat. <i>Theoretical and Applied Genetics</i> , 2020, 133, 653-664.	3.6	10
2331	Genome-wide association study of differences in 14 agronomic traits under low- and high-density planting models based on the 660k SNP array for common wheat. <i>Plant Breeding</i> , 2020, 139, 272-283.	1.9	14
2332	Haplotype structure in commercial maize breeding programs in relation to key founder lines. <i>Theoretical and Applied Genetics</i> , 2020, 133, 547-561.	3.6	23
2333	Single nucleotide polymorphisms (SNPs) provide unprecedented resolution of species boundaries, phylogenetic relationships, and genetic diversity in the mastiff bats ( <i>Molossus</i> ). <i>Molecular Phylogenetics and Evolution</i> , 2020, 143, 106690.	2.7	36

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2334	Genome-wide association mapping for seed protein content in finger millet ( <i>Eleusine coracana</i> ) global collection through genotyping by sequencing. <i>Journal of Cereal Science</i> , 2020, 91, 102888.	3.7	25
2335	Candidate genes-association study to identify loci related to oleic acid in <i>Brassica napus</i> using SNP markers and their heterologous expression in yeast. <i>Plant Physiology and Biochemistry</i> , 2020, 146, 294-302.	5.8	6
2336	Genomic analysis for virulence determinants in feline herpesvirus type-1 isolates. <i>Virus Genes</i> , 2020, 56, 49-57.	1.6	7
2337	Genetic structure and biogeographic history of the Bicknell's Thrush/ Gray-cheeked Thrush species complex. <i>Auk</i> , 2020, 137, .	1.4	7
2338	Exome association analysis sheds light onto leaf rust ( <i>Puccinia triticina</i> ) resistance genes currently used in wheat breeding ( <i>Triticum aestivum</i> L.). <i>Plant Biotechnology Journal</i> , 2020, 18, 1396-1408.	8.3	13
2339	BnaMPK6 is a determinant of quantitative disease resistance against <i>Sclerotinia sclerotiorum</i> in oilseed rape. <i>Plant Science</i> , 2020, 291, 110362.	3.6	19
2340	A genome-wide association study uncovers consistent quantitative trait loci for resistance to <i>Verticillium</i> wilt and <i>Fusarium</i> wilt race 4 in the US Upland cotton. <i>Theoretical and Applied Genetics</i> , 2020, 133, 563-577.	3.6	57
2341	Effect of Divergent Selection for Intramuscular Fat Content on Muscle Lipid Metabolism in Chickens. <i>Animals</i> , 2020, 10, 4.	2.3	23
2342	Genome-Wide Analyses and Prediction of Resistance to MLN in Large Tropical Maize Germplasm. <i>Genes</i> , 2020, 11, 16.	2.4	34
2343	Genomic-wide association study for white spot resistance in a tropical maize germplasm. <i>Euphytica</i> , 2020, 216, 1.	1.2	6
2344	Habitat-Specific Clock Variation and Its Consequence on Reproductive Fitness. <i>Journal of Biological Rhythms</i> , 2020, 35, 134-144.	2.6	8
2345	Assessment of heterotic patterns of tropical low-nitrogen-tolerant maize ( <i>Zea mays</i> L.) inbred lines using testcross performance, morphological traits and SNP markers. <i>Plant Breeding</i> , 2020, 139, 1113-1124.	1.9	4
2346	Genome-wide dissection of hybridization for fiber quality and yield-related traits in upland cotton. <i>Plant Journal</i> , 2020, 104, 1285-1300.	5.7	9
2347	A combination of genome-wide association study and transcriptome analysis in leaf epidermis identifies candidate genes involved in cuticular wax biosynthesis in <i>Brassica napus</i> . <i>BMC Plant Biology</i> , 2020, 20, 458.	3.6	7
2348	Genetic characterization for lesion mimic and other traits in relation to spot blotch resistance in spring wheat. <i>PLoS ONE</i> , 2020, 15, e0240029.	2.5	4
2349	Genome-Wide Association Study Reveals Genomic Regions Associated With Ten Agronomical Traits in Wheat Under Late-Sown Conditions. <i>Frontiers in Plant Science</i> , 2020, 11, 549743.	3.6	16
2350	Genomic Analysis of Selected Maize Landraces from Sahel and Coastal West Africa Reveals Their Variability and Potential for Genetic Enhancement. <i>Genes</i> , 2020, 11, 1054.	2.4	5
2351	Diallelic Analysis of Tropical Maize Germplasm Response to Spontaneous Chromosomal Doubling. <i>Plants</i> , 2020, 9, 1224.	3.5	0

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2353	Voxel carving-based 3D reconstruction of sorghum identifies genetic determinants of light interception efficiency. Plant Direct, 2020, 4, e00255.	1.9	21
2354	Loci and candidate gene identification for soybean resistance to Phytophthora root rot race 1 in combination with association and linkage mapping. Molecular Breeding, 2020, 40, 1.	2.1	6
2355	Identification of hybridization and introgression between Cinnamomum kanehirae Hayata and C. camphora (L.) Presl using genotyping-by-sequencing. Scientific Reports, 2020, 10, 15995.	3.3	5
2356	Interspecific introgression and natural selection in the evolution of Japanese apricot ( <i>Prunus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 5	5.7	16
2357	Genetic dissection of eating and cooking qualities in different subpopulations of cultivated rice ( <i>Oryza sativa</i> L.) through association mapping. BMC Genetics, 2020, 21, 119.	2.7	7
2358	Identification of the First Oomycete Mating-type Locus Sequence in the Grapevine Downy Mildew Pathogen, <i>Plasmopara viticola</i> . Current Biology, 2020, 30, 3897-3907.e4.	3.9	23
2359	Genetic Diversity and Population Structure of Asian and European Common Wheat Accessions Based on Genotyping-By-Sequencing. Frontiers in Genetics, 2020, 11, 580782.	2.3	31
2360	Identification of loci and candidate gene GmSPX-RING1 responsible for phosphorus efficiency in soybean via genome-wide association analysis. BMC Genomics, 2020, 21, 725.	2.8	12
2361	Toward "Smart Canopy" Sorghum: Discovery of the Genetic Control of Leaf Angle Across Layers. Plant Physiology, 2020, 184, 1927-1940.	4.8	20
2362	Identification of miRNA-eQTLs in maize mature leaf by GWAS. BMC Genomics, 2020, 21, 689.	2.8	6
2363	Population structure analysis and identification of genomic regions under selection associated with low-nitrogen tolerance in tropical maize lines. PLoS ONE, 2020, 15, e0239900.	2.5	4
2364	Origin and adaptation to high altitude of Tibetan semi-wild wheat. Nature Communications, 2020, 11, 5085.	12.8	104
2365	Starch Metabolism in Wheat: Gene Variation and Association Analysis Reveal Additive Effects on Kernel Weight. Frontiers in Plant Science, 2020, 11, 562008.	3.6	5
2366	Genome-wide association study (GWAS) reveals genetic basis of ear-related traits in maize. Euphytica, 2020, 216, 1.	1.2	9
2367	Unlocking the relationships among population structure, plant architecture, growing season, and environmental adaptation in Henan wheat cultivars. BMC Plant Biology, 2020, 20, 469.	3.6	4
2368	Genome-Wide Association Study (GWAS) Analysis of Camelina Seedling Germination under Salt Stress Condition. Agronomy, 2020, 10, 1444.	3.0	16
2369	Genetic structure and diversity of Iranian Cannabis populations based on phytochemical, agro-morphological and molecular markers. Industrial Crops and Products, 2020, 158, 112950.	5.2	12

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2371	Genome-wide association mapping for wheat blast resistance in CIMMYT's international screening nurseries evaluated in Bolivia and Bangladesh. <i>Scientific Reports</i> , 2020, 10, 15972.	3.3	27
2372	The Genetic Architecture of Emerging Fungicide Resistance in Populations of a Global Wheat Pathogen. <i>Genome Biology and Evolution</i> , 2020, 12, 2231-2244.	2.5	29
2373	High-Resolution Genome-wide Association Study Identifies Genomic Regions and Candidate Genes for Important Agronomic Traits in Wheat. <i>Molecular Plant</i> , 2020, 13, 1311-1327.	8.3	130
2374	Unraveling waterlogging tolerance-related traits with QTL analysis in reciprocal intervarietal introgression lines using genotyping by sequencing in rapeseed ( <i>Brassica napus</i> L.). <i>Journal of Integrative Agriculture</i> , 2020, 19, 1974-1983.	3.5	12
2375	Divergence of defensive cucurbitacins in independent <i>Cucurbita pepo</i> domestication events leads to differences in specialist herbivore preference. <i>Plant, Cell and Environment</i> , 2020, 43, 2812-2825.	5.7	16
2376	Genetic diversity among early provitamin A quality protein maize inbred lines and the performance of derived hybrids under contrasting nitrogen environments. <i>BMC Genetics</i> , 2020, 21, 78.	2.7	13
2377	Genome-wide analysis and prediction of Fusarium head blight resistance in soft red winter wheat. <i>Crop Science</i> , 2020, 60, 2882-2900.	1.8	24
2378	Association mapping and genomic prediction for ear rot disease caused by <i>Fusarium verticillioides</i> in a tropical maize germplasm. <i>Crop Science</i> , 2020, 60, 2867-2881.	1.8	8
2379	Identification of loci controlling phenology, fruit quality and post-harvest quantitative parameters in Japanese plum ( <i>Prunus salicina</i> Lindl.). <i>Postharvest Biology and Technology</i> , 2020, 169, 111292.	6.0	14
2380	Genome-wide mapping and allelic fingerprinting provide insights into the genetics of resistance to wheat stripe rust in India, Kenya and Mexico. <i>Scientific Reports</i> , 2020, 10, 10908.	3.3	8
2381	Combined GWAS and eQTL analysis uncovers a genetic regulatory network orchestrating the initiation of secondary cell wall development in cotton. <i>New Phytologist</i> , 2020, 226, 1738-1752.	7.3	74
2382	Phenotypic and genetic variation in phosphorus-deficiency-tolerance traits in Chinese wheat landraces. <i>BMC Plant Biology</i> , 2020, 20, 330.	3.6	19
2383	Identification of candidate tolerance genes to low-temperature during maize germination by GWAS and RNA-seq approaches. <i>BMC Plant Biology</i> , 2020, 20, 333.	3.6	53
2384	The improved FASTmrEMMA and GCIM algorithms for genome-wide association and linkage studies in large mapping populations. <i>Crop Journal</i> , 2020, 8, 723-732.	5.2	10
2385	The accuracy of different strategies for building training sets for genomic predictions in segregating soybean populations. <i>Crop Science</i> , 2020, 60, 3115-3126.	1.8	7
2386	Molecular characterization of popular rice ( <i>Oryza sativa</i> L.) varieties of India and association analysis for blast resistance. <i>Genetic Resources and Crop Evolution</i> , 2020, 67, 2225-2236.	1.6	2
2387	Identification of molecular markers for starch content in barley ( <i>Hordeum vulgare</i> L.) by genome-wide association studies based on bulked samples. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2020, 18, 111-119.	0.8	1



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2389	Genome-wide association study and genomic selection for tolerance of soybean biomass to soybean cyst nematode infestation. PLoS ONE, 2020, 15, e0235089.	2.5	28
2390	QTL identification for salt tolerance related traits at the seedling stage in indica rice using a multi-parent advanced generation intercross (MAGIC) population. Plant Growth Regulation, 2020, 92, 365-373.	3.4	14
2391	Genome-wide association study of shank length and diameter at different developmental stages in chicken F2 resource population. Animal Genetics, 2020, 51, 722-730.	1.7	12
2392	Identification of QTNs Controlling 100-Seed Weight in Soybean Using Multilocus Genome-Wide Association Studies. Frontiers in Genetics, 2020, 11, 689.	2.3	26
2393	A durum wheat adult plant stripe rust resistance QTL and its relationship with the bread wheat Yr80 locus. Theoretical and Applied Genetics, 2020, 133, 3049-3066.	3.6	10
2394	Historic recombination in a durum wheat breeding panel enables high-resolution mapping of Fusarium head blight resistance quantitative trait loci. Scientific Reports, 2020, 10, 7567.	3.3	12
2395	Whole genome resequencing of four Italian sweet pepper landraces provides insights on sequence variation in genes of agronomic value. Scientific Reports, 2020, 10, 9189.	3.3	18
2396	Characterizing the impact of an exotic soybean line on elite cultivar development. PLoS ONE, 2020, 15, e0235434.	2.5	1
2397	Four genetic loci control compact plant size with yellow pear-shaped fruit in ornamental tomato ( <i>Solanum lycopersicum</i> L.). Plant Genome, 2020, 13, e20017.	2.8	9
2398	Genome-wide lncRNAs identification and association analysis for cold-responsive genes at the booting stage in rice ( <i>Oryza sativa</i> L.). Plant Genome, 2020, 13, e20020.	2.8	12
2399	Investigation of Heat-Induced Changes in the Grain Yield and Grains Metabolites, with Molecular Insights on the Candidate Genes in Barley. Agronomy, 2020, 10, 1730.	3.0	24
2400	simplePHENOTYPES: SIMulation of pleiotropic, linked and epistatic phenotypes. BMC Bioinformatics, 2020, 21, 491.	2.6	11
2401	Multiple Loci Control Variation in Plasticity to Foliar Shade Throughout Development in <i>Arabidopsis thaliana</i> . G3: Genes, Genomes, Genetics, 2020, 10, 4103-4114.	1.8	1
2402	Genetic Diversity, Population Structure, and Andean Introgression in Brazilian Common Bean Cultivars after Half a Century of Genetic Breeding. Genes, 2020, 11, 1298.	2.4	20
2403	Natural variation of physiological traits, molecular markers, and chlorophyll catabolic genes associated with heat tolerance in perennial ryegrass accessions. BMC Plant Biology, 2020, 20, 520.	3.6	17
2404	Identification and Validation of New Stable QTLs for Grain Weight and Size by Multiple Mapping Models in Common Wheat. Frontiers in Genetics, 2020, 11, 584859.	2.3	8
2405	Genetic Dissection of Resistance to Gray Leaf Spot by Combining Genome-Wide Association, Linkage Mapping, and Genomic Prediction in Tropical Maize Germplasm. Frontiers in Plant Science, 2020, 11, 572027.	3.6	20

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2407	Detection of QTL and QTN and candidate genes for oil content in soybean using a combination of four-way-RIL and germplasm populations. <i>Crop Journal</i> , 2020, 8, 802-811.	5.2	7
2408	Population structure of Nepali spring wheat ( <i>Triticum aestivum</i> L.) germplasm. <i>BMC Plant Biology</i> , 2020, 20, 530.	3.6	9
2409	Natural Sequence Variations and Combinations of GNP1 and NAL1 Determine the Grain Number per Panicle in Rice. <i>Rice</i> , 2020, 13, 14.	4.0	21
2410	Identification of QTLs/Defense Genes Effective at Seedling Stage Against Prevailing Races of Wheat Stripe Rust in India. <i>Frontiers in Genetics</i> , 2020, 11, 572975.	2.3	17
2411	Exploration of genetic structure and association mapping for fibre quality traits in global flax ( <i>Linum</i> ) Tj ETQq1 1 0.784314 rgBT /Overl	2.3	6
2412	Genome-wide association analysis of the strength of the MAMP-elicited defense response and resistance to target leaf spot in sorghum. <i>Scientific Reports</i> , 2020, 10, 20817.	3.3	12
2413	Genome-wide association analysis of sucrose concentration in soybean ( <i>Glycine max</i> L.) seed based on high-throughput sequencing. <i>Plant Genome</i> , 2020, 13, e20059.	2.8	15
2414	European landrace diversity for common bean biofortification: a genome-wide association study. <i>Scientific Reports</i> , 2020, 10, 19775.	3.3	21
2415	Genome-Wide Association Analysis Identified BMPRI1A as a Novel Candidate Gene Affecting the Number of Thoracic Vertebrae in a Large White × Minzhu Intercross Pig Population. <i>Animals</i> , 2020, 10, 2186.	2.3	13
2416	Genome-Wide Association Analysis Identifies Resistance Loci for Bacterial Leaf Streak Resistance in Rice ( <i>Oryza sativa</i> L.). <i>Plants</i> , 2020, 9, 1673.	3.5	14
2417	Identification and diversity of tropical maize inbred lines with resistance to common rust ( <i>Puccinia sorghi</i> Schwein). <i>Crop Science</i> , 2020, 60, 2971-2989.	1.8	8
2418	Genomic Regions Associated with the Control of Flowering Time in Durum Wheat. <i>Plants</i> , 2020, 9, 1628.	3.5	15
2419	Genome-wide association studies and whole-genome prediction reveal the genetic architecture of KRN in maize. <i>BMC Plant Biology</i> , 2020, 20, 490.	3.6	14
2420	Study of plant height as a dynamic trait by multistage phenotyping in chickpea under heat stress identifies common as well as stage specific marker-trait associations. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2020, 18, 330-333.	0.8	1
2421	Genome-Wide Association Studies Detect Multiple QTLs for Productivity in Mesoamerican Diversity Panel of Common Bean Under Drought Stress. <i>Frontiers in Plant Science</i> , 2020, 11, 574674.	3.6	24
2422	Identification of New Leaf Rust Resistance Loci in Wheat and Wild Relatives by Array-Based SNP Genotyping and Association Genetics. <i>Frontiers in Plant Science</i> , 2020, 11, 583738.	3.6	29
2423	Genome-wide association studies of Ca and Mn in the seeds of the common bean ( <i>Phaseolus vulgaris</i> ) Tj ETQq1 1 0.784314 rgBT /Overl	2.9	12

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2424	Multi-locus genome-wide association studies reveal novel genomic regions associated with vegetative stage salt tolerance in bread wheat ( <i>Triticum aestivum</i> L.). <i>Genomics</i> , 2020, 112, 4608-4621.	2.9	32
2425	The casein kinase 2 $\beta$ subunit CK2B1 is required for swollen stem formation via cell cycle control in vegetable <i>Brassica juncea</i> . <i>Plant Journal</i> , 2020, 104, 706-717.	5.7	16
2426	Dissection of identical-by-descent segments during the formation of foundation parents derived from Suwan germplasm of maize. <i>Plant Breeding</i> , 2020, 139, 862-869.	1.9	1
2427	Stable SNP Allele Associations With High Grain Zinc Content in Polished Rice ( <i>Oryza sativa</i> L.) Identified Based on ddRAD Sequencing. <i>Frontiers in Genetics</i> , 2020, 11, 763.	2.3	11
2428	Identifying inbred lines with resistance to endemic diseases in exotic maize germplasm. <i>Crop Science</i> , 2020, 60, 3141-3150.	1.8	5
2429	Genome-wide association mapping reveals novel genes associated with coleoptile length in a worldwide collection of barley. <i>BMC Plant Biology</i> , 2020, 20, 346.	3.6	12
2430	Genetic diversity and population structure analysis of chickpea ( <i>Cicer arietinum</i> L.) advanced breeding lines using whole-genome DArTseq-generated SilicoDART markers. <i>Revista Brasileira De Botanica</i> , 2020, 43, 541-549.	1.3	6
2431	Identification of resistance loci in Chinese and Canadian canola/rapeseed varieties against <i>Leptosphaeria maculans</i> based on genome-wide association studies. <i>BMC Genomics</i> , 2020, 21, 501.	2.8	17
2432	Marker-Trait Association Analysis of Seed Traits in Accessions of Common Bean ( <i>Phaseolus vulgaris</i> L.) in China. <i>Frontiers in Genetics</i> , 2020, 11, 698.	2.3	15
2433	Identification of Ear Morphology Genes in Maize ( <i>Zea mays</i> L.) Using Selective Sweeps and Association Mapping. <i>Frontiers in Genetics</i> , 2020, 11, 747.	2.3	10
2434	The Frequency of Sex: Population Genomics Reveals Differences in Recombination and Population Structure of the Aflatoxin-Producing Fungus <i>Aspergillus flavus</i> . <i>MBio</i> , 2020, 11, .	4.1	27
2435	Genome-wide prediction in a hybrid maize population adapted to Northwest China. <i>Crop Journal</i> , 2020, 8, 830-842.	5.2	14
2436	A cost-effective barcode system for maize genetic discrimination based on bi-allelic InDel markers. <i>Plant Methods</i> , 2020, 16, 101.	4.3	3
2437	Genome-Wide Association Study Using Individual Single-Nucleotide Polymorphisms and Haplotypes for Erythrocyte Traits in Alpine Merino Sheep. <i>Frontiers in Genetics</i> , 2020, 11, 848.	2.3	7
2438	Allopatric instead of parapatric divergence in an ectomycorrhizal fungus ( <i>Laccaria</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Jf 50 182 Jd (trichoderm)	1.6	2
2439	Genetic analysis of QTLs controlling allelopathic characteristics in sorghum. <i>PLoS ONE</i> , 2020, 15, e0235896.	2.5	12
2440	Genome-wide association study of turnip mosaic virus resistance in non-heading Chinese cabbage. <i>3 Biotech</i> , 2020, 10, 363.	2.2	5
2441	Association of microsatellite markers with growth and wood mechanical traits in <i>Eucalyptus cloeziana</i> F. Muell. ( <i>Myrtaceae</i> ). <i>Industrial Crops and Products</i> , 2020, 154, 112702.	5.2	3

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2442	Insights into the Genetic Architecture of Bran Friability and Water Retention Capacity, Two Important Traits for Whole Grain End-Use Quality in Winter Wheat. <i>Genes</i> , 2020, 11, 838.	2.4	3
2443	Genetic dissection of bread wheat diversity and identification of adaptive loci in response to elevated tropospheric ozone. <i>Plant, Cell and Environment</i> , 2020, 43, 2650-2665.	5.7	26
2444	Genomic diversity in pearl millet inbred lines derived from landraces and improved varieties. <i>BMC Genomics</i> , 2020, 21, 469.	2.8	12
2445	Temporal Variation in Genetic Composition of Migratory <i>Helicoverpa Zea</i> in Peripheral Populations. <i>Insects</i> , 2020, 11, 463.	2.2	6
2446	A single- $\epsilon$ population GWAS identified <i>AtMATE</i> expression level polymorphism caused by promoter variants is associated with variation in aluminum tolerance in a local <i>Arabidopsis</i> population. <i>Plant Direct</i> , 2020, 4, e00250.	1.9	14
2447	Molecular mapping of QTLs for yield related traits in recombinant inbred line (RIL) population derived from the popular rice hybrid KRH-2 and their validation through SNP genotyping. <i>Scientific Reports</i> , 2020, 10, 13695.	3.3	27
2448	Uncovering Candidate Genes Controlling Major Fruit-Related Traits in Pepper via Genotype-by-Sequencing Based QTL Mapping and Genome-Wide Association Study. <i>Frontiers in Plant Science</i> , 2020, 11, 1100.	3.6	24
2449	Association Mapping and Development of Marker-Assisted Selection Tools for the Resistance to White Pine Blister Rust in the Alberta Limber Pine Populations. <i>Frontiers in Plant Science</i> , 2020, 11, 557672.	3.6	5
2450	Multi-Trait Genomic Prediction of Yield-Related Traits in US Soft Wheat under Variable Water Regimes. <i>Genes</i> , 2020, 11, 1270.	2.4	26
2451	Genome-wide association for $\beta^2$ -glucan content, population structure, and linkage disequilibrium in elite oat germplasm adapted to subtropical environments. <i>Molecular Breeding</i> , 2020, 40, 1.	2.1	14
2452	Evolutionary and functional genomics of DNA methylation in maize domestication and improvement. <i>Nature Communications</i> , 2020, 11, 5539.	12.8	59
2453	Genetic dissection of 2-heptenal content in soybean ( <i>Glycine max</i> ) seed through genome-wide association study. <i>Crop and Pasture Science</i> , 2020, 71, 884.	1.5	2
2454	Transgressive segregation and gene regions controlling thermotolerance of fruit set and pollen germination in <i>Capsicum chinense</i> . <i>Euphytica</i> , 2020, 216, 1.	1.2	1
2455	The genotype-dependent phenotypic landscape of quinoa in salt tolerance and key growth traits. <i>DNA Research</i> , 2020, 27, .	3.4	15
2456	Genome-wide association study of leaf rust resistance in Russian spring wheat varieties. <i>BMC Plant Biology</i> , 2020, 20, 135.	3.6	17
2457	Genomic Prediction and Selection for Fruit Traits in Winter Squash. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3601-3610.	1.8	15
2458	In-depth genetic analysis reveals conditioning of polyphenol oxidase activity in wheat grains by cis regulation of TaPPO2A-1 expression level. <i>Genomics</i> , 2020, 112, 4690-4700.	2.9	10
2459	Association mapping identifies quantitative trait loci (QTL) for digestibility in rice straw. <i>Biotechnology for Biofuels</i> , 2020, 13, 165.	6.2	7

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2460	Host-symbiont coevolution, cryptic structure, and bleaching susceptibility, in a coral species complex (Scleractinia; Poritidae). Scientific Reports, 2020, 10, 16995.	3.3	33
2461	Genome-wide association mapping revealed numerous novel genomic loci for grain nutritional and yield-related traits in rice ( <i>Oryza sativa</i> L.) landraces. 3 Biotech, 2020, 10, 487.	2.2	11
2462	Formation and diversification of a paradigm biosynthetic gene cluster in plants. Nature Communications, 2020, 11, 5354.	12.8	50
2463	Candidate gene mapping identifies genomic variations in the fire blight susceptibility genes HIPM and DIPM across the <i>Malus</i> germplasm. Scientific Reports, 2020, 10, 16317.	3.3	10
2464	Subspecies Variation of <i>Daucus carota</i> Coastal (‘Gummifer’) Morphotypes (Apiaceae) Using Genotyping-by-Sequencing. Systematic Botany, 2020, 45, 688-702.	0.5	4
2465	Development of SSR markers and association studies of markers with phenology and yield-related traits in grass pea ( <i>Lathyrus sativus</i> ). Crop and Pasture Science, 2020, 71, 768.	1.5	6
2466	Identification of quantitative trait nucleotides and candidate genes for soybean seed weight by multiple models of genome-wide association study. BMC Plant Biology, 2020, 20, 404.	3.6	28
2467	Genome-wide association studies of fruit quality traits in jujube germplasm collections using genotyping-by-sequencing. Plant Genome, 2020, 13, e20036.	2.8	14
2468	Retrospective Quantitative Genetic Analysis and Genomic Prediction of Global Wheat Yields. Frontiers in Plant Science, 2020, 11, 580136.	3.6	7
2469	Combined Analyses of Phenotype, Genotype and Climate Implicate Local Adaptation as a Driver of Diversity in <i>Eucalyptus microcarpa</i> (Grey Box). Forests, 2020, 11, 495.	2.1	6
2470	Genome-wide association study for phosphate deficiency responsive root hair elongation in chickpea. Functional and Integrative Genomics, 2020, 20, 775-786.	3.5	15
2471	Association analysis between agronomic traits and AFLP markers in a wide germplasm of proso millet ( <i>Panicum miliaceum</i> L.) under normal and salinity stress conditions. BMC Plant Biology, 2020, 20, 427.	3.6	7
2472	Use of a <i>Plasmodium vivax</i> genetic barcode for genomic surveillance and parasite tracking in Sri Lanka. Malaria Journal, 2020, 19, 342.	2.3	6
2473	Mapping a Partial Andromonoecy Locus in <i>Citrullus lanatus</i> Using BSA-Seq and GWAS Approaches. Frontiers in Plant Science, 2020, 11, 1243.	3.6	15
2474	Population Structure and Genetic Diversity in Korean Cowpea Germplasm Based on SNP Markers. Plants, 2020, 9, 1190.	3.5	15
2475	A high-density SNP-based linkage map using genotyping-by-sequencing and its utilization for improved genome assembly of chickpea ( <i>Cicer arietinum</i> L.). Functional and Integrative Genomics, 2020, 20, 763-773.	3.5	6
2476	Comparisons of sampling methods for assessing intra- and inter-accession genetic diversity in three rice species using genotyping by sequencing. Scientific Reports, 2020, 10, 13995.	3.3	13
2477	Assessing the genetic diversity of cowpea [ <i>Vigna unguiculata</i> (L.) Walp.] germplasm collections using phenotypic traits and SNP markers. BMC Genetics, 2020, 21, 110.	2.7	32

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2478	Genetic Characterization of Russian Rapeseed Collection and Association Mapping of Novel Loci Affecting Glucosinolate Content. <i>Genes</i> , 2020, 11, 926.	2.4	4
2479	Extensive haplotypes are associated with population differentiation and environmental adaptability in Upland cotton ( <i>Gossypium hirsutum</i> ). <i>Theoretical and Applied Genetics</i> , 2020, 133, 3273-3285.	3.6	15
2480	Natural variation and genomic prediction of growth, physiological traits, and nitrogen-use efficiency in perennial ryegrass under low-nitrogen stress. <i>Journal of Experimental Botany</i> , 2020, 71, 6670-6683.	4.8	9
2481	Genomic islands of divergence infer a phenotypic landscape in Pacific lamprey. <i>Molecular Ecology</i> , 2020, 29, 3841-3856.	3.9	26
2482	Efficiencies of Heterotic Grouping Methods for Classifying Early Maturing Maize Inbred Lines. <i>Agronomy</i> , 2020, 10, 1198.	3.0	15
2483	Marker association study of yield attributing traits in common bean ( <i>Phaseolus vulgaris</i> L.). <i>Molecular Biology Reports</i> , 2020, 47, 6769-6783.	2.3	14
2484	The climatic association of population divergence and future extinction risk of <i>Solanum pimpinellifolium</i> . <i>AoB PLANTS</i> , 2020, 12, plaa012.	2.3	9
2485	Optimization of the genotyping-by-sequencing SNP calling for diversity analysis in cape gooseberry ( <i>Physalis peruviana</i> L.) and related taxa. <i>PLoS ONE</i> , 2020, 15, e0238383.	2.5	5
2486	Narrow genetic base shapes population structure and linkage disequilibrium in an industrial oilseed crop, <i>Brassica carinata</i> A. Braun. <i>Scientific Reports</i> , 2020, 10, 12629.	3.3	13
2487	What is truth: Consensus and discordance in next-generation phylogenetic analyses of <i>Daucus</i> . <i>Journal of Systematics and Evolution</i> , 2020, 58, 1059-1070.	3.1	11
2488	Selection Signatures Analysis Reveals Genes Associated with High-Altitude Adaptation in Tibetan Goats from Nagqu, Tibet. <i>Animals</i> , 2020, 10, 1599.	2.3	21
2489	Genome-wide association study of resistance to Mal de R� Cuarto disease in maize. <i>Agronomy Journal</i> , 2020, 112, 4624-4633.	1.8	3
2490	SNP discovery for genetic diversity and population structure analysis coupled with restriction-associated DNA (RAD) sequencing in walnut cultivars of Sichuan Province, China. <i>Biotechnology and Biotechnological Equipment</i> , 2020, 34, 652-664.	1.3	9
2491	Association of molecular markers with physio-biochemical traits related to seed vigour in rice. <i>Physiology and Molecular Biology of Plants</i> , 2020, 26, 1989-2003.	3.1	14
2492	Genome Wide Association Studies in Multiple Spinach Breeding Populations Refine Downy Mildew Race 13 Resistance Genes. <i>Frontiers in Plant Science</i> , 2020, 11, 563187.	3.6	23
2493	Genomic Selection for Grain Yield in the CIMMYT Wheat Breeding Program��Status and Perspectives. <i>Frontiers in Plant Science</i> , 2020, 11, 564183.	3.6	27
2494	Maximum <i>a posteriori</i> Threshold Genomic Prediction Model for Ordinal Traits. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 4083-4102.	1.8	4
2495	Genome-wide association mapping and comparative genomics identifies genomic regions governing grain nutritional traits in finger millet ( <i>Eleusine coracana</i> L. Gaertn.). <i>Plants People Planet</i> , 2020, 2, 649-662.	3.3	50



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2497	Genomic variation among populations provides insight into the causes of metacommunity survival. <i>Ecology</i> , 2020, 101, e03182.	3.2	5
2498	Association Mapping of Seed Quality Traits Under Varying Conditions of Nitrogen Application in <i>Brassica juncea</i> L. Czern & Coss. <i>Frontiers in Genetics</i> , 2020, 11, 744.	2.3	16
2499	Identification of Loci and Candidate Genes Analyses for Tocopherol Concentration of Soybean Seed. <i>Frontiers in Plant Science</i> , 2020, 11, 539460.	3.6	19
2500	Genetic architecture of agronomic and quality traits in a nested association mapping population of spring wheat. <i>Plant Genome</i> , 2020, 13, e20051.	2.8	11
2501	Genome-Wide Association Study and Identification of Candidate Genes for Nitrogen Use Efficiency in Barley ( <i>Hordeum vulgare</i> L.). <i>Frontiers in Plant Science</i> , 2020, 11, 571912.	3.6	23
2502	A Narrow Endemic or a Species Showing Disjunct Distribution? Studies on <i>Meehania montis-koyae</i> Ohwi (Lamiaceae). <i>Plants</i> , 2020, 9, 1159.	3.5	4
2503	A Deep Learning-Based System (Microscan) for the Identification of Pollen Development Stages and Its Application to Obtaining Doubled Haploid Lines in Eggplant. <i>Biology</i> , 2020, 9, 272.	2.8	4
2504	CC-NBS-LRR, a set of VvCRP markers, can distinguish cultivars with ripe rot resistance to <i>Colletotrichum</i> pathogens in grapevine. <i>Horticulture Environment and Biotechnology</i> , 2020, 61, 915-927.	2.1	5
2505	Identification of SNPs and InDels associated with berry size in table grapes integrating genetic and transcriptomic approaches. <i>BMC Plant Biology</i> , 2020, 20, 365.	3.6	18
2506	Evaluation of variant calling tools for large plant genome re-sequencing. <i>BMC Bioinformatics</i> , 2020, 21, 360.	2.6	27
2507	A transcriptomic variation map provides insights into the genetic basis of <i>Pinus massoniana</i> Lamb. evolution and the association with oleoresin yield. <i>BMC Plant Biology</i> , 2020, 20, 375.	3.6	9
2508	Population genomic and genome-wide association analysis of lignin content in a global collection of 206 forage sorghum accessions. <i>Molecular Breeding</i> , 2020, 40, 1.	2.1	10
2509	The Multisite <i>PeachRefPop</i> Collection: A True Cultural Heritage and International Scientific Tool for Fruit Trees. <i>Plant Physiology</i> , 2020, 184, 632-646.	4.8	12
2510	The Dawn of the Age of Multi-Parent MAGIC Populations in Plant Breeding: Novel Powerful Next-Generation Resources for Genetic Analysis and Selection of Recombinant Elite Material. <i>Biology</i> , 2020, 9, 229.	2.8	31
2511	Genome-wide association study of resistance to anthracnose and angular leaf spot in Brazilian Mesoamerican and Andean common bean cultivars. <i>Crop Science</i> , 2020, 60, 2931-2950.	1.8	14
2512	Mining of candidate genes for nitrogen use efficiency in maize based on genome-wide association study. <i>Molecular Breeding</i> , 2020, 40, 1.	2.1	8
2513	Genome-Wide Association Mapping for Stripe Rust Resistance in Pakistani Spring Wheat Genotypes. <i>Plants</i> , 2020, 9, 1056.	3.5	11

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2514	Association mapping of several nut characters in walnut ( <i>Juglans regia</i> L.). <i>Türk Tarım Ve Ormancılık Dergisi/Turkish Journal of Agriculture and Forestry</i> , 2020, 44, 208-227.	2.1	6
2515	Comparative assessment of genetic diversity matrices and clustering methods in white Guinea yam ( <i>Dioscorea rotundata</i> ) based on morphological and molecular markers. <i>Scientific Reports</i> , 2020, 10, 13191.	3.3	32
2516	Genome-wide association analysis of resistance to <i>Pythium ultimum</i> in common bean ( <i>Phaseolus</i> ). <i>Trends in Plant Science</i> , 2020, 15, 1-10.	1.9	8
2517	Maize Introgression Library Provides Evidence for the Involvement of <i>liguleless1</i> in Resistance to Northern Leaf Blight. <i>Genes, Genomes, Genetics</i> , 2020, 10, 3611-3622.	1.8	17
2518	GWAS Based on RNA-Seq SNPs and High-Throughput Phenotyping Combined with Climatic Data Highlights the Reservoir of Valuable Genetic Diversity in Regional Tomato Landraces. <i>Genes</i> , 2020, 11, 1387.	2.4	14
2519	Genome-Wide Association Study (GWAS) for Resistance to <i>Sclerotinia sclerotiorum</i> in Common Bean. <i>Genes</i> , 2020, 11, 1496.	2.4	10
2520	Accumulation of mutations in genes associated with sexual reproduction contributed to the domestication of a vegetatively propagated staple crop, enset. <i>Horticulture Research</i> , 2020, 7, 185.	6.3	10
2521	Genome-wide association study uncovers genomic regions associated with grain iron, zinc and protein content in pearl millet. <i>Scientific Reports</i> , 2020, 10, 19473.	3.3	33
2522	mrMLM v4.0.2: An R Platform for Multi-locus Genome-wide Association Studies. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 481-487.	6.9	91
2523	A Deep Learning Approach to Population Structure Inference in Inbred Lines of Maize. <i>Frontiers in Genetics</i> , 2020, 11, 543459.	2.3	13
2524	The Global Durum Wheat Panel (GDP): An International Platform to Identify and Exchange Beneficial Alleles. <i>Frontiers in Plant Science</i> , 2020, 11, 569905.	3.6	44
2525	A New Diversity Panel for Winter Rapeseed ( <i>Brassica napus</i> L.) Genome-Wide Association Studies. <i>Agronomy</i> , 2020, 10, 2006.	3.0	6
2526	Characterization of the Genetic Architecture for Fusarium Head Blight Resistance in Durum Wheat: The Complex Association of Resistance, Flowering Time, and Height Genes. <i>Frontiers in Plant Science</i> , 2020, 11, 592064.	3.6	18
2527	Marker-Trait Associations for Tolerance to Ash Dieback in Common Ash ( <i>Fraxinus excelsior</i> L.). <i>Forests</i> , 2020, 11, 1083.	2.1	5
2528	Use of Targeted Amplicon Sequencing in Peanut to Generate Allele Information on Allotetraploid Sub-Genomes. <i>Genes</i> , 2020, 11, 1220.	2.4	3
2529	Genetic structure and diversity of upland rice germplasm using diversity array technology (DART)-based single nucleotide polymorphism (SNP) markers. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2020, 18, 343-350.	0.8	5
2530	A simple, cost-effective high-throughput image analysis pipeline improves genomic prediction accuracy for days to maturity in wheat. <i>Plant Methods</i> , 2020, 16, 146.	4.3	8
2531	The In-Silico Development of DNA Markers for Breeding of Spring Barley Varieties That Are Resistant to Spot Blotch in Russia. <i>Agriculture (Switzerland)</i> , 2020, 10, 505.	3.1	0

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2532	Genome-Wide SNP Discovery and Mapping QTLs for Seed Iron and Zinc Concentrations in Chickpea ( <i>Cicer arietinum</i> L.). <i>Frontiers in Nutrition</i> , 2020, 7, 559120.	3.7	29
2533	Perspectives on Low Temperature Tolerance and Vernalization Sensitivity in Barley: Prospects for Facultative Growth Habit. <i>Frontiers in Plant Science</i> , 2020, 11, 585927.	3.6	19
2534	Detailed Genetic Analysis for Identifying QTLs Associated with Drought Tolerance at Seed Germination and Seedling Stages in Barley. <i>Plants</i> , 2020, 9, 1425.	3.5	25
2535	Identification, Association of Natural Variation and Expression Analysis of ZmNAC9 Gene Response to Low Phosphorus in Maize Seedling Stage. <i>Plants</i> , 2020, 9, 1447.	3.5	1
2536	Association mapping of resistance to emerging stem rust pathogen races in spring wheat using genotyping-by-sequencing. <i>Plant Genome</i> , 2020, 13, e20050.	2.8	8
2537	Genome-Wide Association Study for Plant Architecture and Bioenergy Traits in Diverse Sorghum and Sudangrass Germplasm. <i>Agronomy</i> , 2020, 10, 1602.	3.0	10
2538	Evaluation of agronomic performance and exploratory genome-wide association study of a diverse oat panel for forage use in Taiwan. <i>Grassland Science</i> , 2020, 66, 249-260.	1.1	4
2539	Genetic interactions among Pto-miR319 family members and their targets influence growth and wood properties in <i>Populus tomentosa</i> . <i>Molecular Genetics and Genomics</i> , 2020, 295, 855-870.	2.1	2
2540	Genome-wide association studies for waxy starch in cassava. <i>Euphytica</i> , 2020, 216, 1.	1.2	13
2541	Genetic Architecture of Early Vigor Traits in Wild Soybean. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3105.	4.1	3
2542	Genome-wide association study of partial resistance to sclerotinia stem rot of cultivated soybean based on the detached leaf method. <i>PLoS ONE</i> , 2020, 15, e0233366.	2.5	9
2543	KASP Genotyping as a Molecular Tool for Diagnosis of Cassava-Colonizing <i>Bemisia tabaci</i> . <i>Insects</i> , 2020, 11, 305.	2.2	9
2544	Genome-Wide Association Study for Maize Leaf Cuticular Conductance Identifies Candidate Genes Involved in the Regulation of Cuticle Development. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1671-1683.	1.8	13
2545	Chloroplast genomes of Rubiaceae: Comparative genomics and molecular phylogeny in subfamily Ixoroideae. <i>PLoS ONE</i> , 2020, 15, e0232295.	2.5	18
2546	Genome-Wide Association Study of Grain Size Traits in Indica Rice Multiparent Advanced Generation Intercross (MAGIC) Population. <i>Frontiers in Plant Science</i> , 2020, 11, 395.	3.6	19
2547	Genome-Wide Association Study identify the genetic loci conferring resistance to Coffee Berry Disease ( <i>Colletotrichum kahawae</i> ) in <i>Coffea arabica</i> var. Rume Sudan. <i>Euphytica</i> , 2020, 216, 1.	1.2	16
2548	Genome-wide association study of Striga resistance in early maturing white tropical maize inbred lines. <i>BMC Plant Biology</i> , 2020, 20, 203.	3.6	29
2549	Genome-wide association study leads to novel genetic insights into resistance to <i>Aspergillus flavus</i> in maize kernels. <i>BMC Plant Biology</i> , 2020, 20, 206.	3.6	8

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2551	Genome-wide association analyses identify known and novel loci for teat number in Duroc pigs using single-locus and multi-locus models. <i>BMC Genomics</i> , 2020, 21, 344.	2.8	43
2552	Genome-wide association study of leaf chemistry traits in tobacco. <i>Breeding Science</i> , 2020, 70, 253-264.	1.9	1
2553	<i>Ms3</i> dominant genetic male sterility for wheat improvement with molecular breeding. <i>Crop Science</i> , 2020, 60, 1362-1372.	1.8	7
2554	Association Mapping of Quantitative Trait Loci for Grain Size in Introgression Line Derived from <i>Oryza Rufipogon</i> . <i>Rice Science</i> , 2020, 27, 246-254.	3.9	8
2555	“MNâ€Clearwater”, the first foodâ€grade intermediate wheatgrass ( <i>Kernza</i> perennial grain) cultivar. <i>Journal of Plant Registrations</i> , 2020, 14, 288-297.	0.5	58
2556	Differentially evolved drought stress indices determine the genetic variation of <i>Brassica napus</i> at seedling traits by genome-wide association mapping. <i>Journal of Advanced Research</i> , 2020, 24, 447-461.	9.5	29
2557	Genomic prediction of maternal haploid induction rate in maize. <i>Plant Genome</i> , 2020, 13, e20014.	2.8	14
2558	Using public databases for genomic prediction of tropical maize lines. <i>Plant Breeding</i> , 2020, 139, 697-707.	1.9	6
2559	Principles and approaches of association mapping in plant breeding. <i>Tropical Plant Biology</i> , 2020, 13, 212-224.	1.9	37
2560	The genetic architecture of the maize progenitor, teosinte, and how it was altered during maize domestication. <i>PLoS Genetics</i> , 2020, 16, e1008791.	3.5	27
2561	An improved 7K SNP array, the C7AIR, provides a wealth of validated SNP markers for rice breeding and genetics studies. <i>PLoS ONE</i> , 2020, 15, e0232479.	2.5	51
2562	Genetic Dissection of Nitrogen Use Efficiency in Tropical Maize Through Genome-Wide Association and Genomic Prediction. <i>Frontiers in Plant Science</i> , 2020, 11, 474.	3.6	33
2563	Key Genes and Genetic Interactions of Plant-Pathogen Functional Modules in Poplar Infected by <i>Marssonina brunnea</i> . <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1080-1090.	2.6	11
2564	Genomic data reveal two distinct species from the widespread alpine ginger <i>Roscoea tibetica</i> Batalin (Zingiberaceae). <i>Journal of Systematics and Evolution</i> , 2021, 59, 1232-1243.	3.1	13
2565	Identification of two novel Hessian fly resistance genes H35 and H36 in a hard winter wheat line SD06165. <i>Theoretical and Applied Genetics</i> , 2020, 133, 2343-2353.	3.6	31
2566	Characterization of sources of resistance to fusarium wilt in chickpea. <i>Indian Phytopathology</i> , 2020, 73, 701-705.	1.2	0
2567	Molecular delimitation of European leafy liverworts of the genus <i>Calypogeia</i> based on plastid super-barcodes. <i>BMC Plant Biology</i> , 2020, 20, 243.	3.6	25

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2569	QTL mapping and GWAS for identification of loci conferring partial resistance to <i>Pythium sylvaticum</i> in soybean ( <i>Glycine max</i> (L.) Merr). Molecular Breeding, 2020, 40, 1.	2.1	16
2570	Genetic diversity of Asian rice gall midge based on mtCOI gene sequences and identification of a novel resistance locus gm12 in rice cultivar MN62M. Molecular Biology Reports, 2020, 47, 4273-4283.	2.3	10
2571	Long-read bitter melon ( <i>Momordica charantia</i> ) genome and the genomic architecture of nonclassic domestication. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 14543-14551.	7.1	43
2572	Genomic prediction of maize microphenotypes provides insights for optimizing selection and mining diversity. Plant Biotechnology Journal, 2020, 18, 2456-2465.	8.3	20
2573	Negative dominance and dominance-by-dominance epistatic effects reduce grain-yield heterosis in wide crosses in wheat. Science Advances, 2020, 6, eaay4897.	10.3	40
2574	Characterization of <i>Hemerocallis citrina</i> Transcriptome and Development of EST-SSR Markers for Evaluation of Genetic Diversity and Population Structure of <i>Hemerocallis</i> Collection. Frontiers in Plant Science, 2020, 11, 686.	3.6	14
2575	Genome-Wide Mapping of Loci Associated With Resistance to Clubroot in <i>Brassica napus</i> ssp. <i>napobrassica</i> (Rutabaga) Accessions From Nordic Countries. Frontiers in Plant Science, 2020, 11, 742.	3.6	14
2576	Rapid local adaptation linked with phenotypic plasticity. Evolution Letters, 2020, 4, 345-359.	3.3	17
2577	Fine mapping of the Ca3GT gene controlling anthocyanin biosynthesis in mature unripe fruit of <i>Capsicum annuum</i> L.. Theoretical and Applied Genetics, 2020, 133, 2729-2742.	3.6	18
2578	Identification, association, and expression analysis of ZmNAC134 gene response to phosphorus deficiency tolerance traits in maize at seedling stage. Euphytica, 2020, 216, 1.	1.2	3
2579	Whole-genome resequencing of wild and domestic sheep identifies genes associated with morphological and agronomic traits. Nature Communications, 2020, 11, 2815.	12.8	142
2580	Increased Power and Accuracy of Causal Locus Identification in Time Series Genome-wide Association in Sorghum. Plant Physiology, 2020, 183, 1898-1909.	4.8	39
2581	Exploring natural diversity of <i>Medicago truncatula</i> reveals phenotypes and loci associated with the response of seedling performance to nitrate supply. Physiologia Plantarum, 2020, 170, 227-247.	5.2	2
2582	Improving Prediction Accuracy Using Multi-allelic Haplotype Prediction and Training Population Optimization in Wheat. G3: Genes, Genomes, Genetics, 2020, 10, 2265-2273.	1.8	20
2583	Genome-wide association analysis of root system architecture features and agronomic traits in durum wheat. Molecular Breeding, 2020, 40, 1.	2.1	18
2584	Determining the Genetic Control of Common Bean Early-Growth Rate Using Unmanned Aerial Vehicles. Remote Sensing, 2020, 12, 1748.	4.0	12
2585	Genome-Wide Association Mapping of Adult-Plant Resistance to Stripe Rust in Common Wheat ( <i>Triticum aestivum</i> ). Plant Disease, 2020, 104, 2174-2180.	1.4	6

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2586	Evolution and Functional Divergence of the Fructokinase Gene Family in Populus. <i>Frontiers in Plant Science</i> , 2020, 11, 484.	3.6	6
2587	Genome-wide association studies using 50K rice genic SNP chip unveil genetic architecture for anaerobic germination of deep-water rice population of Assam, India. <i>Molecular Genetics and Genomics</i> , 2020, 295, 1211-1226.	2.1	25
2588	Allelic sequence variation in the Sub1A, Sub1B and Sub1C genes among diverse rice cultivars and its association with submergence tolerance. <i>Scientific Reports</i> , 2020, 10, 8621.	3.3	14
2589	The relevance of gene flow with wild relatives in understanding the domestication process. <i>Royal Society Open Science</i> , 2020, 7, 191545.	2.4	18
2590	Weedy Rice as a Novel Gene Resource: A Genome-Wide Association Study of Anthocyanin Biosynthesis and an Evaluation of Nutritional Quality. <i>Frontiers in Plant Science</i> , 2020, 11, 878.	3.6	11
2591	Vis/NIR hyperspectral imaging distinguishes sub-population, production environment, and physicochemical grain properties in rice. <i>Scientific Reports</i> , 2020, 10, 9284.	3.3	29
2592	SNP genotyping reveals substructuring in weakly differentiated populations of Atlantic cod ( <i>Gadus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	3.3	10
2593	Mining for Candidate Genes Controlling Secondary Growth of the Carrot Storage Root. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4263.	4.1	7
2594	Adaptive genetic potential and plasticity of trait variation in the foundation prairie grass <i>Andropogon gerardii</i> across the US Great Plains climate gradient: Implications for climate change and restoration. <i>Evolutionary Applications</i> , 2020, 13, 2333-2356.	3.1	12
2595	Genotypic diversity in willow ( <i>Salix</i> spp.) is associated with chemical and morphological polymorphism, suggesting human-assisted dissemination in the Eastern Mediterranean. <i>Biochemical Systematics and Ecology</i> , 2020, 91, 104081.	1.3	6
2596	Upâ€regulating <i>GmETO1</i> improves phosphorus uptake and use efficiency by promoting root growth in soybean. <i>Plant, Cell and Environment</i> , 2020, 43, 2080-2094.	5.7	31
2597	Dissection of the genetic basis of oil content in Chinese peanut cultivars through association mapping. <i>BMC Genetics</i> , 2020, 21, 60.	2.7	7
2598	Genomic Prediction of Kernel Zinc Concentration in Multiple Maize Populations Using Genotyping-by-Sequencing and Repeat Amplification Sequencing Markers. <i>Frontiers in Plant Science</i> , 2020, 11, 534.	3.6	30
2599	Quantitative Trait Loci Associated with <i>Rotylenchulus reniformis</i> Host Suitability in Soybean. <i>Phytopathology</i> , 2020, 110, 1511-1521.	2.2	8
2600	Recommendations for Choosing the Genotyping Method and Best Practices for Quality Control in Crop Genome-Wide Association Studies. <i>Frontiers in Genetics</i> , 2020, 11, 447.	2.3	48
2601	Genome-Wide Association Study Reveals the Genetic Architecture of Stripe Rust Resistance at the Adult Plant Stage in Chinese Endemic Wheat. <i>Frontiers in Plant Science</i> , 2020, 11, 625.	3.6	8
2602	A Genome-Wide Association Study of Coleoptile Length in Different Chinese Wheat Landraces. <i>Frontiers in Plant Science</i> , 2020, 11, 677.	3.6	14
2603	Genome-Wide Association Studies in Diverse Spring Wheat Panel for Stripe, Stem, and Leaf Rust Resistance. <i>Frontiers in Plant Science</i> , 2020, 11, 748.	3.6	44



#	ARTICLE	IF	CITATIONS
2604	Genetic Diversity, Population Structure and Marker-Trait Association for 100-Seed Weight in International Safflower Panel Using SilicoDART Marker Information. <i>Plants</i> , 2020, 9, 652.	3.5	18
2605	Root-knot nematode genetic diversity associated with host compatibility to sweetpotato cultivars. <i>Molecular Plant Pathology</i> , 2020, 21, 1088-1098.	4.2	10
2606	Genome-Wide Diversity, Population Structure and Demographic History of Dromedaries in the Central Desert of Iran. <i>Genes</i> , 2020, 11, 599.	2.4	5
2607	Association Analysis of Traits in Watermelon Genotypes Using Molecular Markers. <i>Iranian Journal of Science and Technology, Transaction A: Science</i> , 2020, 44, 361-369.	1.5	3
2608	Identification of a transcriptional regulatory module that reduces leaf temperature in poplar under heat stress. <i>Tree Physiology</i> , 2020, 40, 1108-1125.	3.1	5
2609	Sex-specific impact of inbreeding on pathogen load in the striped dolphin. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20200195.	2.6	7
2610	Haplotype diversity underlying quantitative traits in Canadian soybean breeding germplasm. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1967-1976.	3.6	10
2611	Adaptive fitness of <i>Sapindus emarginatus</i> Vahl populations towards future climatic regimes and the limiting factors of its distribution. <i>Scientific Reports</i> , 2020, 10, 3803.	3.3	4
2612	Dispersal patterns of <i>Trypanosoma cruzi</i> in Arequipa, Peru. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0007910.	3.0	4
2613	Genome-Wide Association Mapping to Identify Genetic Loci for Cold Tolerance and Cold Recovery During Germination in Rice. <i>Frontiers in Genetics</i> , 2020, 11, 22.	2.3	27
2614	Genome-Wide Association Study of Salinity Tolerance During Germination in Barley ( <i>Hordeum vulgare</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T	3.6	73
2615	A connected half-sib family training population for genomic prediction in barley. <i>Crop Science</i> , 2020, 60, 262-281.	1.8	7
2616	Genome-Wide Detection of SNP Markers Associated with Four Physiological Traits in Groundnut ( <i>Arachis hypogaea</i> L.) Mini Core Collection. <i>Agronomy</i> , 2020, 10, 192.	3.0	10
2617	Comparison of array- and sequencing-based markers for genome-wide association mapping and genomic prediction in spring wheat. <i>Crop Science</i> , 2020, 60, 211-225.	1.8	11
2618	Identification of QTLs in oil palm ( <i>Elaeis guineensis</i> Jacq.) using SSR markers through association mapping. <i>Journal of Genetics</i> , 2020, 99, 1.	0.7	12
2619	A 62K genic-SNP chip array for genetic studies and breeding applications in pigeonpea ( <i>Cajanus cajan</i> L.) Tj ETQq1 1 0.784314 rgBT /Ov	3.3	19
2620	The Circadian Clock Gene, TaPRR1, Is Associated With Yield-Related Traits in Wheat ( <i>Triticum aestivum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10	3.6	17
2621	Shared Genetic Control of Root System Architecture between <i>Zea mays</i> and <i>Sorghum bicolor</i> . <i>Plant Physiology</i> , 2020, 182, 977-991.	4.8	57

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2622	Whole-genome sequencing of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> mutant isolates identifies avirulence gene candidates. <i>BMC Genomics</i> , 2020, 21, 247.	2.8	23
2623	Genome-Wide Association Mapping of Dark Green Color Index using a Diverse Panel of Soybean Accessions. <i>Scientific Reports</i> , 2020, 10, 5166.	3.3	13
2624	Genetic structure, gene flow pattern, and association analysis of superior germplasm resources in domesticated upland cotton ( <i>Gossypium hirsutum</i> L.). <i>Plant Diversity</i> , 2020, 42, 189-197.	3.7	9
2625	Diverse genetic mechanisms underlie worldwide convergent rice feralization. <i>Genome Biology</i> , 2020, 21, 70.	8.8	55
2626	Effect of drought stress on agro-morphological traits in sunflower ( <i>Helianthus annuus</i> L.) genotypes and identification of informative ISSR markers. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2020, 18, 49-62.	0.8	5
2627	Genome wide association mapping and candidate gene analysis for pod shatter resistance in <i>Brassica juncea</i> and its progenitor species. <i>Molecular Biology Reports</i> , 2020, 47, 2963-2974.	2.3	14
2628	Genome-wide association study identifies various loci underlying agronomic and morphological traits in diversified potato panel. <i>Physiology and Molecular Biology of Plants</i> , 2020, 26, 1003-1020.	3.1	17
2629	Genetic Basis Dissection for Eating and Cooking Qualities of Japonica Rice in Northeast China. <i>Agronomy</i> , 2020, 10, 423.	3.0	10
2630	Tomato SD1, encoding a kinase-interacting protein, is a major locus controlling stem development. <i>Journal of Experimental Botany</i> , 2020, 71, 3575-3587.	4.8	12
2631	Diversity and heterotic patterns in North American proprietary dent maize germplasm. <i>Crop Science</i> , 2020, 60, 100-114.	1.8	42
2632	Identification of genome-wide single-nucleotide polymorphisms among geographically diverse radish accessions. <i>DNA Research</i> , 2020, 27, .	3.4	15
2633	Unraveling hierarchical genetic structure in a marine metapopulation: A comparison of three high-throughput genotyping approaches. <i>Molecular Ecology</i> , 2020, 29, 2189-2203.	3.9	26
2634	Genome-wide association studies and QTL mapping uncover the genetic architecture of ear tip barrenness in maize. <i>Physiologia Plantarum</i> , 2020, 170, 27-39.	5.2	28
2635	IntAssoPlot: An R Package for Integrated Visualization of Genome-Wide Association Study Results With Gene Structure and Linkage Disequilibrium Matrix. <i>Frontiers in Genetics</i> , 2020, 11, 260.	2.3	22
2636	Loci associated with variation in gene expression and growth in juvenile salmon are influenced by the presence of a growth hormone transgene. <i>BMC Genomics</i> , 2020, 21, 185.	2.8	5
2637	Identification of quantitative trait loci associated with nitrogen use efficiency in winter wheat. <i>PLoS ONE</i> , 2020, 15, e0228775.	2.5	18
2638	Genome-Wide Association Analyses Reveal Genomic Regions Controlling Canopy Wilting in Soybean. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1413-1425.	1.8	18
2639	Linkage Analysis and Multi-Locus Genome-Wide Association Studies Identify QTNs Controlling Soybean Plant Height. <i>Frontiers in Plant Science</i> , 2020, 11, 9.	3.6	20

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2640	Genomic Prediction Accuracy of Seven Breeding Selection Traits Improved by QTL Identification in Flax. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1577.	4.1	21
2641	Identification of Two Novel Peanut Genotypes Resistant to Aflatoxin Production and Their SNP Markers Associated with Resistance. <i>Toxins</i> , 2020, 12, 156.	3.4	15
2642	VviUCC1 Nucleotide Diversity, Linkage Disequilibrium and Association with Rachis Architecture Traits in Grapevine. <i>Genes</i> , 2020, 11, 598.	2.4	7
2643	Genome-wide association analysis of stem water-soluble carbohydrate content in bread wheat. <i>Theoretical and Applied Genetics</i> , 2020, 133, 2897-2914.	3.6	20
2644	Harness the power of genomic selection and the potential of germplasm in crop breeding for global food security in the era with rapid climate change. <i>Crop Journal</i> , 2020, 8, 688-700.	5.2	43
2645	Identification of regions under selection and loci controlling agronomic traits in a soft red winter wheat population. <i>Plant Genome</i> , 2020, 13, e20031.	2.8	12
2646	Genome-wide association study of grain mold resistance in sorghum association panel as affected by inoculation with <i>Alternaria alternata</i> alone and <i>Alternaria alternata</i> , <i>Fusarium thapsinum</i> , and <i>Curvularia lunata</i> combined. <i>European Journal of Plant Pathology</i> , 2020, 157, 783-798.	1.7	11
2647	Multi-Location Evaluation of Global Wheat Lines Reveal Multiple QTL for Adult Plant Resistance to <i>Septoria Nodorum</i> Blotch (SNB) Detected in Specific Environments and in Response to Different Isolates. <i>Frontiers in Plant Science</i> , 2020, 11, 771.	3.6	17
2648	Genetic Basis of Maize Resistance to Multiple Insect Pests: Integrated Genome-Wide Comparative Mapping and Candidate Gene Prioritization. <i>Genes</i> , 2020, 11, 689.	2.4	21
2649	Detection of Genomic Regions Associated with Resistance to Stem Rust in Russian Spring Wheat Varieties and Breeding Germplasm. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4706.	4.1	13
2650	Multi-parent populations in crops: a toolbox integrating genomics and genetic mapping with breeding. <i>Heredity</i> , 2020, 125, 396-416.	2.6	124
2651	Identification of genetic loci associated with forage quality in response to water deficit in autotetraploid alfalfa ( <i>Medicago sativa</i> L.). <i>BMC Plant Biology</i> , 2020, 20, 303.	3.6	27
2652	Identification of novel genetic factors underlying the host-pathogen interaction between barley ( <i>Hordeum vulgare</i> L.) and powdery mildew ( <i>Blumeria graminis</i> f. sp. <i>hordei</i> ). <i>PLoS ONE</i> , 2020, 15, e0235565.	2.5	6
2653	Mapping regulatory variants controlling gene expression in drought response and tolerance in maize. <i>Genome Biology</i> , 2020, 21, 163.	8.8	76
2654	Genetic markers associated with seed longevity and vitamin E in diverse Aus rice varieties. <i>Seed Science Research</i> , 2020, 30, 133-141.	1.7	11
2655	Genome wide association analysis of a stemborer egg induced "call-for-help" defence trait in maize. <i>Scientific Reports</i> , 2020, 10, 11205.	3.3	20
2656	Development of a single nucleotide polymorphism array for population genomic studies in four European pine species. <i>Molecular Ecology Resources</i> , 2020, 20, 1697-1705.	4.8	25
2657	Genetic analysis of callus formation in a diversity panel of 96 rose genotypes. <i>Plant Cell, Tissue and Organ Culture</i> , 2020, 142, 505-517.	2.3	11

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2658	Genome-wide association analysis reveals loci and candidate genes involved in fiber quality traits in sea island cotton ( <i>Gossypium barbadense</i> ). <i>BMC Plant Biology</i> , 2020, 20, 289.	3.6	13
2659	QTL analysis and GWAS of agronomic traits in sweetpotato (<i>Ipomoea batatas</i> L.) using genome wide SNPs. <i>Breeding Science</i> , 2020, 70, 283-291.	1.9	9
2660	Quantitative trait loci for agronomic traits in tetraploid wheat for enhancing grain yield in Kazakhstan environments. <i>PLoS ONE</i> , 2020, 15, e0234863.	2.5	19
2661	Genome wide association mapping for tocopherol concentration in soybean seeds across multiple environments. <i>Industrial Crops and Products</i> , 2020, 154, 112674.	5.2	10
2662	Genetic diversity analysis of specialty glutinous and low-amylose rice ( <i>Oryza sativa</i> L.) landraces of Assam based on Wx locus and microsatellite diversity. <i>Journal of Biosciences</i> , 2020, 45, 1.	1.1	4
2663	Molecular genetic analysis of spring wheat core collection using genetic diversity, population structure, and linkage disequilibrium. <i>BMC Genomics</i> , 2020, 21, 434.	2.8	44
2664	ZEAMAP, a Comprehensive Database Adapted to the Maize Multi-Omics Era. <i>IScience</i> , 2020, 23, 101241.	4.1	63
2665	HAPPI GWAS: Holistic Analysis with Pre- and Post-Integration GWAS. <i>Bioinformatics</i> , 2020, 36, 4655-4657.	4.1	10
2666	Multi-level patterns of genetic structure and isolation by distance in the widespread plant <i>Mimulus guttatus</i> . <i>Heredity</i> , 2020, 125, 227-239.	2.6	23
2667	Identification of QTL and genes for pod number in soybean by linkage analysis and genome-wide association studies. <i>Molecular Breeding</i> , 2020, 40, 1.	2.1	14
2668	Characterization of Genetic Diversity and Genome-Wide Association Mapping of Three Agronomic Traits in Qingke Barley ( <i>Hordeum Vulgare</i> L.) in the Qinghai-Tibet Plateau. <i>Frontiers in Genetics</i> , 2020, 11, 638.	2.3	14
2669	Fine mapping and candidate gene analysis of qKW7b, a major QTL for kernel width in maize. <i>Molecular Breeding</i> , 2020, 40, 1.	2.1	4
2670	Progress and Prospects of Association Mapping in Sugarcane ( <i>Saccharum Species Hybrid</i> ), a Complex Polyploid Crop. <i>Sugar Tech</i> , 2020, 22, 939-953.	1.8	12
2671	A genome-wide association study of hexanal content related to soymilk off-flavours in seed of soybean ( <i>Glycine max</i> ). <i>Crop and Pasture Science</i> , 2020, 71, 552.	1.5	3
2672	The regulatory landscape of early maize inflorescence development. <i>Genome Biology</i> , 2020, 21, 165.	8.8	32
2673	Parallel and nonparallel genomic responses contribute to herbicide resistance in <i>Ipomoea purpurea</i> , a common agricultural weed. <i>PLoS Genetics</i> , 2020, 16, e1008593.	3.5	39
2674	Genomic Prediction and Indirect Selection for Grain Yield in US Pacific Northwest Winter Wheat Using Spectral Reflectance Indices from High-Throughput Phenotyping. <i>International Journal of Molecular Sciences</i> , 2020, 21, 165.	4.1	29
2675	Potential of Genome-Wide Association Studies and Genomic Selection to Improve Productivity and Quality of Commercial Timber Species in Tropical Rainforest, a Case Study of <i>Shorea platyclados</i> . <i>Forests</i> , 2020, 11, 239.	2.1	11

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2676	Seed Weight as a Covariate in Association and Prediction Studies for Biomass Traits in Maize Seedlings. <i>Plants</i> , 2020, 9, 275.	3.5	2
2677	High-density NGS-based map construction and genetic dissection of fruit shape and rind netting in <i>Cucumis melo</i> . <i>Theoretical and Applied Genetics</i> , 2020, 133, 1927-1945.	3.6	21
2678	Pipette and paper: Combining molecular and genealogical methods to assess a Nile tilapia ( <i>Oreochromis niloticus</i> ) breeding program. <i>Aquaculture</i> , 2020, 523, 735171.	3.5	4
2679	Genetic analysis of adventitious root formation in vivo and in vitro in a diversity panel of roses. <i>Scientia Horticulturae</i> , 2020, 266, 109277.	3.6	13
2680	Genome-Wide Association Study Uncovers Novel Genomic Regions Associated With Coleoptile Length in Hard Winter Wheat. <i>Frontiers in Genetics</i> , 2019, 10, 1345.	2.3	26
2681	Transcriptome-Based Prediction of Complex Traits in Maize. <i>Plant Cell</i> , 2020, 32, 139-151.	6.6	80
2682	DARTseq Molecular Markers Associated with the Spiny-Tip Leaf Margin in Pineapple ( <i>Ananas comosus</i> ) Tj ETQq0 0 0.0rgBT /Overlock 10 Tf	1.9	3
2683	Development of a PCR-based genetic sex identification method in spinyhead croaker ( <i>Collichthys</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 27	3.5	27
2684	In-depth genome diversity, population structure and linkage disequilibrium analysis of worldwide diverse safflower ( <i>Carthamus tinctorius</i> L.) accessions using NGS data generated by DARTseq technology. <i>Molecular Biology Reports</i> , 2020, 47, 2123-2135.	2.3	21
2685	Identification of QTL for early vigor and leaf senescence across two tropical maize doubled haploid populations under nitrogen deficient conditions. <i>Euphytica</i> , 2020, 216, 1.	1.2	5
2686	Next generation sequencing data in the phylogenetic relationships of the genus <i>Molossus</i> (Chiroptera, Molossidae). <i>Data in Brief</i> , 2020, 29, 105276.	1.0	5
2687	A serine/threonine protein kinase encoding gene <i>KERNEL NUMBER PER ROW6</i> regulates maize grain yield. <i>Nature Communications</i> , 2020, 11, 988.	12.8	82
2688	Current Affairs of Microbial Genome-Wide Association Studies: Approaches, Bottlenecks and Analytical Pitfalls. <i>Frontiers in Microbiology</i> , 2019, 10, 3119.	3.5	54
2689	Genomic Prediction for Grain Yield and Yield-Related Traits in Chinese Winter Wheat. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1342.	4.1	27
2690	Haplotyping the <i>Vitis</i> collinear core genome with rhAmpSeq improves marker transferability in a diverse genus. <i>Nature Communications</i> , 2020, 11, 413.	12.8	52
2691	Dissecting the Genetic Complexity of <i>Fusarium</i> Crown Rot Resistance in Wheat. <i>Scientific Reports</i> , 2020, 10, 3200.	3.3	15
2692	Genome-wide association mapping reveals loci for shelf life and developmental rate of lettuce. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1947-1966.	3.6	29
2693	An SNP based GWAS analysis of seed longevity in wheat. <i>Cereal Research Communications</i> , 2020, 48, 149-156.	1.6	19

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2694	Dissecting the genetic mechanisms of waterlogging tolerance in <i>Brassica napus</i> through linkage mapping and a genome-wide association study. <i>Industrial Crops and Products</i> , 2020, 147, 112269.	5.2	12
2695	Genome-wide association mapping for grain shape and color traits in Ethiopian durum wheat ( <i>Triticum</i> ) Tj ETQq1 1 0,784314,rgBT /Over	5.2	38
2696	Genome-wide association study (GWAS) reveals genetic loci of lead (Pb) tolerance during seedling establishment in rapeseed ( <i>Brassica napus</i> L.). <i>BMC Genomics</i> , 2020, 21, 139.	2.8	14
2697	Mining of favorable alleles for seed reserve utilization efficiency in <i>Oryza sativa</i> by means of association mapping. <i>BMC Genetics</i> , 2020, 21, 4.	2.7	7
2698	Maize genomes to fields (G2F): 2014–2017 field seasons: genotype, phenotype, climatic, soil, and inbred ear image datasets. <i>BMC Research Notes</i> , 2020, 13, 71.	1.4	38
2699	Genetic Differentiation in Hatchery and Stocked Populations of Sea Trout in the Southern Baltic: Selection Evidence at SNP Loci. <i>Genes</i> , 2020, 11, 184.	2.4	7
2700	Natural Variation in Lignin and Pectin Biosynthesis-Related Genes in Switchgrass ( <i>Panicum virgatum</i> L.) and Association of SNP Variants with Dry Matter Traits. <i>Bioenergy Research</i> , 2020, 13, 79-99.	3.9	4
2701	Substantial genetic divergence and lack of recent gene flow support cryptic speciation in a colour polymorphic bumble bee ( <i>Bombus bifarius</i> ) species complex. <i>Systematic Entomology</i> , 2020, 45, 635-652.	3.9	36
2702	A Large Transposon Insertion in the <i>stiff1</i> Promoter Increases Stalk Strength in Maize. <i>Plant Cell</i> , 2020, 32, 152-165.	6.6	40
2703	Nested association mapping of important agronomic traits in three interspecific soybean populations. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1039-1054.	3.6	12
2704	Complex patterns of differentiation and gene flow underly the divergence of aposematic phenotypes in <i>Oophaga</i> poison frogs. <i>Molecular Ecology</i> , 2020, 29, 1944-1956.	3.9	17
2705	The <i>Ficus erecta</i> genome aids <i>Ceratocystis</i> canker resistance breeding in common fig ( <i>F. carica</i> ). <i>Plant Journal</i> , 2020, 102, 1313-1322.	5.7	15
2706	CUBIC: an atlas of genetic architecture promises directed maize improvement. <i>Genome Biology</i> , 2020, 21, 20.	8.8	57
2707	Genomic Predictions Using Low-Density SNP Markers, Pedigree and GWAS Information: A Case Study with the Non-Model Species <i>Eucalyptus cladocalyx</i> . <i>Plants</i> , 2020, 9, 99.	3.5	23
2708	Genome-wide association mapping revealed syntenic loci QFhb-4AL and QFhb-5DL for Fusarium head blight resistance in common wheat ( <i>Triticum aestivum</i> L.). <i>BMC Plant Biology</i> , 2020, 20, 29.	3.6	21
2709	Genomic Regions Associated with Virulence in <i>Pyrenophora teres</i> f. <i>teres</i> Identified by Genome-Wide Association Analysis and Biparental Mapping. <i>Phytopathology</i> , 2020, 110, 881-891.	2.2	21
2710	Phenotypic diversity and genome-wide association mapping of earliness-related traits in cultivated tomato ( <i>Solanum lycopersicum</i> L.). <i>Scientia Horticulturae</i> , 2020, 264, 109194.	3.6	3
2711	Whole-genome diversity, population structure and linkage disequilibrium analysis of globally diverse wheat genotypes using genotyping-by-sequencing DArTseq platform. <i>3 Biotech</i> , 2020, 10, 48.	2.2	5



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2712	Host and symbiont genetic determinants of nutritional phenotype in a natural population of the pea aphid. <i>Molecular Ecology</i> , 2020, 29, 848-858.	3.9	15
2713	Rediscovery of Genetic and Genomic Resources for Future Food Security. , 2020, , .		11
2714	Multiregional origins of the domesticated tetraploid wheats. <i>PLoS ONE</i> , 2020, 15, e0227148.	2.5	27
2715	Uncovering Phenotypic Diversity and DArTseq Marker Loci Associated with Antioxidant Activity in Common Bean. <i>Genes</i> , 2020, 11, 36.	2.4	26
2716	Genetic Dissection of Grain Yield and Agronomic Traits in Maize under Optimum and Low-Nitrogen Stressed Environments. <i>International Journal of Molecular Sciences</i> , 2020, 21, 543.	4.1	18
2717	Urbanization and Population Genetic Structure of the Panama City crayfish ( <i>Procambarus econfinae</i> ). <i>Journal of Heredity</i> , 2020, 111, 204-215.	2.4	2
2718	Identification of Candidate Growth-Related SNPs and Genes Using GWAS in Brown-Marbled Grouper ( <i>Epinephelus fuscoguttatus</i> ). <i>Marine Biotechnology</i> , 2020, 22, 153-166.	2.4	38
2719	Cryptic variation in RNA-directed DNA-methylation controls lateral root development when auxin signalling is perturbed. <i>Nature Communications</i> , 2020, 11, 218.	12.8	18
2720	Drought response of flax accessions and identification of quantitative trait nucleotides (QTNs) governing agronomic and root traits by genome-wide association analysis. <i>Molecular Breeding</i> , 2020, 40, 1.	2.1	12
2721	SNP-based genetic diversity assessment among hungarian bread wheat ( <i>Triticum aestivum</i> L.) genotypes. <i>Cereal Research Communications</i> , 2020, 48, 1-7.	1.6	8
2722	High-quality genome sequence of white lupin provides insight into soil exploration and seed quality. <i>Nature Communications</i> , 2020, 11, 492.	12.8	90
2723	Evaluation of genetic diversity, agronomic traits, and anthracnose resistance in the NPCGS Sudan Sorghum Core collection. <i>BMC Genomics</i> , 2020, 21, 88.	2.8	38
2724	Linkage disequilibrium mapping for grain Fe and Zn enhancing QTLs useful for nutrient dense rice breeding. <i>BMC Plant Biology</i> , 2020, 20, 57.	3.6	74
2725	Identification of Loci Through Genome-Wide Association Studies to Improve Tolerance to Sulfur Deficiency in Rice. <i>Frontiers in Plant Science</i> , 2019, 10, 1668.	3.6	17
2726	The origin and current situation of <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> tropical race 4 in Israel and the Middle East. <i>Scientific Reports</i> , 2020, 10, 1590.	3.3	52
2727	A Genome-Wide Association Study of Resistance to <i>Puccinia striiformis</i> f. sp. <i>hordei</i> and <i>P. graminis</i> f. sp. <i>tritici</i> in Barley and Development of Resistant Germplasm. <i>Phytopathology</i> , 2020, 110, 1082-1092.	2.2	5
2728	Gains through selection for grain yield in a winter wheat breeding program. <i>PLoS ONE</i> , 2020, 15, e0221603.	2.5	25
2729	Genotypic and phenotypic characterization of a large, diverse population of maize near-isogenic lines. <i>Plant Journal</i> , 2020, 103, 1246-1255.	5.7	12

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2730	High-Density Genetic Linkage Mapping of <i>Lepidium</i> Based on Genotyping-by-Sequencing SNPs and Segregating Contig Tag Haplotypes. <i>Frontiers in Plant Science</i> , 2020, 11, 448.	3.6	6
2731	Exploring the Genetic Architecture of Root-Related Traits in Mediterranean Bread Wheat Landraces by Genome-Wide Association Analysis. <i>Agronomy</i> , 2020, 10, 613.	3.0	24
2732	Genome-wide selection and genetic improvement during modern maize breeding. <i>Nature Genetics</i> , 2020, 52, 565-571.	21.4	146
2733	Increased Prediction Accuracy Using Combined Genomic Information and Physiological Traits in A Soft Wheat Panel Evaluated in Multi-Environments. <i>Scientific Reports</i> , 2020, 10, 7023.	3.3	12
2734	Identification of additional /novel QTL associated with resistance to cassava green mite in a biparental mapping population. <i>PLoS ONE</i> , 2020, 15, e0231008.	2.5	10
2735	Hybrid Breeding for MLN Resistance: Heterosis, Combining Ability, and Hybrid Prediction. <i>Plants</i> , 2020, 9, 468.	3.5	10
2736	Genomic prediction enables early but low-intensity selection in soybean segregating progenies. <i>Crop Science</i> , 2020, 60, 1346-1361.	1.8	4
2737	Genetic diversity of provitamin-A cassava ( <i>Manihot esculenta</i> Crantz) in Sierra Leone. <i>Genetic Resources and Crop Evolution</i> , 2020, 67, 1193-1208.	1.6	10
2738	Genome-wide association study reveals the genetic basis of cold tolerance in wheat. <i>Molecular Breeding</i> , 2020, 40, 1.	2.1	41
2739	Genetic differentiation of Mutator insertion polymorphisms and association with agronomic traits in waxy and common maize. <i>Genes and Genomics</i> , 2020, 42, 631-638.	1.4	2
2740	Candidate genes association study to identify allele-specific SNP marker of 18:3 fatty acid in <i>Brassica napus</i> . <i>Journal of Plant Physiology</i> , 2020, 248, 153159.	3.5	0
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2742	Genomic regions underlying metabolic and neuronal signaling pathways are temporally consistent in a moving avian hybrid zone. <i>Evolution; International Journal of Organic Evolution</i> , 2020, 74, 1498-1513.	2.3	20
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2744	Development of a multiparent advanced generation intercross (MAGIC) population for genetic exploitation of complex traits in <i>Brassica juncea</i> : Glucosinolate content as an example. <i>Plant Breeding</i> , 2020, 139, 779-789.	1.9	9
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2747	Bridging old and new: diversity and evaluation of high iron-associated stress response of rice cultivated in West Africa. <i>Journal of Experimental Botany</i> , 2020, 71, 4188-4200.	4.8	14

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2750	Identifying heterotic groups and testers for hybrid development in early maturing yellow maize ( <i>Zea mays</i> ) using genomic data. <i>Frontiers in Plant Science</i> , 2020, 11, 1010.	1.9	10
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2752	Genome Wide Association Mapping of Spot Blotch Resistance at Seedling and Adult Plant Stages in Barley. <i>Frontiers in Plant Science</i> , 2020, 11, 642.	3.6	15
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2754	SNP discovery of <i>Camellia oleifera</i> based on RNA-seq and its application for identification of genetic relationships and locus for oil content among different cultivars. <i>Journal of Horticultural Science and Biotechnology</i> , 2020, 95, 687-702.	1.9	1
2755	Identification and characterization of trait-specific SNPs using ddRAD sequencing in water buffalo. <i>Genomics</i> , 2020, 112, 3571-3578.	2.9	14
2756	A sorghum practical haplotype graph facilitates genome-wide imputation and cost-effective genomic prediction. <i>Plant Genome</i> , 2020, 13, e20009.	2.8	54
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2760	Early Drought-Responsive Genes Are Variable and Relevant to Drought Tolerance. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1657-1670.	1.8	13
2761	QTL mapping of spontaneous haploid genome doubling using genotyping-by-sequencing in maize ( <i>Zea mays</i> ) using genomic data. <i>Frontiers in Plant Science</i> , 2020, 11, 1010.	3.6	12
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2765	Genetic dissection of heat-responsive physiological traits to improve adaptation and increase yield potential in soft winter wheat. <i>BMC Genomics</i> , 2020, 21, 315.	2.8	10

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2767	A Genome-Wide Association Study To Understand the Effect of <i>Fusarium verticillioides</i> Infection on Seedlings of a Maize Diversity Panel. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1685-1696.	1.8	13
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2771	Association mapping for yield traits under drought stress in Autumn rice germplasm collection of Assam. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2021, 30, 26-36.	1.7	8
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2773	Dissecting the phenotypic components and genetic architecture of maize stem vascular bundles using high-throughput phenotypic analysis. <i>Plant Biotechnology Journal</i> , 2021, 19, 35-50.	8.3	25
2774	Resistance and susceptibility QTL identified in a rice MAGIC population by screening with a minor-effect virulence factor from <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . <i>Plant Biotechnology Journal</i> , 2021, 19, 51-63.	8.3	6
2775	A GBS-based GWAS analysis of adaptability and yield traits in bread wheat ( <i>Triticum aestivum</i> L.). <i>Journal of Applied Genetics</i> , 2021, 62, 27-41.	1.9	30
2776	Genome-wide association study of six quality-related traits in common wheat ( <i>Triticum aestivum</i> L.) under two sowing conditions. <i>Theoretical and Applied Genetics</i> , 2021, 134, 399-418.	3.6	22
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2780	Hybrid performance as related to genomic diversity and population structure in public sorghum inbred lines. <i>Crop Science</i> , 2021, 61, 357-371.	1.8	4
2781	Genome-wide association analysis of aluminum tolerance related traits in rapeseed ( <i>Brassica napus</i> L.) during germination. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 335-357.	1.6	6
2782	A linkage disequilibrium-based statistical test for Genome-Wide Epistatic Selection Scans in structured populations. <i>Heredity</i> , 2021, 126, 77-91.	2.6	5
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2786	Genome-wide association study identifies QTL for thousand grain weight in winter wheat under normal- and late-sown stressed environments. <i>Theoretical and Applied Genetics</i> , 2021, 134, 143-157.	3.6	36
2787	Genetics of extra-early maturing yellow and orange quality protein maize inbreds and derived hybrids under low soil nitrogen and <i>Striga</i> infestation. <i>Crop Science</i> , 2021, 61, 1052-1072.	1.8	9
2788	Genetics of days to flowering, maturity and plant height in natural and derived forms of <i>Brassica rapa</i> L.. <i>Theoretical and Applied Genetics</i> , 2021, 134, 473-487.	3.6	12
2789	Genetic Differentiation of <i>Verticillium dahliae</i> Populations Recovered from Symptomatic and Asymptomatic Hosts. <i>Phytopathology</i> , 2021, 111, 149-159.	2.2	9
2790	Genetic diversity of Guatemalan climbing bean collections. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 639-656.	1.6	10
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2792	Downy mildew resistance is genetically mediated by prophylactic production of phenylpropanoids in hop. <i>Plant, Cell and Environment</i> , 2021, 44, 323-338.	5.7	16
2793	<i>FLOWERING LOCUS T4</i> delays flowering and decreases floret fertility in barley. <i>Journal of Experimental Botany</i> , 2021, 72, 107-121.	4.8	18
2794	Loci harboring genes with important role in drought and related abiotic stress responses in flax revealed by multiple GWAS models. <i>Theoretical and Applied Genetics</i> , 2021, 134, 191-212.	3.6	23
2795	Association mapping and genomic selection for sorghum adaptation to tropical soils of Brazil in a sorghum multiparental random mating population. <i>Theoretical and Applied Genetics</i> , 2021, 134, 295-312.	3.6	9
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2797	Novel sources of resistance to blast disease in finger millet. <i>Crop Science</i> , 2021, 61, 250-262.	1.8	14
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2799	Developing KASP Markers for Identification of Basmati Rice Varieties. <i>Food Analytical Methods</i> , 2021, 14, 663-673.	2.6	11
2800	Miniature inverted repeat transposable elements <i>cis</i> -regulate circular RNA expression and promote ethylene biosynthesis, reducing heat tolerance in <i>Populus tomentosa</i> . <i>Journal of Experimental Botany</i> , 2021, 72, 1978-1994.	4.8	9
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2805	The <i>Aegilops ventricosa</i> 2NvS segment in bread wheat: cytology, genomics and breeding. <i>Theoretical and Applied Genetics</i> , 2021, 134, 529-542.	3.6	48
2806	Comparative population genomic analysis provides insights into breeding of modern indica rice in China. <i>Gene</i> , 2021, 768, 145303.	2.2	1
2807	Polymorphisms in <i>cis</i> -elements confer SAUR26 gene expression difference for thermoresponse natural variation in <i>Arabidopsis</i> . <i>New Phytologist</i> , 2021, 229, 2751-2764.	7.3	19
2808	Genome-wide association study of resistance to PstS2 and Warrior races of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> (stripe rust) in bread wheat landraces. <i>Plant Genome</i> , 2021, 14, e20066.	2.8	17
2809	Candidate gene association of gene expression data in sugarcane contrasting for sucrose content. <i>Genomics</i> , 2021, 113, 229-237.	2.9	9
2810	The genome of Shanputao ( <i>Vitis amurensis</i> ) provides a new insight into cold tolerance of grapevine. <i>Plant Journal</i> , 2021, 105, 1495-1506.	5.7	52
2811	New QTLs for Spot Blotch Disease Resistance in Wheat ( <i>Triticum aestivum</i> L.) Using Genome-Wide Association Mapping. <i>Frontiers in Genetics</i> , 2020, 11, 613217.	2.3	24
2812	Flowering time regulation model revisited by pooled sequencing of mass selection populations. <i>Plant Science</i> , 2021, 304, 110797.	3.6	5
2813	Classical and genomic prediction of hybrid sweet corn performance in organic environments. <i>Crop Science</i> , 2021, 61, 1698-1708.	1.8	5
2814	Elite allele mining for growth rate traits in common carp ( <i>Cyprinus carpio</i> ) by association analysis. <i>Aquaculture Research</i> , 2021, 52, 1192-1200.	1.8	2
2815	Single nucleotide polymorphism-based haplotypes associated with <i>Meloidogyne javanica</i> resistance in Brazilian soybean germplasm. <i>Agronomy Journal</i> , 2021, 113, 1008-1019.	1.8	0
2816	Association mapping identifies and confirms loci for soybean seed weight. <i>Crop Science</i> , 2021, 61, 1289-1300.	1.8	4
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2824	Genomic selection of forage agronomic traits in winter wheat. Crop Science, 2021, 61, 410-421.	1.8	5
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2826	Strategies for the utilization of the USDA mung bean germplasm collection for breeding outcomes. Crop Science, 2021, 61, 422-442.	1.8	15
2827	Genetic diversity of <i>Prunus sibirica</i> L. superior accessions based on the SSR markers developed using restriction-site associated DNA sequencing. Genetic Resources and Crop Evolution, 2021, 68, 615-628.	1.6	7
2828	<i>Rpg7</i> : A New Gene for Stem Rust Resistance from <i>Hordeum vulgare</i> ssp. <i>spontaneum</i> . Phytopathology, 2021, 111, 548-558.	2.2	6
2829	Transcriptome analysis and association mapping reveal the genetic regulatory network response to cadmium stress in <i>Populus tomentosa</i> . Journal of Experimental Botany, 2021, 72, 576-591.	4.8	21
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2833	In-vitro anti-fungal assay and association analysis reveal a role for the <i>Pinus monticola</i> PR10 gene (PmPR10-3.1) in quantitative disease resistance to white pine blister rust. Genome, 2021, 64, 693-704.	2.0	7
2834	Molecular Mapping and Breeding in Mango. Compendium of Plant Genomes, 2021, , 153-163.	0.5	1
2835	Genome-wide association mapping reveals potential novel loci controlling stripe rust resistance in a Chinese wheat landrace diversity panel from the southern autumn-sown spring wheat zone. BMC Genomics, 2021, 22, 34.	2.8	18
2836	Genome-Wide Association Study of Morpho-Physiological Traits in <i>Aegilops tauschii</i> to Broaden Wheat Genetic Diversity. Plants, 2021, 10, 211.	3.5	2
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2839	A Two-in-One Strategy: Target and Nontarget Site Mechanisms Both Play Important Role in IMI-Resistant Weedy Rice. <i>International Journal of Molecular Sciences</i> , 2021, 22, 982.	4.1	9
2840	Genome-Wide Association Study Using a Multiparent Advanced Generation Intercross (MAGIC) Population Identified QTLs and Candidate Genes to Predict Shoot and Grain Zinc Contents in Rice. <i>Agriculture (Switzerland)</i> , 2021, 11, 70.	3.1	6
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2842	A GWAS to identify the cereal cyst nematode ( <i>Heterodera filipjevi</i> ) resistance loci in diverse wheat prebreeding lines. <i>Journal of Applied Genetics</i> , 2021, 62, 93-98.	1.9	17
2843	Genetic dissection of <i>Striga hermonthica</i> (Del.) Benth. resistance via genome-wide association and genomic prediction in tropical maize germplasm. <i>Theoretical and Applied Genetics</i> , 2021, 134, 941-958.	3.6	19
2844	Introduction to Bioinformatics. , 2021, , 3-20.		0
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2848	A candidate gene association analysis identifies SNPs potentially involved in drought tolerance in European beech ( <i>Fagus sylvatica</i> L.). <i>Scientific Reports</i> , 2021, 11, 2386.	3.3	16
2849	Whole-Genome Mapping of Date Palm ( <i>Phoenix Dactylifera</i> L.). <i>Compendium of Plant Genomes</i> , 2021, , 181-199.	0.5	0
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2851	Genetic architecture of wild soybean ( <i>Glycine soja</i> Sieb. and Zucc.) populations originating from different East Asian regions. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 1577-1588.	1.6	2
2852	Transcriptome-Derived Amplicon Sequencing Markers Elucidate the U.S. <i>Podosphaera macularis</i> Population Structure Across Feral and Commercial Plantings of <i>Humulus lupulus</i> . <i>Phytopathology</i> , 2021, 111, 194-203.	2.2	15
2853	Association analysis of physiological traits in spring barley ( <i>Hordeum vulgare</i> L.) under water deficit conditions. <i>Food Science and Nutrition</i> , 2021, 9, 1761-1779.	3.4	6
2854	Identification of genetic variation for salt tolerance in <i>Brassica napus</i> using genome-wide association mapping. <i>Molecular Genetics and Genomics</i> , 2021, 296, 391-408.	2.1	16
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2857	Identification of new genes and quantitative trait loci associated with growth curve parameters in F2 chicken population using genome-wide association study. <i>Animal Genetics</i> , 2021, 52, 171-184.	1.7	12
2858	Genome-Wide Association Study of Maize Aboveground Dry Matter Accumulation at Seedling Stage. <i>Frontiers in Genetics</i> , 2020, 11, 571236.	2.3	9
2860	Homozygosity Mapping Reveals Population History and Trait Architecture in Self-Incompatible Pear ( <i>Pyrus</i> spp.). <i>Frontiers in Plant Science</i> , 2020, 11, 590846.	3.6	7
2861	Development of a large set of diagnostic SNP markers using ddRAD-seq to study hybridization in <i>Rhinanthus major</i> and <i>R. minor</i> (Orobanchaceae). <i>Conservation Genetics Resources</i> , 2021, 13, 31-33.	0.8	1
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2864	Date Palm Quantitative Trait Loci. <i>Compendium of Plant Genomes</i> , 2021, , 155-168.	0.5	0
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2866	Status and Prospectives of Genome-Wide Association Studies in Plants. , 2021, , 413-457.		2
2868	Genome-Wide Association for Itraconazole Sensitivity in Non-resistant Clinical Isolates of <i>Aspergillus fumigatus</i> . <i>Frontiers in Fungal Biology</i> , 2021, 1, .	2.0	10
2869	A natural antisense transcript acts as a negative regulator for the maize drought stress response gene <i>ZmNAC48</i> . <i>Journal of Experimental Botany</i> , 2021, 72, 2790-2806.	4.8	28
2870	<i>QDtbn1</i> , an <i>EB-box</i> gene affecting maize tassel branch number by a dominant model. <i>Plant Biotechnology Journal</i> , 2021, 19, 1183-1194.	8.3	14
2871	Genetic Dissection for Maize Forage Digestibility Traits in a Multi-Parent Advanced Generation Intercross (MAGIC) Population. <i>Agronomy</i> , 2021, 11, 104.	3.0	9
2872	Measurement of Genetic Mobility Using a Transposon-Based Marker System in Sorghum. <i>Methods in Molecular Biology</i> , 2021, 2250, 195-205.	0.9	0
2873	Candidate genes and SNPs associated with stomatal conductance under drought stress in <i>Vitis</i> . <i>BMC Plant Biology</i> , 2021, 21, 7.	3.6	12
2874	Assessing Rice Salinity Tolerance: From Phenomics to Association Mapping. <i>Methods in Molecular Biology</i> , 2021, 2238, 339-375.	0.9	4
2875	Genome-Wide Association Mapping of Freezing Tolerance Loci in Canola ( <i>Brassica napus</i> L.). <i>Agronomy</i> , 2021, 11, 233.	3.0	7

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2877	Genome-wide association mapping of leaf rust and stripe rust resistance in wheat accessions using the 90K SNP array. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1233-1251.	3.6	34
2878	Genome-Wide Association Study of Tan Spot Resistance in a Hexaploid Wheat Collection From Kazakhstan. <i>Frontiers in Genetics</i> , 2020, 11, 581214.	2.3	24
2879	QTL identification for nine seed-related traits in <i>Brassica juncea</i> using a multiparent advanced generation intercross (MAGIC) population. <i>Czech Journal of Genetics and Plant Breeding</i> , 2021, 57, 9-18.	0.8	3
2880	Preliminary Phenotypic and SNP-Based Molecular Characterization of Maize ( <i>Zea mays</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Inbred Background of 48-2. <i>American Journal of Plant Sciences</i> , 2021, 12, 1073-1089.	0.8	0
2882	Genetic mapping of pollen fertility restoration QTLs in rye ( <i>Secale cereale</i> L.) with CMS Pampa. <i>Journal of Applied Genetics</i> , 2021, 62, 185-198.	1.9	3
2883	Resistance of European Spring 2-Row Barley Cultivars to <i>Pyrenophora graminea</i> and Detection of Associated Loci. <i>Agronomy</i> , 2021, 11, 374.	3.0	7
2884	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.	3.6	9
2885	Population structure, genetic diversity, and trait association analysis in rice ( <i>Oryza sativa</i> L.) genotypes for brown spot disease resistance. <i>Tropical Plant Pathology</i> , 2021, 46, 265.	1.5	1
2886	Exploitation of Tolerance of Wheat Kernel Weight and Shape-Related Traits from <i>Aegilops tauschii</i> under Heat and Combined Heat-Drought Stresses. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1830.	4.1	12
2887	Multi-Locus Genome-Wide Association Studies Reveal Fruit Quality Hotspots in Peach Genome. <i>Frontiers in Plant Science</i> , 2021, 12, 644799.	3.6	18
2888	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.	1.8	7
2889	Current status and impending progress for cassava structural genomics. <i>Plant Molecular Biology</i> , 2022, 109, 177-191.	3.9	11
2890	Population structure, genetic diversity and genomic selection signatures among a Brazilian common bean germplasm. <i>Scientific Reports</i> , 2021, 11, 2964.	3.3	46
2891	The genetic architecture of the dynamic changes in grain moisture in maize. <i>Plant Biotechnology Journal</i> , 2021, 19, 1195-1205.	8.3	35
2892	Evolutionary gain of oligosaccharide hydrolysis and sugar transport enhanced carbohydrate partitioning in sweet watermelon fruits. <i>Plant Cell</i> , 2021, 33, 1554-1573.	6.6	57
2893	Assessment of heterosis based on parental genetic distance estimated with SSR and SNP markers in upland cotton ( <i>Gossypium hirsutum</i> L.). <i>BMC Genomics</i> , 2021, 22, 123.	2.8	18
2894	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.	0.6	2

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2898	A novel motif in the 5'UTR of an orphan gene <i>Big Root Biomass</i> modulates root biomass in sesame. Plant Biotechnology Journal, 2021, 19, 1065-1079.	8.3	18
2899	OsTPR boosts the superior grains through increase in upper secondary rachis branches without incurring a grain quality penalty. Plant Biotechnology Journal, 2021, 19, 1396-1411.	8.3	9
2900	A worldwide maize panel revealed new genetic variation for cold tolerance. Theoretical and Applied Genetics, 2021, 134, 1083-1094.	3.6	17
2901	Bulk segregant analysis identifies SSR markers associated with leaf- and seed-related traits in Perilla crop ( <i>Perilla frutescens</i> L.). Genes and Genomics, 2021, 43, 323-332.	1.4	14
2902	Characterization of wheat curl mite resistance gene <i>Cmc4</i> in OK05312. Theoretical and Applied Genetics, 2021, 134, 993-1005.	3.6	11
2903	Analysis of the primary sources of quantitative adult plant resistance to stripe rust in U.S. soft red winter wheat germplasm. Plant Genome, 2021, 14, e20082.	2.8	1
2904	Molecular characterization of SIATG18f in response to Tomato leaf curl New Delhi virus infection in tomato and development of a CAPS marker for leaf curl disease tolerance. Theoretical and Applied Genetics, 2021, 134, 1463-1474.	3.6	14
2905	Application of Genomics to Understand Salt Tolerance in Lentil. Genes, 2021, 12, 332.	2.4	12
2906	Genome-Wide Association Studies for Fusarium Head Blight Resistance and Its Trade-Off With Grain Yield in Soft Red Winter Wheat. Plant Disease, 2021, 105, 2435-2444.	1.4	14
2907	Genomic prediction using training population design in interspecific soybean populations. Molecular Breeding, 2021, 41, 1.	2.1	7
2908	Distinguishing HapMap Accessions Through Recursive Set Partitioning in Hierarchical Decision Trees. Frontiers in Plant Science, 2021, 12, 628421.	3.6	0
2910	Genome-wide association study to identify soybean stem pushing resistance and lodging resistance loci. Canadian Journal of Plant Science, 2021, 101, 663-670.	0.9	4
2912	Associations between population epigenetic differentiation and environmental factors in the exotic weed mile-a-minute ( <i>Mikania micrantha</i> ). Weed Science, 2021, 69, 307-332.	1.5	6
2913	Molecular characterization, expression and functional analysis of acyl-CoA-binding protein gene family in maize ( <i>Zea mays</i> ). BMC Plant Biology, 2021, 21, 94.	3.6	12
2914	Integration of high-density genetic mapping with transcriptome analysis uncovers numerous agronomic QTL and reveals candidate genes for the control of tillering in sorghum. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	4
2916	Transcriptomic and genome-wide association study reveal long noncoding RNAs responding to nitrogen deficiency in maize. BMC Plant Biology, 2021, 21, 93.	3.6	18
2917	Genome-wide association mapping identifies <i>HvNIP2;2</i> / <i>HvLsi6</i> accounting for efficient boron transport in barley. Physiologia Plantarum, 2021, 171, 809-822.	5.2	12

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2918	Enhancing grain-yield-related traits by CRISPR-Cas9 promoter editing of maize CLE genes. <i>Nature Plants</i> , 2021, 7, 287-294.	9.3	199
2919	Association mapping for maize stover yield and saccharification efficiency using a multiparent advanced generation intercross (MAGIC) population. <i>Scientific Reports</i> , 2021, 11, 3425.	3.3	16
2920	Identification of genomic loci controlling phenologic and morphologic traits in barley ( <i>Hordeum</i> ). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 6</i> 2021, 22, 291-304.	0.1	0
2921	Genome-wide association of rice response to blast fungus identifies loci for robust resistance under high nitrogen. <i>BMC Plant Biology</i> , 2021, 21, 99.	3.6	14
2922	Genomic Resource Development for <i>Hydrangea</i> ( <i>Hydrangea macrophylla</i> (Thunb.) Ser.)-A Transcriptome Assembly and a High-Density Genetic Linkage Map. <i>Horticulturae</i> , 2021, 7, 25.	2.8	6
2923	Discerning molecular diversity and association mapping for phenological, physiological and yield traits under high temperature stress in chickpea ( <i>Cicer arietinum</i> L.). <i>Journal of Genetics</i> , 2021, 100, 1.	0.7	7
2924	Mining favorable alleles for rice sheath blight resistance by association mapping. <i>Plant Growth Regulation</i> , 2021, 94, 61-72.	3.4	2
2925	A Genome-Wide Genetic Diversity Scan Reveals Multiple Signatures of Selection in a European Soybean Collection Compared to Chinese Collections of Wild and Cultivated Soybean Accessions. <i>Frontiers in Plant Science</i> , 2021, 12, 631767.	3.6	16
2926	Marker-trait association analysis for drought tolerance in smooth brome grass. <i>BMC Plant Biology</i> , 2021, 21, 116.	3.6	1
2927	Combination of Genome-Wide Association Study and QTL Mapping Reveals the Genetic Architecture of Fusarium Stalk Rot in Maize. <i>Frontiers in Agronomy</i> , 2021, 2, .	3.3	7
2928	Evaluating the genetic diversity in two tropical leguminous trees, <i>Dalbergia cochinchinensis</i> and <i>D. nigrescens</i> , in lowland forests in Cambodia and Thailand using MIG-seq. <i>Genes and Genetic Systems</i> , 2021, 96, 41-53.	0.7	1
2929	Association mapping to identify molecular markers associated with resistance genes to stink bugs in soybean. <i>Euphytica</i> , 2021, 217, 1.	1.2	6
2931	Genome-wide association study of cyanogenic glycosides, proline, sugars, and pigments in <i>Eucalyptus cladocalyx</i> after 18 consecutive dry summers. <i>Physiologia Plantarum</i> , 2021, 172, 1550-1569.	5.2	8
2932	Genetic diversity and population structure of popcorn germplasm resources using genome-wide SNPs through genotyping-by-sequencing. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 2379-2389.	1.6	8
2933	Genome wide association analyses to understand genetic basis of flowering and plant height under three levels of nitrogen application in <i>Brassica juncea</i> (L.) Czern & Coss. <i>Scientific Reports</i> , 2021, 11, 4278.	3.3	18
2934	Evaluating the accuracy of genomic prediction for the management and conservation of relictual natural tree populations. <i>Tree Genetics and Genomes</i> , 2021, 17, 1.	1.6	32
2935	Chromosome-Level Genome Assembly of the American Cranberry ( <i>Vaccinium macrocarpon</i> Ait.) and Its Wild Relative <i>Vaccinium microcarpum</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 633310.	3.6	29
2936	Population Genomic Analysis of <i>Listeria monocytogenes</i> From Food Reveals Substrate-Specific Genome Variation. <i>Frontiers in Microbiology</i> , 2021, 12, 620033.	3.5	6



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2937	Association Mapping of Verticillium Wilt Disease in a Worldwide Collection of Cotton ( <i>Gossypium</i> ) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	3.5	9
2938	Genome-Wide Association Study of Topsoil Root System Architecture in Field-Grown Soybean [ <i>Glycine max</i> (L.) Merr.]. <i>Frontiers in Plant Science</i> , 2020, 11, 590179.	3.6	7
2939	Effects of high temperature on spikelet sterility in rice ( <i>Oryza sativa</i> L.): association between molecular markers and allelic phenotypic effect in field condition. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 1923-1935.	1.6	5
2940	A Single Nucleotide Mutation in a GLUTAMATE RECEPTOR-LIKE Gene Confers Resistance to Fusarium Wilt in <i>Gossypium hirsutum</i> . <i>Advanced Science</i> , 2021, 8, 2002723.	11.2	37
2941	Genome-wide association study of low nitrogen tolerance traits at the seedling stage of rapeseed. <i>Biologia Plantarum</i> , 0, 65, 10-18.	1.9	3
2943	Genotyping-by-sequencing (GBS) for SNP-based linkage map construction for two <i>Prunus</i> rootstocks from a peach rootstock breeding program. <i>Acta Horticulturae</i> , 2021, , 113-120.	0.2	3
2944	Association Mapping of Thousand Grain Weight using SSR and SNP Markers in Rice ( <i>Oryza sativa</i> L.) Across Six Environments. <i>Tropical Plant Biology</i> , 2021, 14, 143-155.	1.9	4
2945	A classic approach for determining genomic prediction accuracy under terminal drought stress and well-watered conditions in wheat landraces and cultivars. <i>PLoS ONE</i> , 2021, 16, e0247824.	2.5	6
2946	Genetic parameter estimation and selection in advanced breeding population of white Guinea yam. <i>Journal of Crop Improvement</i> , 2021, 35, 790-815.	1.7	7
2947	Association Mapping and Transcriptome Analysis Reveal the Genetic Architecture of Maize Kernel Size. <i>Frontiers in Plant Science</i> , 2021, 12, 632788.	3.6	3
2949	Genetic characterization of a <i>Sorghum bicolor</i> multiparent mapping population emphasizing carbon-partitioning dynamics. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	23
2950	Genome sequence and genetic diversity analysis of an under-domesticated orphan crop, white fonio ( <i>Digitaria exilis</i> ). <i>GigaScience</i> , 2021, 10, .	6.4	23
2951	Manipulating <i>ZmEXPA4</i> expression ameliorates the drought-induced prolonged anthesis and silking interval in maize. <i>Plant Cell</i> , 2021, 33, 2058-2071.	6.6	33
2952	Seascape genomics reveals candidate molecular targets of heat stress adaptation in three coral species. <i>Molecular Ecology</i> , 2021, 30, 1892-1906.	3.9	14
2953	Genetic Diversity of Soybeans ( <i>Glycine max</i> (L.) Merr.) with Black Seed Coats and Green Cotyledons in Korean Germplasm. <i>Agronomy</i> , 2021, 11, 581.	3.0	20
2954	Regional association analysis coupled with transcriptome analyses reveal candidate genes affecting seed oil accumulation in <i>Brassica napus</i> . <i>Theoretical and Applied Genetics</i> , 2021, 134, 1545-1555.	3.6	7
2955	Evaluation and genome-wide association study of resistance to bacterial blight race 18 in U.S. Upland cotton germplasm. <i>Molecular Genetics and Genomics</i> , 2021, 296, 719-729.	2.1	7
2956	Labelling Selective Sweeps Used in Durum Wheat Breeding from a Diverse and Structured Panel of Landraces and Cultivars. <i>Biology</i> , 2021, 10, 258.	2.8	6

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2958	Population genomics of Mediterranean oat ( <i>A. sativa</i> ) reveals high genetic diversity and three loci for heading date. <i>Theoretical and Applied Genetics</i> , 2021, 134, 2063-2077.	3.6	10
2959	Large Genetic Diversity and Strong Positive Selection in F-Box and GPCR Genes among the Wild Isolates of <i>Caenorhabditis elegans</i> . <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	13
2960	High-resolution genome-wide association study pinpoints metal transporter and chelator genes involved in the genetic control of element levels in maize grain. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	18
2961	A linear regression model for the prediction of rice sheath blight field resistance. <i>Plant Disease</i> , 2021, , PDIS08201681RE.	1.4	1
2962	Genomic and Phenotypic Diversity of Cultivated and Wild Tomatoes with Varying Levels of Heat Tolerance. <i>Genes</i> , 2021, 12, 503.	2.4	10
2963	Genomic region associated with pod color variation in pea ( <i>Pisum sativum</i> ). <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	9
2965	Pairwise linkage disequilibrium estimation for polyploids. <i>Molecular Ecology Resources</i> , 2021, 21, 1230-1242.	4.8	18
2967	Gene disruption by structural mutations drives selection in US rice breeding over the last century. <i>PLoS Genetics</i> , 2021, 17, e1009389.	3.5	6
2968	Genome-Wide Association of Stem Carbohydrate Accumulation and Remobilization during Grain Growth in Bread Wheat ( <i>Triticum aestivum</i> L.) in Mediterranean Environments. <i>Plants</i> , 2021, 10, 539.	3.5	2
2970	Genetic dissection of the volatilome-fruit texture interplay in apple. <i>Acta Horticulturae</i> , 2021, , 383-390.	0.2	0
2971	Emergence and diversification of a highly invasive chestnut pathogen lineage across southeastern Europe. <i>ELife</i> , 2021, 10, .	6.0	24
2972	Mining QTL and genes for root traits and biochemical parameters under vegetative drought in South Indian genotypes of finger millet ( <i>Eleusine coracana</i> (L.) Gaertn) by association mapping and in silico comparative genomics. <i>Biocatalysis and Agricultural Biotechnology</i> , 2021, 32, 101935.	3.1	9
2973	Genetic loci mediating circadian clock output plasticity and crop productivity under barley domestication. <i>New Phytologist</i> , 2021, 230, 1787-1801.	7.3	14
2974	Detection of breeding signatures in wheat using a linkage disequilibrium-corrected mapping approach. <i>Scientific Reports</i> , 2021, 11, 5527.	3.3	18
2975	Genome-wide association study to identify chromosomal regions related to panicle architecture in rice ( <i>Oryza sativa</i> ). <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 2849-2865.	1.6	2
2976	Maize germplasm chronosequence shows crop breeding history impacts recruitment of the rhizosphere microbiome. <i>ISME Journal</i> , 2021, 15, 2454-2464.	9.8	49
2977	Identification of Bacterial Blight Resistance Loci in Rice ( <i>Oryza sativa</i> L.) against Diverse Xoo Thai Strains by Genome-Wide Association Study. <i>Plants</i> , 2021, 10, 518.	3.5	8

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2978	Genotyping-by-Sequencing in <i>Vigna unguiculata</i> Landraces and Its Utility for Assessing Taxonomic Relationships. <i>Plants</i> , 2021, 10, 509.	3.5	10
2979	Genome-wide association mapping identifies novel loci underlying fire blight resistance in apple. <i>Plant Genome</i> , 2021, 14, e20087.	2.8	11
2980	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.	3.3	14
2981	Interdisciplinary strategies to enable data-driven plant breeding in a changing climate. <i>One Earth</i> , 2021, 4, 372-383.	6.8	20
2982	Identification of major QTL for waterlogging tolerance in maize using genome-wide association study and bulked sample analysis. <i>Journal of Applied Genetics</i> , 2021, 62, 405-418.	1.9	15
2983	Genome-wide association analysis uncovers stable QTLs for yield and quality traits of spring bread wheat ( <i>Triticum aestivum</i> ) across contrasting environments. <i>Plant Gene</i> , 2021, 25, 100269.	2.3	17
2984	rMVP: A Memory-efficient, Visualization-enhanced, and Parallel-accelerated Tool for Genome-wide Association Study. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 619-628.	6.9	396
2985	A comparative assessment of GBS-SNPs aligned to scaffold and pseudo-chromosome level of the pear reference genome. <i>Acta Horticulturae</i> , 2021, , 255-260.	0.2	0
2988	Genome-Wide Association Studies of Mineral Content in Common Bean. <i>Frontiers in Plant Science</i> , 2021, 12, 636484.	3.6	26
2989	Association analysis and molecular tagging of phytochemicals in the endangered medicinal plant licorice ( <i>Glycyrrhiza glabra</i> L.). <i>Phytochemistry</i> , 2021, 183, 112629.	2.9	11
2990	Population genetic structure and association mapping for iron toxicity tolerance in rice. <i>PLoS ONE</i> , 2021, 16, e0246232.	2.5	20
2991	<i>Arabidopsis thaliana</i> Genes Associated with Cucumber mosaic virus Virulence and Their Link to Virus Seed Transmission. <i>Microorganisms</i> , 2021, 9, 692.	3.6	13
2992	Dissecting nematode resistance regions in soybean revealed pleiotropic effect of soybean cyst and reniform nematode resistance genes. <i>Plant Genome</i> , 2021, 14, e20083.	2.8	12
2993	A global barley panel revealing genomic signatures of breeding in modern Australian cultivars. <i>Plant Journal</i> , 2021, 106, 419-434.	5.7	19
2994	Genome-wide association studies reveal the coordinated regulatory networks underlying photosynthesis and wood formation in <i>Populus</i> . <i>Journal of Experimental Botany</i> , 2021, 72, 5372-5389.	4.8	12
2995	Genome-wide diversity and structure variation among lablab [ <i>Lablab purpureus</i> (L.) Sweet] accessions and their implication in a Forage breeding program. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 2997-3010.	1.6	14
2998	Joint analysis of days to flowering reveals independent temperate adaptations in maize. <i>Heredity</i> , 2021, 126, 929-941.	2.6	4
2999	Genetic Mapping by Sequencing More Precisely Detects Loci Responsible for Anaerobic Germination Tolerance in Rice. <i>Plants</i> , 2021, 10, 705.	3.5	7

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3000	New genomic approaches for enhancing maize genetic improvement. <i>Current Opinion in Plant Biology</i> , 2021, 60, 101977.	7.1	9
3001	Genetic diversity, population structure, and selection signature in Ethiopian sorghum [ <i>Sorghum bicolor</i> L. (Moench)] germplasm. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	13
3003	GWAS of pod morphological and color characters in common bean. <i>BMC Plant Biology</i> , 2021, 21, 184.	3.6	20
3004	Linkage disequilibrium patterns, population structure and diversity analysis in a worldwide durum wheat collection including Argentinian genotypes. <i>BMC Genomics</i> , 2021, 22, 233.	2.8	17
3005	Genetic diversity and population structure of advanced clones selected over forty years by a potato breeding program in the USA. <i>Scientific Reports</i> , 2021, 11, 8344.	3.3	33
3006	Genetic dissection of flowering time in flax ( <i>Linum usitatissimum</i> L.) through single- and multi-locus genome-wide association studies. <i>Molecular Genetics and Genomics</i> , 2021, 296, 877-891.	2.1	16
3007	Cotton pan-genome retrieves the lost sequences and genes during domestication and selection. <i>Genome Biology</i> , 2021, 22, 119.	8.8	76
3008	Genome-wide association study (GWAS) of major QTLs for bunch and oil yield related traits in <i>Elaeis guineensis</i> L. <i>Plant Science</i> , 2021, 305, 110810.	3.6	7
3009	Evolutionary genomics of endangered Hawaiian tree snails (Achatinellidae: Achatinellinae) for conservation of adaptive capacity. <i>PeerJ</i> , 2021, 9, e10993.	2.0	7
3011	Validation of functional polymorphisms affecting maize plant height by unoccupied aerial systems discovers novel temporal phenotypes. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	18
3012	Genetic diversity structure of western-type carrots. <i>BMC Plant Biology</i> , 2021, 21, 200.	3.6	8
3014	Genomic regions associated with leaf wilting traits under drought stress in spring wheat at the seedling stage revealed by GWAS. <i>Environmental and Experimental Botany</i> , 2021, 184, 104393.	4.2	29
3015	Crop breeding for a changing climate: integrating phenomics and genomics with bioinformatics. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1677-1690.	3.6	38
3016	SNP detection and population structure evaluation of <i>Salix gordejewii</i> Y. L. Chang et Skv. in Hunshandake Sandland, Inner Mongolia, China. <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 997-1005.	3.1	1
3017	Genome-Wide Association and Prediction of Male and Female Floral Hybrid Potential Traits in Elite Spring Bread Wheat Genotypes. <i>Plants</i> , 2021, 10, 895.	3.5	4
3018	Genetic variation and population structure in China summer maize germplasm. <i>Scientific Reports</i> , 2021, 11, 8012.	3.3	16
3019	Genome-wide association mapping for agronomic traits in an 8-way Upland cotton MAGIC population by SLAF-seq. <i>Theoretical and Applied Genetics</i> , 2021, 134, 2459-2468.	3.6	10
3020	Marker-Assisted Introgression and Stacking of Major QTLs Controlling Grain Number (Gn1a) and Number of Primary Branching (WFP) to NERICA Cultivars. <i>Plants</i> , 2021, 10, 844.	3.5	31

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3024	Genomic prediction for growth using a low-density SNP panel in dromedary camels. <i>Scientific Reports</i> , 2021, 11, 7675.	3.3	10
3025	Genome-wide association study for adult plant resistance to yellow rust in spring bread wheat ( <i>Triticum aestivum</i> L.). <i>Euphytica</i> , 2021, 217, 1.	1.2	10
3026	Allelic Diversity at Abiotic Stress Responsive Genes in Relationship to Ecological Drought Indices for Cultivated Tepary Bean, <i>Phaseolus acutifolius</i> A. Gray, and Its Wild Relatives. <i>Genes</i> , 2021, 12, 556.	2.4	38
3028	Genetic Diversity and Association Analysis among Germplasms of <i>Diospyros kaki</i> in Zhejiang Province Based on SSR Markers. <i>Forests</i> , 2021, 12, 422.	2.1	6
3029	Nitrogen Use Efficiency in Sorghum: Exploring Native Variability for Traits Under Variable N-Regimes. <i>Frontiers in Plant Science</i> , 2021, 12, 643192.	3.6	13
3030	QTL mapping of five forage quality traits in sorghum <i>—</i> sudangrass. <i>Pakistan Journal of Botany</i> , 2021, 53, .	0.5	1
3031	A genomics resource for genetics, physiology, and breeding of West African sorghum. <i>Plant Genome</i> , 2021, 14, e20075.	2.8	14
3032	Pathway-based analysis of anthocyanin diversity in diploid potato. <i>PLoS ONE</i> , 2021, 16, e0250861.	2.5	9
3033	Association mapping of genomic loci linked with <i>Fusarium</i> wilt resistance ( <i>Foc</i> 2) in chickpea. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2021, 19, 195-202.	0.8	9
3034	A capture-based assay for detection and characterization of transposon polymorphisms in maize. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	1
3035	Classical phenotyping and deep learning concur on genetic control of stomatal density and area in sorghum. <i>Plant Physiology</i> , 2021, 186, 1562-1579.	4.8	26
3036	Introgression between <i>Sphyrapicus nuchalis</i> and <i>S. varius</i> sapsuckers in a hybrid zone in west-central Alberta. <i>Journal of Avian Biology</i> , 2021, 52, .	1.2	4
3037	Sources of Resistance to Common Bacterial Blight and Charcoal Rot Disease for the Production of Mesoamerican Common Beans in the Southern United States. <i>Plants</i> , 2021, 10, 998.	3.5	7
3040	Genome-wide association study for grain mineral content in a Brazilian common bean diversity panel. <i>Theoretical and Applied Genetics</i> , 2021, 134, 2795-2811.	3.6	15
3041	Plastid genome sequencing, identification of nuclear SNP markers, and quality assessment of medicinal rhizomatous herb <i>Polygonatum odoratum</i> (Asparagaceae) cultivars. <i>Ecology and Evolution</i> , 2021, 11, 7660-7676.	1.9	4
3042	A review on cobia, <i>Rachycentron canadum</i> , aquaculture. <i>Journal of the World Aquaculture Society</i> , 2021, 52, 691-709.	2.4	16
3043	Genome resequencing reveals DNA polymorphisms associated with seed size/weight determination in chickpea. <i>Genomics</i> , 2021, 113, 1458-1468.	2.9	7

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3045	MultiGWAS: An integrative tool for Genome Wide Association Studies in tetraploid organisms. <i>Ecology and Evolution</i> , 2021, 11, 7411-7426.	1.9	5
3046	Genome sequencing sheds light on the contribution of structural variants to <i>Brassica oleracea</i> diversification. <i>BMC Biology</i> , 2021, 19, 93.	3.8	41
3048	The UCR Minicore: a resource for cowpea research and breeding. , 2021, 3, e95.		26
3050	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, .	1.8	7
3051	Genome-wide association study of seed coat color in sesame ( <i>Sesamum indicum</i> L.). <i>PLoS ONE</i> , 2021, 16, e0251526.	2.5	23
3052	Genome-wide association mapping reveals race-specific SNP markers associated with anthracnose resistance in carioca common beans. <i>PLoS ONE</i> , 2021, 16, e0251745.	2.5	4
3053	Regions of Chromosome 2A of Bread Wheat ( <i>Triticum aestivum</i> L.) Associated with Variation in Physiological and Agronomical Traits under Contrasting Water Regimes. <i>Plants</i> , 2021, 10, 1023.	3.5	8
3056	Identifying Anti-Oxidant Biosynthesis Genes in Pearl Millet [ <i>Pennisetum glaucum</i> (L.) R. Br.] Using Genome-Wide Association Analysis. <i>Frontiers in Plant Science</i> , 2021, 12, 599649.	3.6	11
3057	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> Å— J. regia hybrids. <i>Horticulture Research</i> , 2021, 8, 111.	6.3	4
3058	Identification of glutathione transferase gene associated with partial resistance to <i>Sclerotinia</i> stem rot of soybean using genome-wide association and linkage mapping. <i>Theoretical and Applied Genetics</i> , 2021, 134, 2699-2709.	3.6	10
3059	Specific adaptation for early maturity and height stability in Icelandic spring barley. <i>Crop Science</i> , 2021, 61, 2306-2323.	1.8	3
3060	Genome-wide simple sequence repeats (SSR) markers discovered from whole-genome sequence comparisons of multiple spinach accessions. <i>Scientific Reports</i> , 2021, 11, 9999.	3.3	38
3061	Genetic variation in a radish ( <i>Raphanus sativus</i> L.) geodiversity collection. <i>Genetic Resources and Crop Evolution</i> , 2022, 69, 163-171.	1.6	5
3062	Novel Loci for Kernel Hardness Appeared as a Response to Heat and Combined Heat-Drought Conditions in Wheat Harboring <i>Aegilops tauschii</i> Diversity. <i>Agronomy</i> , 2021, 11, 1061.	3.0	11
3063	Association mapping and domestication analysis to dissect genetic improvement process of upland cotton yield-related traits in China. <i>Journal of Cotton Research</i> , 2021, 4, .	2.5	5
3065	Single nucleotide polymorphisms reveal genetic diversity in New Mexican chile peppers ( <i>Capsicum</i> spp.). <i>BMC Genomics</i> , 2021, 22, 356.	2.8	14
3067	Identification of Novel Marker-Trait Associations for Lint Yield Contributing Traits in Upland Cotton ( <i>Gossypium hirsutum</i> L.) Using SSRs. <i>Frontiers in Plant Science</i> , 2021, 12, 653270.	3.6	6
3069	Genome-Wide Association Study of Kernel Traits in <i>Aegilops tauschii</i> . <i>Frontiers in Genetics</i> , 2021, 12, 651785.	2.3	4



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3070	Identification of candidate SNPs and genes associated with anti-RGNV using GWAS in the red-spotted grouper, <i>Epinephelus akaara</i> . <i>Fish and Shellfish Immunology</i> , 2021, 112, 31-37.	3.6	8
3071	Genome-Wide Association Study Reveals Genomic Regions Associated with Fusarium Wilt Resistance in Common Bean. <i>Genes</i> , 2021, 12, 765.	2.4	15
3072	Cryptic introgressions contribute to transgressive segregation for early blight resistance in tomato. <i>Theoretical and Applied Genetics</i> , 2021, 134, 2561-2575.	3.6	6
3073	Genetic dissection of soybean partial resistance to sclerotinia stem rot through genome wide association study and high throughout single nucleotide polymorphisms. <i>Genomics</i> , 2021, 113, 1262-1271.	2.9	15
3074	Toward the identification of molecular markers associated with phytochemical traits in the Iranian sumac ( <i>Rhus coriaria</i> L.) population. <i>Food Science and Nutrition</i> , 2021, 9, 3142-3154.	3.4	4
3075	Genetic variation and association analyses identify genes linked to fruit set-related traits in grapevine. <i>Plant Science</i> , 2021, 306, 110875.	3.6	5
3076	Unoccupied aerial systems discovered overlooked loci capturing the variation of entire growing period in maize. <i>Plant Genome</i> , 2021, 14, e20102.	2.8	16
3078	Genetic diversity among Brazilian carioca common bean cultivars for nitrogen use efficiency. <i>Crop Science</i> , 2021, 61, 2534-2547.	1.8	1
3079	Genome-wide association analysis for yield-related traits at the R6 stage in a Chinese soybean mini core collection. <i>Genes and Genomics</i> , 2021, 43, 897-912.	1.4	8
3080	Identification of Prospective Soybean Accessions for the Creation of a Genebank Core Collection Based on High Density DNA Marker Data. <i>IOP Conference Series: Earth and Environmental Science</i> , 2021, 762, 012069.	0.3	0
3081	Genome wide association study for the identification of genes associated with tail fat deposition in Chinese sheep breeds. <i>Biology Open</i> , 2021, 10, .	1.2	16
3082	Genetic Diversity, Linkage Disequilibrium and Population Structure of Bulgarian Bread Wheat Assessed by Genome-Wide Distributed SNP Markers: From Old Germplasm to Semi-Dwarf Cultivars. <i>Plants</i> , 2021, 10, 1116.	3.5	15
3083	Genome-wide association mapping of the “super-soft”™ kernel texture in white winter wheat. <i>Theoretical and Applied Genetics</i> , 2021, 134, 2547-2559.	3.6	12
3084	Genetic Effects and Expression Patterns of the Nitrate Transporter (NRT) Gene Family in <i>Populus tomentosa</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 661635.	3.6	16
3085	Genetic study of the resistance of faba bean ( <i>Vicia faba</i> ) against the fungus <i>Ascochyta fabae</i> through a genome-wide association analysis. <i>Plant Breeding</i> , 2021, 140, 442-452.	1.9	9
3086	Evolutionary Processes Involved in the Emergence and Expansion of an Atypical <i>O. sativa</i> Group in Madagascar. <i>Rice</i> , 2021, 14, 44.	4.0	3
3089	The landscape of gene “CDS” haplotype diversity in rice: Properties, population organization, footprints of domestication and breeding, and implications for genetic improvement. <i>Molecular Plant</i> , 2021, 14, 787-804.	8.3	58
3090	The Genetic Base for Peanut Height-Related Traits Revealed by a Meta-Analysis. <i>Plants</i> , 2021, 10, 1058.	3.5	7

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3091	A combination of genome-wide and transcriptome-wide association studies reveals genetic elements leading to male sterility during high temperature stress in cotton. <i>New Phytologist</i> , 2021, 231, 165-181.	7.3	33
3092	Identification of Resistance Sources and Genome-Wide Association Mapping of Septoria Tritici Blotch Resistance in Spring Bread Wheat Germplasm of ICARDA. <i>Frontiers in Plant Science</i> , 2021, 12, 600176.	3.6	8
3093	Genetic characterization of global collection of flax ( <i>L. Usitatissimum</i> L.) utilizing molecular marker. <i>Ecological Genetics and Genomics</i> , 2021, 19, 100084.	0.5	1
3094	Genome-Wide Association Study Uncover the Genetic Architecture of Salt Tolerance-Related Traits in Common Wheat ( <i>Triticum aestivum</i> L.). <i>Frontiers in Genetics</i> , 2021, 12, 663941.	2.3	15
3095	Barley Viridis-k links an evolutionarily conserved C-type ferredoxin to chlorophyll biosynthesis. <i>Plant Cell</i> , 2021, 33, 2834-2849.	6.6	4
3096	Rapid sequence evolution driven by transposable elements at a virulence locus in a fungal wheat pathogen. <i>BMC Genomics</i> , 2021, 22, 393.	2.8	18
3097	Dissection of the Genetic Basis of Yield-Related Traits in the Chinese Peanut Mini-Core Collection Through Genome-Wide Association Studies. <i>Frontiers in Plant Science</i> , 2021, 12, 637284.	3.6	18
3098	Genome wide association study reveals plant loci controlling heritability of the rhizosphere microbiome. <i>ISME Journal</i> , 2021, 15, 3181-3194.	9.8	97
3099	Underground heterosis for yield improvement in melon. <i>Journal of Experimental Botany</i> , 2021, 72, 6205-6218.	4.8	11
3100	Genome-Wide Association Analysis for Stem Cross Section Properties, Height and Heading Date in a Collection of Spanish Durum Wheat Landraces. <i>Plants</i> , 2021, 10, 1123.	3.5	9
3102	Genome-wide association study reveals early seedling vigour-associated quantitative trait loci in indica rice. <i>Euphytica</i> , 2021, 217, 1.	1.2	1
3103	Genetic basis of some physiological traits and yield in early and late sowing conditions in bread wheat ( <i>Triticum aestivum</i> L.). <i>Journal of Applied Genetics</i> , 2021, 62, 601-605.	1.9	3
3104	Genome-wide association analysis permits characterization of <i>Stagonospora nodorum</i> blotch (SNB) resistance in hard winter wheat. <i>Scientific Reports</i> , 2021, 11, 12570.	3.3	13
3105	Elucidating SNP-based genetic diversity and population structure of advanced breeding lines of bread wheat ( <i>Triticum aestivum</i> L.). <i>PeerJ</i> , 2021, 9, e11593.	2.0	5
3106	Genome-Wide Association Study and Genomic Prediction for Soybean Cyst Nematode Resistance in USDA Common Bean ( <i>Phaseolus vulgaris</i> ) Core Collection. <i>Frontiers in Plant Science</i> , 2021, 12, 624156.	3.6	20
3107	Molecular genetic diversity and population structure analyses of rutabaga accessions from Nordic countries as revealed by single nucleotide polymorphism markers. <i>BMC Genomics</i> , 2021, 22, 442.	2.8	7
3108	PIP-SNP: a pipeline for processing SNP data featured as linkage disequilibrium bin mapping, genotype imputing and marker synthesizing. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab060.	3.2	1
3109	Genetic variation and association mapping in the F2 population of the Perilla crop ( <i>Perilla frutescens</i> ) Tj ETQq1 1 0.784314 rgBT /Overlo	1.2	11

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3110	Genome Wide Association Mapping of Root Traits in the Andean Genepool of Common Bean ( <i>Phaseolus</i> ) Tj ETQq0.0 rgBT /Overlock 1	3.6	10
3111	Association between the Polymorphisms of fads2a and fads2b and Poly-Unsaturated Fatty Acids in Common Carp ( <i>Cyprinus carpio</i> ). <i>Animals</i> , 2021, 11, 1780.	2.3	5
3113	Genome Wide Association Study of Rice ( <i>Oryza sativa</i> L.) during Heading Stage under a High Temperature. <i>Plant Breeding and Biotechnology</i> , 2021, 9, 104-111.	0.9	2
3114	Machine-learning predicts genomic determinants of meiosis-driven structural variation in a eukaryotic pathogen. <i>Nature Communications</i> , 2021, 12, 3551.	12.8	21
3115	Natural Genetic Diversity in Tomato Flavor Genes. <i>Frontiers in Plant Science</i> , 2021, 12, 642828.	3.6	16
3116	Genome-wide association analysis of drought adaptive traits in common bean. <i>Crop Science</i> , 2021, 61, 3232-3253.	1.8	11
3117	Genetic Diversity, Population Structure and Screening of Molecular Markers Associated to Agronomic Traits in Safflower ( <i>Carthamus tinctorius</i> L.). <i>Iranian Journal of Science and Technology, Transaction A: Science</i> , 2021, 45, 1549-1560.	1.5	6
3119	Genotyping-by-Sequencing-Based Genome-Wide Association Studies of Fusarium Wilt Resistance in Radishes ( <i>Raphanus sativus</i> L.). <i>Genes</i> , 2021, 12, 858.	2.4	9
3120	Genome-wide association analysis of resistance to aluminum toxicity in the roots of common bean seedlings. <i>Crop Science</i> , 2021, 61, 2271-2279.	1.8	2
3122	Evaluation of Septoria Nodorum Blotch (SNB) Resistance in Glumes of Wheat ( <i>Triticum aestivum</i> L.) and the Genetic Relationship With Foliar Disease Response. <i>Frontiers in Genetics</i> , 2021, 12, 681768.	2.3	4
3123	Genome-Wide Association Study Reveals a Genomic Region Associated with Mite-Recruitment Phenotypes in the Domesticated Grapevine ( <i>Vitis vinifera</i> ). <i>Genes</i> , 2021, 12, 1013.	2.4	8
3124	Genetic dissection of natural variation in oilseed traits of camelina by whole-genome resequencing and QTL mapping. <i>Plant Genome</i> , 2021, 14, e20110.	2.8	24
3125	Dissecting the trade-off of grain number and size in wheat. <i>Planta</i> , 2021, 254, 3.	3.2	13
3126	Genome-Wide Association Study on Root Traits Under Different Growing Environments in Wheat ( <i>Triticum aestivum</i> L.). <i>Frontiers in Genetics</i> , 2021, 12, 646712.	2.3	8
3127	Genome-wide association mapping of seedling and adult plant response to stem rust in a durum wheat panel. <i>Plant Genome</i> , 2021, 14, e20105.	2.8	5
3128	Environmental association modelling with loci under divergent selection predicts the distribution range of a lizard. <i>Molecular Ecology</i> , 2021, 30, 3856-3868.	3.9	5
3129	A recessive gene pepy-1 encoding Pelota confers resistance to begomovirus isolates of PepYLCIV and PepYLCAV in <i>Capsicum annuum</i> . <i>Theoretical and Applied Genetics</i> , 2021, 134, 2947-2964.	3.6	27
3130	Using high-throughput multiple optical phenotyping to decipher the genetic architecture of maize drought tolerance. <i>Genome Biology</i> , 2021, 22, 185.	8.8	47

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3132	Identification of the PmWEEP locus controlling weeping traits in <i>Prunus mume</i> through an integrated genome-wide association study and quantitative trait locus mapping. <i>Horticulture Research</i> , 2021, 8, 131.	6.3	10
3133	Overview on domestication, breeding, genetic gain and improvement of tuber quality traits of potato using fast forwarding technique (GWAS): A review. <i>Plant Breeding</i> , 2021, 140, 519-542.	1.9	19
3134	High resolution mapping and candidate gene identification of downy mildew race 16 resistance in spinach. <i>BMC Genomics</i> , 2021, 22, 478.	2.8	14
3135	High-resolution genome-wide association study and genomic prediction for disease resistance and cold tolerance in wheat. <i>Theoretical and Applied Genetics</i> , 2021, 134, 2857-2873.	3.6	15
3136	Genetic diversity and inter-trait relationship of tropical extra-early maturing quality protein maize inbred lines under low soil nitrogen stress. <i>PLoS ONE</i> , 2021, 16, e0252506.	2.5	10
3137	An overview of current population genomics methods for the analysis of whole-genome resequencing data in eukaryotes. <i>Molecular Ecology</i> , 2021, 30, 6036-6071.	3.9	38
3138	Genomic prediction of the performance of hybrids and the combining abilities for line by tester trials in maize. <i>Crop Journal</i> , 2022, 10, 109-116.	5.2	7
3139	Development of an Aus-Derived Nested Association Mapping (Aus-NAM) Population in Rice. <i>Plants</i> , 2021, 10, 1255.	3.5	23
3140	Natural variations in the non-coding region of ZmNAC080308 contributes maintaining grain yield under drought stress in maize. <i>BMC Plant Biology</i> , 2021, 21, 305.	3.6	12
3141	Identifying suitable tester for evaluating <i>Striga</i> resistant lines using DArTseq markers and agronomic traits. <i>PLoS ONE</i> , 2021, 16, e0253481.	2.5	5
3143	Integration of genome wide association studies and co-expression networks reveal roles of <i>PtoWRKY42</i> and <i>PtoUGT76C1</i> in trans-zeatin metabolism and cytokinin sensitivity in poplar. <i>New Phytologist</i> , 2021, 231, 1462-1477.	7.3	13
3144	Genetic Diversity and Association Analysis of Lint Percentage Variation Population in <i>Gossypium Hirsutum</i> L. Based on Microsatellite Markers. <i>Journal of Natural Fibers</i> , 0, , 1-10.	3.1	1
3145	Candidate Gene Analysis for Nitrogen Absorption and Utilization in Japonica Rice at the Seedling Stage Based on a Genome-Wide Association Study. <i>Frontiers in Plant Science</i> , 2021, 12, 670861.	3.6	8
3146	Genetic dissection and identification of candidate genes for brown planthopper, <i>Nilaparvata lugens</i> (Delphacidae: Hemiptera) resistance in farmers' varieties of rice in Odisha. <i>Crop Protection</i> , 2021, 144, 105600.	2.1	10
3147	Evaluation of Bayesian alphabet and GBLUP based on different marker density for genomic prediction in Alpine Merino sheep. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	8
3148	New PCR-specific markers for pollen fertility restoration QRfp-4R in rye ( <i>Secale cereale</i> L.) with Pampa sterilizing cytoplasm. <i>Journal of Applied Genetics</i> , 2021, 62, 545-557.	1.9	1
3149	Identification of Gene Associated with Sweetness in Corn ( <i>Zea mays</i> L.) by Genome-Wide Association Study (GWAS) and Development of a Functional SNP Marker for Predicting Sweet Corn. <i>Plants</i> , 2021, 10, 1239.	3.5	13
3150	Genome-Wide Association Mapping for Yield and Related Traits Under Drought Stressed and Non-stressed Environments in Wheat. <i>Frontiers in Genetics</i> , 2021, 12, 649988.	2.3	14

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3151	GENOME-WIDE ASSOCIATION STUDY OF GRAIN QUALITY TRAITS IN SPRING BARLEY COLLECTION GROWN IN KYZYLORDA REGION. <i>Experimental Biology</i> , 2021, 87, .	0.0	1
3152	Genome-wide association analysis of agronomical and physiological traits linked to drought tolerance in a diverse potatoes ( <i>Solanum tuberosum</i> ) panel. <i>Plant Breeding</i> , 2021, 140, 654-664.	1.9	7
3153	Genome-Wide Association Mapping and Gene Expression Analysis Reveal the Negative Role of OsMYB21 in Regulating Bacterial Blight Resistance in Rice. <i>Rice</i> , 2021, 14, 58.	4.0	11
3154	Genetic parameter estimates and identification of SNPs associated with growth traits in Senegalese sole. <i>Aquaculture</i> , 2021, 539, 736665.	3.5	7
3156	<i>GmRAV</i> confers ecological adaptation through photoperiod control of flowering time and maturity in soybean. <i>Plant Physiology</i> , 2021, 187, 361-377.	4.8	19
3157	Genome-Wide Association Analysis for Triazole Resistance in <i>Aspergillus fumigatus</i> . <i>Pathogens</i> , 2021, 10, 701.	2.8	17
3158	Whole-genome variation of transposable element insertions in a maize diversity panel. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	16
3159	Genetic basis of kernel starch content decoded in a maize multi-parent population. <i>Plant Biotechnology Journal</i> , 2021, 19, 2192-2205.	8.3	27
3160	Natural variations in the P-type ATPase heavy metal transporter gene <i>ZmHMA3</i> control cadmium accumulation in maize grains. <i>Journal of Experimental Botany</i> , 2021, 72, 6230-6246.	4.8	37
3162	Rapid adaptation through genomic and epigenomic responses following translocations in an endangered salmonid. <i>Evolutionary Applications</i> , 2021, 14, 2470-2489.	3.1	10
3163	Large-scale Multi-omics Genome-wide Association Studies (Mo-GWAS): Guidelines for Sample Preparation and Normalization. <i>Journal of Visualized Experiments</i> , 2021, , .	0.3	0
3164	Genetic diversity and population structure of ridge gourd ( <i>Luffa acutangula</i> ) accessions in a Thailand collection using SNP markers. <i>Scientific Reports</i> , 2021, 11, 15311.	3.3	4
3166	Genomic and Chemical Diversity of Commercially Available High-CBD Industrial Hemp Accessions. <i>Frontiers in Genetics</i> , 2021, 12, 682475.	2.3	12
3167	Genome-wide association studies for sulfur-containing amino acids in soybean seeds. <i>Euphytica</i> , 2021, 217, 1.	1.2	6
3168	Genomic selection to introgress exotic maize germplasm into elite maize in China to improve kernel dehydration rate. <i>Euphytica</i> , 2021, 217, 1.	1.2	1
3169	Genome wide association study of agronomic and seed traits in a world collection of proso millet ( <i>Panicum miliaceum</i> L.). <i>BMC Plant Biology</i> , 2021, 21, 330.	3.6	25
3170	Multi-Allelic Haplotype-Based Association Analysis Identifies Genomic Regions Controlling Domestication Traits in Intermediate Wheatgrass. <i>Agriculture (Switzerland)</i> , 2021, 11, 667.	3.1	9
3171	QTL mapping in an interspecific sorghum population uncovers candidate regulators of salinity tolerance. <i>Plant Stress</i> , 2021, 2, 100024.	5.5	12

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3172	Rapid Identification of QTL for Mesocotyl Length in Rice Through Combining QTL-seq and Genome-Wide Association Analysis. <i>Frontiers in Genetics</i> , 2021, 12, 713446.	2.3	11
3173	Genetic diversity and population structure analysis of bambara groundnut ( <i>Vigna subterrene</i> L) landraces using DArT SNP markers. <i>PLoS ONE</i> , 2021, 16, e0253600.	2.5	17
3174	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.	3.9	9
3176	Association mapping of sponge cake volume in U.S. Pacific Northwest elite soft white wheat ( <i>Triticum</i> ) TJ ETQq1 1 0.784314 rgBT /Overlook	3.7	3
3177	Development and application of molecular markers for TSW (thousand-seed weight) related gene BnaGRF7.C02 in <i>Brassica napus</i> . <i>Oil Crop Science</i> , 2021, 6, 145-150.	2.0	1
3178	Integrating GWAS and transcriptomics to identify genes involved in seed dormancy in rice. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3553-3562.	3.6	6
3179	Genetic basis and network underlying synergistic roots and shoots biomass accumulation revealed by genome-wide association studies in rice. <i>Scientific Reports</i> , 2021, 11, 13769.	3.3	4
3180	The CCCH zinc finger family of soybean ( <i>Glycine max</i> L.): genome-wide identification, expression, domestication, GWAS and haplotype analysis. <i>BMC Genomics</i> , 2021, 22, 511.	2.8	9
3181	Genome-wide association mapping of <i>Pyrenophora teres</i> f. <i>maculata</i> and <i>Pyrenophora teres</i> f. <i>teres</i> resistance loci utilizing natural Turkish wild and landrace barley populations. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	3
3182	Genome-Environment Association Analysis for Bio-Climatic Variables in Common Bean ( <i>Phaseolus</i> ) TJ ETQq1 1 0.784314 rgBT /Overlook	3.5	5
3183	The Use of "Genotyping-by-Sequencing" to Recover Shared Genealogy in Genetically Diverse <i>Eucalyptus</i> Populations. <i>Forests</i> , 2021, 12, 904.	2.1	4
3184	Identification and Confirmation of Loci Associated With Canopy Wilting in Soybean Using Genome-Wide Association Mapping. <i>Frontiers in Plant Science</i> , 2021, 12, 698116.	3.6	9
3185	Construction of high density genetic map and QTL mapping in sorghum—sudangrass. <i>Euphytica</i> , 2021, 217, 1.	1.2	7
3186	Genome-wide association screening and verification of potential genes associated with root architectural traits in maize ( <i>Zea mays</i> L.) at multiple seedling stages. <i>BMC Genomics</i> , 2021, 22, 558.	2.8	16
3187	Validation of a novel associative transcriptomics pipeline in <i>Brassica oleracea</i> : identifying candidates for vernalisation response. <i>BMC Genomics</i> , 2021, 22, 539.	2.8	6
3188	Haplotype Analysis of BADH1 by Next-Generation Sequencing Reveals Association with Salt Tolerance in Rice during Domestication. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7578.	4.1	11
3189	Characterization of the genetic basis of local adaptation of wheat landraces from Iran and Pakistan using genome-wide association study. <i>Plant Genome</i> , 2021, 14, e20096.	2.8	8
3190	Genomic variation within the maize stiff-stalk heterotic germplasm pool. <i>Plant Genome</i> , 2021, 14, e20114.	2.8	14



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3191	The Chicken Pan-Genome Reveals Gene Content Variation and a Promoter Region Deletion in <i>IGF2BP1</i> Affecting Body Size. <i>Molecular Biology and Evolution</i> , 2021, 38, 5066-5081.	8.9	70
3192	Genomic Selection for End-Use Quality and Processing Traits in Soft White Winter Wheat Breeding Program with Machine and Deep Learning Models. <i>Biology</i> , 2021, 10, 689.	2.8	37
3193	Agronomic, Physiological and Genetic Changes Associated With Evolution, Migration and Modern Breeding in Durum Wheat. <i>Frontiers in Plant Science</i> , 2021, 12, 674470.	3.6	15
3195	Genotypic Variation in Cultivated and Wild Sorghum Genotypes in Response to <i>Striga hermonthica</i> Infestation. <i>Frontiers in Plant Science</i> , 2021, 12, 671984.	3.6	7
3196	Effects of a saponin-based insect resistance and a systemic pathogen resistance on field performance of the wild crucifer <i>Barbarea vulgaris</i> . <i>Arthropod-Plant Interactions</i> , 2021, 15, 683-698.	1.1	1
3197	Contrasting genetic signal of recolonization after rainforest fragmentation in African trees with different dispersal abilities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	4
3198	Genome-Wide Variation in Betacoronaviruses. <i>Journal of Virology</i> , 2021, 95, e0049621.	3.4	4
3199	The chromosome-level reference genome assembly for <i>Dendrobium officinale</i> and its utility of functional genomics research and molecular breeding study. <i>Acta Pharmaceutica Sinica B</i> , 2021, 11, 2080-2092.	12.0	54
3200	Clubroot resistance derived from the European <i>Brassica napus</i> cv. 'Tosca' is not effective against virulent <i>Plasmodiophora brassicae</i> isolates from Alberta, Canada. <i>Scientific Reports</i> , 2021, 11, 14472.	3.3	3
3201	Multi-Locus Genome-Wide Association Study and Genomic Selection of Kernel Moisture Content at the Harvest Stage in Maize. <i>Frontiers in Plant Science</i> , 2021, 12, 697688.	3.6	5
3202	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.	0.8	12
3203	Genome-wide association mapping reveals new loci associated with light-colored seed coat at harvest and slow darkening in carioca beans. <i>BMC Plant Biology</i> , 2021, 21, 343.	3.6	4
3204	Machine learning-enabled phenotyping for GWAS and TWAS of WUE traits in 869 field-grown sorghum accessions. <i>Plant Physiology</i> , 2021, 187, 1481-1500.	4.8	44
3205	Molecular and genetic dissection of the USDA rice mini-core collection using high-density SNP markers. <i>Plant Science</i> , 2021, 308, 110910.	3.6	5
3206	MegaLMM: Mega-scale linear mixed models for genomic predictions with thousands of traits. <i>Genome Biology</i> , 2021, 22, 213.	8.8	25
3207	Genome-Wide Association Study of Nitrogen Use Efficiency and Agronomic Traits in Upland Rice. <i>Rice Science</i> , 2021, 28, 379-390.	3.9	14
3208	Genome-wide association study of yield components in spring wheat collection harvested under two water regimes in Northern Kazakhstan. <i>PeerJ</i> , 2021, 9, e11857.	2.0	8
3209	Identifying SSR Markers Related to Seed Fatty Acid Content in Perilla Crop ( <i>Perilla frutescens</i> L.). <i>Plants</i> , 2021, 10, 1404.	3.5	14

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3213	Long-read genome assembly and genetic architecture of fruit shape in the bottle gourd. <i>Plant Journal</i> , 2021, 107, 956-968.	5.7	23
3214	Does rice breeding affect the ability of plants to interact with earthworms in nutrient-depleted Ferralsols?. <i>Applied Soil Ecology</i> , 2021, 163, 103958.	4.3	4
3215	Genomic Predictions With Nonadditive Effects Improved Estimates of Additive Effects and Predictions of Total Genetic Values in <i>Pinus sylvestris</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 666820.	3.6	9
3216	Genetic control of kernel compositional variation in a maize diversity panel. <i>Plant Genome</i> , 2021, 14, e20115.	2.8	7
3217	Genetic Dissection of Quantitative Resistance to Common Rust ( <i>Puccinia sorghi</i> ) in Tropical Maize ( <i>Zea mays</i> ) Using GWAS. <i>Frontiers in Plant Science</i> , 2021, 12, 692205.	3.6	14
3218	Genetic basis of maize kernel oil-related traits revealed by high-density SNP markers in a recombinant inbred line population. <i>BMC Plant Biology</i> , 2021, 21, 344.	3.6	10
3219	Identification and validation of a novel locus, Qpm-3BL, for adult plant resistance to powdery mildew in wheat using multilocus GWAS. <i>BMC Plant Biology</i> , 2021, 21, 357.	3.6	14
3220	Genetic Dissection of Grain Yield of Maize and Yield-Related Traits Through Association Mapping and Genomic Prediction. <i>Frontiers in Plant Science</i> , 2021, 12, 690059.	3.6	19
3221	GWAS and WGCNA uncover hub genes controlling salt tolerance in maize ( <i>Zea mays</i> L.) seedlings. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3305-3318.	3.6	54
3222	Semidwarf winter wheat roots contain fewer organic acids than wild-type varieties under phosphorus stress. <i>Crop Science</i> , 2021, 61, 3586-3597.	1.8	4
3223	Identification of Candidate Gene-Based Markers for Girth Growth in Rubber Trees. <i>Plants</i> , 2021, 10, 1440.	3.5	3
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3225	Genome-Wide Association Study of Root and Shoot Related Traits in Spring Soybean ( <i>Glycine max</i> L.) at Seedling Stages Using SLAF-Seq. <i>Frontiers in Plant Science</i> , 2021, 12, 568995.	3.6	17
3226	Phylogenomics of <i>Palythoa</i> (Hexacorallia: Scleractinia): probing species boundaries in a globally distributed genus. <i>Coral Reefs</i> , 2021, 40, 1.	2.2	2
3227	Genetic Dissection of Seedling Root System Architectural Traits in a Diverse Panel of Hexaploid Wheat through Multi-Locus Genome-Wide Association Mapping for Improving Drought Tolerance. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7188.	4.1	20
3228	Genotyping and lipid profiling of 601 cultivated sunflower lines reveals novel genetic determinants of oil fatty acid content. <i>BMC Genomics</i> , 2021, 22, 505.	2.8	16

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3230	Morphometric relationships and their contribution to biomass and cannabinoid yield in hybrids of hemp (<i>Cannabis sativa</i>). Journal of Experimental Botany, 2021, 72, 7694-7709.	4.8	18
3231	Gene duplication drove the loss of awn in sorghum. Molecular Plant, 2021, 14, 1831-1845.	8.3	19
3232	Major QTLs and Potential Candidate Genes for Heat Stress Tolerance Identified in Chickpea (Cicer) Tj ETQq1 1 0.784314 rgBT /Overlook	3.6	38
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3237	Genomic Prediction of Resistance to Tar Spot Complex of Maize in Multiple Populations Using Genotyping-by-Sequencing SNPs. Frontiers in Plant Science, 2021, 12, 672525.	3.6	6
3238	Integrating Genome-Wide Association Analysis With Transcriptome Sequencing to Identify Candidate Genes Related to Blooming Time in Prunus mume. Frontiers in Plant Science, 2021, 12, 690841.	3.6	11
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3240	Using Genomic Selection to Leverage Resources among Breeding Programs: Consortium-Based Breeding. Agronomy, 2021, 11, 1555.	3.0	6
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3242	Predicting phenotypes from genetic, environment, management, and historical data using CNNs. Theoretical and Applied Genetics, 2021, 134, 3997-4011.	3.6	20
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3244	Genetic diversity and inter-gene pool introgression of Mesoamerican Diversity Panel in common beans. Journal of Applied Genetics, 2021, 62, 585-600.	1.9	1
3245	Association mapping and pathway analysis of ear rot disease caused by <i>Aspergillus flavus</i> in a panel of tropical maize germplasm. Crop Science, 2021, 61, 4128-4138.	1.8	3
3246	Breeding Driven Enrichment of Genetic Variation for Key Yield Components and Grain Starch Content Under Drought Stress in Winter Wheat. Frontiers in Plant Science, 2021, 12, 684205.	3.6	16
3247	Identification of Markers for Root Traits Related to Drought Tolerance Using Traditional Rice Germplasm. Molecular Biotechnology, 2021, 63, 1280-1292.	2.4	4

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3249	Genome-wide association studies of leaf angle in maize. <i>Molecular Breeding</i> , 2021, 41, 1.	2.1	9
3250	Genetic diversity among a collection of bitter melon ( <i>Momordica charantia</i> L.) cultivars. <i>Genetic Resources and Crop Evolution</i> , 2022, 69, 729-735.	1.6	4
3251	<i>Rhododendron kuomeianum</i> (Ericaceae), a new species from northeastern Yunnan (China), based on morphological and genomic data. <i>Plant Diversity</i> , 2021, 43, 292-298.	3.7	6
3252	Genome-Wide Association Study of Waterlogging Tolerance in Barley ( <i>Hordeum vulgare</i> L.) Under Controlled Field Conditions. <i>Frontiers in Plant Science</i> , 2021, 12, 711654.	3.6	23
3253	A transposon-mediated reciprocal translocation promotes environmental adaptation but compromises domesticability of wild soybeans. <i>New Phytologist</i> , 2021, 232, 1765-1777.	7.3	5
3254	A triple threat: the <i>Parastagonospora nodorum</i> SnTox267 effector exploits three distinct host genetic factors to cause disease in wheat. <i>New Phytologist</i> , 2022, 233, 427-442.	7.3	22
3255	Genetic diversity and population structure of <i>Leptosphaeria maculans</i> isolates in Western Canada. <i>Journal of Genetics and Genomics</i> , 2021, 48, 994-1006.	3.9	0
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3257	A natural single-nucleotide polymorphism variant in <i>sulfite reductase</i> influences sulfur assimilation in maize. <i>New Phytologist</i> , 2021, 232, 692-704.	7.3	2
3258	Identification of a major QTL for Hessian fly resistance in wheat cultivar "Chokwang". <i>Crop Journal</i> , 2022, 10, 775-782.	5.2	10
3259	Revealing the genetic diversity and population structure in <i>Aegilops crassa</i> and <i>Aegilops cylindrica</i> species using molecular markers and physio-chemical traits. <i>Cereal Research Communications</i> , 2022, 50, 347-356.	1.6	1
3260	Genomic Assessment of Global Population Structure in a Highly Migratory and Habitat Versatile Apex Predator, the Tiger Shark ( <i>Galeocerdo cuvier</i> ). <i>Journal of Heredity</i> , 2021, 112, 497-507.	2.4	10
3261	Genomic Diversity of Azole-Resistant <i>Aspergillus fumigatus</i> in the United States. <i>MBio</i> , 2021, 12, e0180321.	4.1	17
3262	Association analysis for agronomic traits in wheat under terminal heat stress. <i>Saudi Journal of Biological Sciences</i> , 2021, 28, 7404-7415.	3.8	6
3264	The Genetic Diversity and Population Structure of Different Geographical Populations of Bottle Gourd ( <i>Lagenaria siceraria</i> ) Accessions Based on Genotyping-by-Sequencing. <i>Agronomy</i> , 2021, 11, 1677.	3.0	9
3265	Genome-Wide Association Study Reveals Key Genes for Differential Lead Accumulation and Tolerance in Natural <i>Arabidopsis thaliana</i> Accessions. <i>Frontiers in Plant Science</i> , 2021, 12, 689316.	3.6	3
3266	Intimate genetic relationships and fungicide resistance in multiple strains of <i>Aspergillus fumigatus</i> isolated from a plant bulb. <i>Environmental Microbiology</i> , 2021, 23, 5621-5638.	3.8	7

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3271	Global range expansion history of pepper ( <i>Capsicum</i> spp.) revealed by over 10,000 genebank accessions. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	48
3272	Classical and genomic prediction of synthetic open-pollinated sweet corn performance in organic environments. Crop Science, 2021, 61, 3382-3391.	1.8	2
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3275	Natural variation in a type-A response regulator confers maize chilling tolerance. Nature Communications, 2021, 12, 4713.	12.8	63
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3277	New high-quality peach ( <i>Prunus persica</i> L. Batsch) genome assembly to analyze the molecular evolutionary mechanism of volatile compounds in peach fruits. Plant Journal, 2021, 108, 281-295.	5.7	31
3278	Genomic selection in salmonids: new discoveries and future perspectives. Aquaculture International, 2021, 29, 2259-2289.	2.2	13
3279	The genetics and evolution of eye color in domestic pigeons ( <i>Columba livia</i> ). PLoS Genetics, 2021, 17, e1009770.	3.5	6
3280	De novo assembly, annotation, and comparative analysis of 26 diverse maize genomes. Science, 2021, 373, 655-662.	12.6	282
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3282	Genome-wide association study and genomic selection for yield and related traits in soybean. PLoS ONE, 2021, 16, e0255761.	2.5	28
3283	Evaluation of maize root growth and genome-wide association studies of root traits in response to low nitrogen supply at seedling emergence. Crop Journal, 2021, 9, 794-804.	5.2	26
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3285	Association Study and Mendelian Randomization Analysis Reveal Effects of the Genetic Interaction Between PtoMIR403b and PtoGT31B-1 on Wood Formation in <i>Populus tomentosa</i> . Frontiers in Plant Science, 2021, 12, 704941.	3.6	2

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3288	Genome-Wide Association Study for Body Length, Body Height, and Total Teat Number in Large White Pigs. <i>Frontiers in Genetics</i> , 2021, 12, 650370.	2.3	12
3289	Population genomics of transposable element activation in the highly repressive genome of an agricultural pathogen. <i>Microbial Genomics</i> , 2021, 7, .	2.0	8
3290	The Informal Seed Business: Focus on Yellow Bean in Tanzania. <i>Sustainability</i> , 2021, 13, 8897.	3.2	8
3291	Multi-Trait Multi-Environment Genomic Prediction of Agronomic Traits in Advanced Breeding Lines of Winter Wheat. <i>Frontiers in Plant Science</i> , 2021, 12, 709545.	3.6	25
3292	Mining QTLs for elevated protein and other major seed composition traits from diverse soybean germplasm. <i>Molecular Breeding</i> , 2021, 41, 1.	2.1	5
3293	Phenotyping stomatal closure by thermal imaging for GWAS and TWAS of water use efficiency-related genes. <i>Plant Physiology</i> , 2021, 187, 2544-2562.	4.8	23
3294	Concerted genomic and epigenomic changes accompany stabilization of Arabidopsis allopolyploids. <i>Nature Ecology and Evolution</i> , 2021, 5, 1382-1393.	7.8	41
3295	Genome-wide analysis of genomic imprinting in the endosperm and allelic variation in flax. <i>Plant Journal</i> , 2021, 107, 1697-1710.	5.7	6
3296	Evaluation of genetic diversity and association mapping for seed weight and size in vegetable soybean germplasm. <i>Crop Science</i> , 2021, 61, 3516-3528.	1.8	2
3297	Validation of Genes Affecting Rice Grain Zinc Content Through Candidate Gene-Based Association Analysis. <i>Frontiers in Genetics</i> , 2021, 12, 701658.	2.3	4
3298	Getting back to the grass roots: harnessing specialized metabolites for improved crop stress resilience. <i>Current Opinion in Biotechnology</i> , 2021, 70, 174-186.	6.6	13
3299	An IBD-based mixed model approach for QTL mapping in multiparental populations. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3643-3660.	3.6	9
3300	Megabase-scale presence-absence variation with <i>Tripsacum</i> origin was under selection during maize domestication and adaptation. <i>Genome Biology</i> , 2021, 22, 237.	8.8	21
3301	Genome-Wide Scanning Enabled SNP Discovery, Linkage Disequilibrium Patterns and Population Structure in a Panel of Fonio ( <i>Digitaria exilis</i> [Kippist] Stapf) Germplasm. <i>Frontiers in Sustainable Food Systems</i> , 2021, 5, .	3.9	5
3302	Genetic sources and loci for wheat head blast resistance identified by genome-wide association analysis. <i>Crop Journal</i> , 2021, , .	5.2	9
3304	Genome-Wide Comparative Analysis of Genetic Diversity of Regular and Specialty Maize Inbred Lines Through Genotyping by Target Sequencing (GBTS). <i>Plant Molecular Biology Reporter</i> , 2022, 40, 221-231.	1.8	1
3305	Development of high-resolution multiple-SNP arrays for genetic analyses and molecular breeding through genotyping by target sequencing and liquid chip. <i>Plant Communications</i> , 2021, 2, 100230.	7.7	38



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3308	Integrative analysis of GWAS and transcriptome to reveal novel loci regulation flowering time in semi-winter rapeseed. <i>Plant Science</i> , 2021, 310, 110980.	3.6	14
3310	Identification of putative key genes for thermal adaptation in the Japanese mantis shrimp ( <i>Oratosquilla</i> ) Tj ETQq1 1 0.784314 rgBT /Ove <i>Genomics and Proteomics</i> , 2021, 39, 100828.	1.0	1
3311	QTL mapping for bioenergy traits in sweet sorghum recombinant inbred lines. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	3
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3313	Genome wide association and prediction studies of agronomic and quality traits in spring beard wheat ( <i>Triticum aestivum</i> L.) under rain-fed environment with terminal moisture stress. <i>Journal of Cereal Science</i> , 2021, 101, 103278.	3.7	6
3314	Genetic Diversity and Population Structure of Cowpea [ <i>Vigna unguiculata</i> (L.) Walp.] Germplasm Collected from Togo Based on DArT Markers. <i>Genes</i> , 2021, 12, 1451.	2.4	16
3315	Association analysis of <sc><i>GmMAPKs</i></sc> and functional characterization of <sc><i>GmMMK1</i></sc> to salt stress response in soybean. <i>Physiologia Plantarum</i> , 2021, 173, 2026-2040.	5.2	7
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3319	DNA Variation in a Diversity Panel of Tomato Genetic Resources. <i>Journal of the American Society for Horticultural Science</i> , 2021, 146, 339-345.	1.0	0
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3322	A Genome-Wide Association Study Identifies Candidate Genes Associated With Shell Color in Bay Scallop <i>Argopecten irradians irradians</i> . <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	10
3323	Inferring multilayer interactome networks shaping phenotypic plasticity and evolution. <i>Nature Communications</i> , 2021, 12, 5304.	12.8	13
3324	Local auxin biosynthesis acts downstream of brassinosteroids to trigger root foraging for nitrogen. <i>Nature Communications</i> , 2021, 12, 5437.	12.8	37
3326	Genome-Wide Association Study Reveals Novel Genetic Loci for Quantitative Resistance to Septoria Tritici Blotch in Wheat ( <i>Triticum aestivum</i> L.). <i>Frontiers in Plant Science</i> , 2021, 12, 671323.	3.6	8

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3328	Characterization of PmBN418 , a wheat powdery mildew resistance gene on the rye 1RS chromosome arm. <i>Crop Science</i> , 2021, 61, 4194.	1.8	1
3329	High genetic and epigenetic variation of transposable elements: Potential drivers to rapid adaptive evolution for the noxious invasive weed <i>Mikania micrantha</i> . <i>Ecology and Evolution</i> , 2021, 11, 13501-13517.	1.9	8
3330	Polyphenol oxidase genes as integral part of the evolutionary history of domesticated tetraploid wheat. <i>Genomics</i> , 2021, 113, 2989-3001.	2.9	8
3331	Comparative analyses of responses to exogenous and endogenous antiherbivore elicitors enable a forward genetics approach to identify maize gene candidates mediating sensitivity to herbivore-associated molecular patterns. <i>Plant Journal</i> , 2021, 108, 1295-1316.	5.7	9
3333	Genome-Wide Association and Selective Sweep Studies Reveal the Complex Genetic Architecture of DMI Fungicide Resistance in <i>Cercospora beticola</i> . <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	12
3334	Integrating a genome-wide association study with transcriptomic data to predict candidate genes and favourable haplotypes influencing <i>Brassica napus</i> seed phytate. <i>DNA Research</i> , 2021, 28, .	3.4	14
3336	Genomic background selection to reduce the mutation load after random mutagenesis. <i>Scientific Reports</i> , 2021, 11, 19404.	3.3	8
3337	Evaluation of Advanced Backcrosses of Eggplant with <i>Solanum elaeagnifolium</i> Introgressions under Low N Conditions. <i>Agronomy</i> , 2021, 11, 1770.	3.0	11
3338	Genomic basis underlying the metabolome-mediated drought adaptation of maize. <i>Genome Biology</i> , 2021, 22, 260.	8.8	44
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3340	Modified expression of <i>TaCYP78A5</i> enhances grain weight with yield potential by accumulating auxin in wheat ( <i>Triticum aestivum</i> L.). <i>Plant Biotechnology Journal</i> , 2022, 20, 168-182.	8.3	29
3341	The details are in the genome-wide SNPs: Fine scale evolution of the Malaysian weedy rice. <i>Plant Science</i> , 2021, 310, 110985.	3.6	1
3342	Whole-genome sequencing of brown-marbled grouper ( <i>Epinephelus fuscoguttatus</i> ) provides insights into adaptive evolution and growth differences. <i>Molecular Ecology Resources</i> , 2022, 22, 711-723.	4.8	16
3343	Genome-Wide Association Study to Map Genomic Regions Related to the Initiation Time of Four Growth Stage Traits in Soybean. <i>Frontiers in Genetics</i> , 2021, 12, 715529.	2.3	3
3344	Genome-wide association analysis of root length traits in <i>Brassica napus</i> at germination stage under sodium carbonate stress. <i>Euphytica</i> , 2021, 217, 1.	1.2	3
3345	Exploration into natural variation for genes associated with fruit shape and size among <i>Capsicum chinense</i> collections. <i>Genomics</i> , 2021, 113, 3002-3014.	2.9	10
3347	Discovery of the REN11 Locus From <i>Vitis aestivalis</i> for Stable Resistance to Grapevine Powdery Mildew in a Family Segregating for Several Unstable and Tissue-Specific Quantitative Resistance Loci. <i>Frontiers in Plant Science</i> , 2021, 12, 733899.	3.6	26

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3349	Genotyping-by-Sequencing Based Genetic Mapping Identified Major and Consistent Genomic Regions for Productivity and Quality Traits in Peanut. <i>Frontiers in Plant Science</i> , 2021, 12, 668020.	3.6	19
3350	Population Structure and Genetic Diversity of Two-Rowed Barley Accessions from Kazakhstan Based on SNP Genotyping Data. <i>Plants</i> , 2021, 10, 2025.	3.5	10
3351	Genetic diversity in rice ( <i>Oryza sativa</i> L.) landraces of Sikkim-Himalaya and early insight into their use in genome-wide association analysis. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 0, , 1-10.	0.8	3
3352	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, , .	1.4	4
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3354	Genetic diversity assessment of Georgia peanut cultivars developed during ninety years of breeding. <i>Plant Genome</i> , 2021, 14, e20141.	2.8	4
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3795	Genomic predictions in diploid <i>Actinidia chinensis</i> (kiwifruit). European Journal of Horticultural Science, 2019, 84, 213-217.	0.7	4
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3805	Genetic analysis of drupelet count in black raspberry ( <i>Rubus occidentalis</i> ). Acta Horticulturae, 2020, , 65-72.	0.2	0
3813	Identification of SNP Markers Associated with Iron and Zinc Concentrations in Cicer Seeds. Current Genomics, 2020, 21, 212-223.	1.6	7
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3817	Effect of Population Size on Genome-Wide Association Study of Agronomic Traits in Soybean. Proceedings of the Latvian Academy of Sciences, 2020, 74, 244-251.	0.1	1
3818	Genomic regions of <i>Solanum tuberosum</i> L. associated with the tuber eye depth. Vavilovskii Zhurnal Genetiki I Selektzii, 2020, 24, 465-473.	1.1	3
3820	Genome-Wide Association Study of Rice Rooting Ability at the Seedling Stage. Rice, 2020, 13, 59.	4.0	12
3821	Identification and Fine Mapping of a Locus Related to Leaf Up-Curling Trait (Bnuc3) in <i>Brassica napus</i> . International Journal of Molecular Sciences, 2021, 22, 11693.	4.1	2
3822	Key genes and mechanisms underlying natural variation of silique length in oilseed rape ( <i>Brassica</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 5.2 8		
3823	Identification of genes for drought resistance and prediction of gene candidates in soybean seedlings based on linkage and association mapping. Crop Journal, 2022, 10, 830-839.	5.2	10
3824	A Genome-Wide Association Study Pinpoints Quantitative Trait Genes for Plant Height, Heading Date, Grain Quality, and Yield in Rye ( <i>Secale cereale</i> L.). Frontiers in Plant Science, 2021, 12, 718081.	3.6	12
3825	Genome-wide association study uncovers major genetic loci associated with seed flooding tolerance in soybean. BMC Plant Biology, 2021, 21, 497.	3.6	13
3828	Genome-based prediction of agronomic traits in spring wheat under conventional and organic management systems. Theoretical and Applied Genetics, 2021, 135, 537.	3.6	10
3829	The <i>APETALA2</i> homolog <i>CaFFN</i> regulates flowering time in pepper. Horticulture Research, 2021, 8, 208.	6.3	5

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3830	Oxidative stress response and programmed cell death guided by NAC013 modulate pithiness in radish taproots. <i>Plant Journal</i> , 2021, , .	5.7	2
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3834	Genotyping by sequencing for SNP marker development in onion. <i>Genome</i> , 2020, 63, 607-613.	2.0	6
3835	SNPViz v2.0: A web-based tool for enhanced haplotype analysis using large scale resequencing datasets and discovery of phenotypes causative gene using allelic variations. , 2020, , .		2
3836	Association Analysis and Validation of Simple Sequence Repeat Markers for Fiber Fineness in Ramie ( <i>Boehmeria nivea</i> L. Gaudich). <i>Journal of Natural Fibers</i> , 2022, 19, 3615-3623.	3.1	2
3837	Using single-plantomics in the field to link maize genes to functions and phenotypes. <i>Molecular Systems Biology</i> , 2020, 16, e9667.	7.2	22
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3842	Genotyping-by-Sequencing Identifies Historical Breeding Stages of the Recently Domesticated American Cranberry. <i>Frontiers in Plant Science</i> , 2020, 11, 607770.	3.6	11
3844	Genetic and Genomic Resources and Their Exploitation for Unlocking Genetic Potential from the Wild Relatives. , 2020, , 193-210.		3
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3847	Genome-wide association study on agronomic traits of temperate japonica rice ( <i>Oryza sativa</i> L.). <i>Crop Breeding and Applied Biotechnology</i> , 2020, 20, .	0.4	5
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3851	Genome-wide association mapping and candidate gene analysis for water-soluble protein concentration in soybean ( <i>Glycine max</i> ) based on high-throughput single nucleotide polymorphism markers. <i>Crop and Pasture Science</i> , 2020, 71, 239.	1.5	0
3855	Development of core-collections for Guizhou tea genetic resources and GWAS of leaf size using SNP developed by genotyping-by-sequencing. <i>PeerJ</i> , 2020, 8, e8572.	2.0	14
3862	A conserved genetic architecture among populations of the maize progenitor, teosinte, was radically altered by domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	1
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3865	Novel QTLs for salinity tolerance revealed by genome-wide association studies of biomass, chlorophyll and tissue ion content in 176 rice landraces from Bangladesh. <i>PLoS ONE</i> , 2021, 16, e0259456.	2.5	3
3866	Genome-wide SNP discovery, linkage mapping, and analysis of QTL for morpho-physiological traits in rice during vegetative stage under drought stress. <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 2635-2650.	3.1	5
3868	Genome-wide association mapping and genomic prediction for adult stage sclerotinia stem rot resistance in <i>Brassica napus</i> (L) under field environments. <i>Scientific Reports</i> , 2021, 11, 21773.	3.3	21
3869	Genome-wide association links candidate genes to fruit firmness, fruit flesh color, flowering time, and soluble solid content in apricot ( <i>Prunus armeniaca</i> L.). <i>Molecular Biology Reports</i> , 2022, 49, 5283-5291.	2.3	2
3870	In Silico Functional Prediction and Expression Analysis of C2H2 Zinc-Finger Family Transcription Factor Revealed Regulatory Role of ZmZFP126 in Maize Growth. <i>Frontiers in Genetics</i> , 2021, 12, 770427.	2.3	6
3871	The long-read genome assembly of hop ( <i>Humulus lupulus</i> ) uncovers the pseudoautosomal region and other genomic features. <i>Acta Horticulturae</i> , 2021, , 1-16.	0.2	2
3872	Comparative Association Mapping Reveals Conservation of Major Gene Resistance to White Pine Blister Rust in Southwestern White Pine ( <i>Pinus strobiformis</i> ) and Limber Pine ( <i>P. flexilis</i> ). <i>Phytopathology</i> , 2022, 112, 1093-1102.	2.2	3
3873	A Pathway Association Study Tool for GWAS Analyses of Metabolic Pathway Information. <i>Journal of Visualized Experiments</i> , 2020, , .	0.3	0
3884	Genome-wide discovery and characterization of long noncoding RNAs in African oil palm ( <i>Elaeis</i> Tj ETQq1 1 0.784314 rgBT /Overl	2.0	3
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3891	Identification of single nucleotide polymorphisms (SNPs) for maize cell wall hydroxycinnamates using a multi-parent advanced generation intercross (MAGIC) population. <i>Phytochemistry</i> , 2022, 193, 113002.	2.9	1
3892	Prediction of Maize Phenotypic Traits With Genomic and Environmental Predictors Using Gradient Boosting Frameworks. <i>Frontiers in Plant Science</i> , 2021, 12, 699589.	3.6	20
3893	Functional Analysis of the "Green Revolution" Gene Photoperiod-1 and Its Selection Trends During Bread Wheat Breeding. <i>Frontiers in Plant Science</i> , 2021, 12, 745411.	3.6	6
3894	Genetic variation in <i>YIGE1</i> contributes to ear length and grain yield in maize. <i>New Phytologist</i> , 2022, 234, 513-526.	7.3	38
3896	Genome-wide approaches delineate the additive, epistatic, and pleiotropic nature of variants controlling fatty acid composition in peanut ( <i>Arachis hypogaea</i> L.). <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	5
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3899	Insights on Genetic Diversity, Population Structure, and Linkage Disequilibrium in Globally Diverse Coconut Accessions Using Genotyping-by-Sequencing. <i>OMICS A Journal of Integrative Biology</i> , 2021, 25, 796-809.	2.0	8

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3903	Marker-trait association study for root-related traits in chickpea ( <i>Cicer arietinum</i> L.). <i>Acta Agriculturae Slovenica</i> , 2021, 117, 1.	0.3	0
3904	Genomic regions associated with resistance to <i>Fusarium</i> wilt in castor identified through linkage and association mapping approaches. <i>Genome</i> , 2022, 65, 123-136.	2.0	9
3905	Dissecting four correlated growth period traits using a genome-wide association study approach in soybean. <i>Genetic Resources and Crop Evolution</i> , 2022, 69, 1147-1162.	1.6	0
3906	Variation in cis-regulation of a NAC transcription factor contributes to drought tolerance in wheat. <i>Molecular Plant</i> , 2022, 15, 276-292.	8.3	78
3907	Discovery and Validation of a Recessively Inherited Major-Effect QTL Conferring Resistance to Maize Lethal Necrosis (MLN) Disease. <i>Frontiers in Genetics</i> , 2021, 12, 767883.	2.3	10
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3911	Targeted re-sequencing and genome-wide association analysis for wood property traits in breeding population of <i>Eucalyptus tereticornis</i> A— <i>E. grandis</i> . <i>Genomics</i> , 2021, 113, 4276-4292.	2.9	7
3912	Identification of an Elite Core Panel as a Key Breeding Resource to Accelerate the Rate of Genetic Improvement for Irrigated Rice. <i>Rice</i> , 2021, 14, 92.	4.0	19
3913	Trends of genetic changes uncovered by Env- and Eigen-GWAS in wheat and barley. <i>Theoretical and Applied Genetics</i> , 2022, 135, 667-678.	3.6	8
3914	Development of the Wheat Practical Haplotype Graph database as a resource for genotyping data storage and genotype imputation. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	7
3915	Laboratory phenomics predicts field performance and identifies superior indica haplotypes for early seedling vigour in dry direct-seeded rice. <i>Genomics</i> , 2021, 113, 4227-4236.	2.9	5
3916	Bayesian multitrait kernel methods improve multienvironment genome-based prediction. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	8
3917	Electroencephalogram Signatures of Agitation Induced by Sevoflurane and Its Association With Genetic Polymorphisms. <i>Frontiers in Medicine</i> , 2021, 8, 678185.	2.6	3
3918	Genome-Wide Association Mapping of Seedling Vigor and Regrowth Vigor in Winter Wheat. <i>Crops</i> , 2021, 1, 153-165.	1.4	3

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3920	The performance of phenomic selection depends on the genetic architecture of the target trait. <i>Theoretical and Applied Genetics</i> , 2022, 135, 653-665.	3.6	9
3921	Identification of a Diverse Core Set Panel of Rice From the East Coast Region of India Using SNP Markers. <i>Frontiers in Genetics</i> , 2021, 12, 726152.	2.3	6
3922	Intraspecies Genomic Divergence of a Fig Wasp Species Is Due to Geographical Barrier and Adaptation. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	2.2	1
3923	Investigation and Genome-Wide Association Analysis of Fusarium Seedling Blight Resistance in Chinese Elite Wheat Lines. <i>Frontiers in Plant Science</i> , 2021, 12, 777494.	3.6	0
3924	Genetic diversity of Norway spruce ecotypes assessed by GBS-derived SNPs. <i>Scientific Reports</i> , 2021, 11, 23119.	3.3	12
3925	The History and Diversity of Rice Domestication as Resolved From 1464 Complete Plastid Genomes. <i>Frontiers in Plant Science</i> , 2021, 12, 781793.	3.6	16
3926	Genetic Dissection of Mature Root Characteristics by Genome-Wide Association Studies in Rapeseed ( <i>Brassica napus</i> L.). <i>Plants</i> , 2021, 10, 2569.	3.5	10
3927	Genome-wide association analysis uncovers the genetic architecture of tradeoff between flowering date and yield components in sesame. <i>BMC Plant Biology</i> , 2021, 21, 549.	3.6	9
3928	Structure of genetic diversity and genome-wide association studies of bean fly ( <i>Ophiomyia</i> ) Tj ETQq1 1 0.784314 r <sup>2</sup> BT /Overlock 10 Tj S	1.2	3
3929	Genome-wide association identifies candidate genes for drought tolerance in coast redwood and giant sequoia. <i>Plant Journal</i> , 2022, 109, 7-22.	5.7	17
3930	Genome-Wide Association Study for Detecting Salt-Tolerance Loci and Candidate Genes in Rice. <i>Agriculture (Switzerland)</i> , 2021, 11, 1174.	3.1	3
3931	Selective Sweeps and Polygenic Adaptation Drive Local Adaptation along Moisture and Temperature Gradients in Natural Populations of Coast Redwood and Giant Sequoia. <i>Genes</i> , 2021, 12, 1826.	2.4	7
3932	Genetic Architecture of Novel Sources for Reproductive Cold Tolerance in Sorghum. <i>Frontiers in Plant Science</i> , 2021, 12, 772177.	3.6	3
3933	Genetic dissection of maize plant architecture using a novel nested association mapping population. <i>Plant Genome</i> , 2022, 15, e20179.	2.8	5
3934	FunGraph: A statistical protocol to reconstruct omnigenic multilayer interactome networks for complex traits. <i>STAR Protocols</i> , 2021, 2, 100985.	1.2	5
3937	Candidate gene (PHA-E) and phytohemagglutinin content in snap bean ( <i>Phaseolus vulgaris</i> L.): an association study. <i>Biotechnology and Biotechnological Equipment</i> , 2021, 35, 1420-1426.	1.3	1
3938	Genome-wide superior alleles, haplotypes and candidate genes associated with tolerance on sodic-dispersive soils in wheat ( <i>Triticum aestivum</i> L.). <i>Theoretical and Applied Genetics</i> , 2022, 135, 1113-1128.	3.6	3



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3940	Feasibility of genomic prediction for brown rot (<i>Monilinia</i> spp.) resistance in peach. <i>Fruit Research</i> , 2022, 2, 1-12.	2.0	4
3942	Genomic Selection for Wheat Blast in a Diversity Panel, Breeding Panel and Full-Sibs Panel. <i>Frontiers in Plant Science</i> , 2021, 12, 745379.	3.6	13
3943	Phenotypic Diversity and Association Mapping of Ascorbic Acid Content in Spinach. <i>Frontiers in Genetics</i> , 2021, 12, 752313.	2.3	4
3944	The genome of oil-Camellia and population genomics analysis provide insights into seed oil domestication. <i>Genome Biology</i> , 2022, 23, 14.	8.8	68
3945	Identification of Candidate Forage Yield Genes in Sorghum ( <i>Sorghum bicolor</i> L.) Using Integrated Genome-Wide Association Studies and RNA-Seq. <i>Frontiers in Plant Science</i> , 2021, 12, 788433.	3.6	6
3947	TaNRT2.1-6B is a dual-affinity nitrate transporter contributing to nitrogen uptake in bread wheat under both nitrogen deficiency and sufficiency. <i>Crop Journal</i> , 2022, 10, 993-1005.	5.2	13
3948	Identification of genes associated with carotenoids accumulation in scallop ( <i>Patinopecten</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T5	3.5	9
3949	Genomic regions associated with virulence in <i>Setosphaeria turcica</i> identified by linkage mapping in a biparental population. <i>Fungal Genetics and Biology</i> , 2022, 159, 103655.	2.1	6
3951	CWAS for low radiation tolerance during grain filling in rice ( <i>Oryza sativa</i> L.). , 2020, , .		0
3952	Genome-Wide Association Analysis of Polysaccharide Content in Young Fruits of Okra. <i>Botanical Research</i> , 2021, 10, 749-760.	0.0	0
3953	Exploring genetic diversity, population structure, and phylogeography in <i>Paracoccidioides</i> species using AFLP markers. <i>Studies in Mycology</i> , 2021, 100, 100129-100129.	7.2	17
3955	Genetic Diversity and Population Structure Analysis of the USDA Olive Germplasm Using Genotyping-By-Sequencing (GBS). <i>Genes</i> , 2021, 12, 2007.	2.4	12
3956	Multiple evolutionary origins of glyphosate resistance in <i>Lolium multiflorum</i> . <i>Evolutionary Applications</i> , 2022, 15, 316-329.	3.1	8
3957	Population structure analysis to explore genetic diversity and geographical distribution characteristics of cultivated-type tea plant in Guizhou Plateau. <i>BMC Plant Biology</i> , 2022, 22, 55.	3.6	7
3958	Development and Genetic Characterization of Peanut Advanced Backcross Lines That Incorporate Root-Knot Nematode Resistance From <i>Arachis stenosperma</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 785358.	3.6	5
3960	An intraspecies <i>Leishmania donovani</i> hybrid from the Indian subcontinent is associated with an atypical phenotype of cutaneous disease. <i>IScience</i> , 2022, 25, 103802.	4.1	12
3961	Genome-wide association study of cassava starch paste properties. <i>PLoS ONE</i> , 2022, 17, e0262888.	2.5	3

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3964	A sorghum genome-wide association study (GWAS) identifies a WRKY transcription factor as a candidate gene underlying sugarcane aphid ( <i>Melanaphis sacchari</i> ) resistance. Planta, 2022, 255, 37.	3.2	10
3966	Identification of Heterotic Groups and Patterns Based on Genotypic and Phenotypic Characteristics Among Rice Accessions of Diverse Origins. Frontiers in Genetics, 2022, 13, 811124.	2.3	9
3967	Single nucleotide polymorphism (SNP) in the doublesex ( <i>dsx</i> ) gene splice sites and relevance for its alternative splicing in the malaria vector <i>Anopheles gambiae</i> . Wellcome Open Research, 0, 7, 31.	1.8	1
3968	Genome-Wide Association Study Reveals Complex Genetic Architecture of Cadmium and Mercury Accumulation and Tolerance Traits in <i>Medicago truncatula</i> . Frontiers in Plant Science, 2021, 12, 806949.	3.6	10
3969	Genomic Analysis Reveals Subdivision of Black Rats ( <i>Rattus rattus</i> ) in India, Origin of the Worldwide Species Spread. Genes, 2022, 13, 267.	2.4	2
3970	Comparison of Single-Trait and Multi-Trait Genome-Wide Association Models and Inclusion of Correlated Traits in the Dissection of the Genetic Architecture of a Complex Trait in a Breeding Program. Frontiers in Plant Science, 2021, 12, 772907.	3.6	10
3971	Selection for resistance to cassava mosaic disease in African cassava germplasm using single nucleotide polymorphism markers. South African Journal of Science, 2022, 118, .	0.7	3
3972	Genome-wide association study for seedling biomass-related traits in <i>Gossypium arboreum</i> L.. BMC Plant Biology, 2022, 22, 54.	3.6	5
3973	Dissection of the genetic architecture of peduncle vascular bundle-related traits in maize by a genome-wide association study. Plant Biotechnology Journal, 2022, 20, 1042-1053.	8.3	8
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3975	Genome-wide association study of the candidate genes for grape berry shape-related traits. BMC Plant Biology, 2022, 22, 42.	3.6	6
3976	Phenotypic and molecular characterization of a set of tropical maize inbred lines from a public breeding program in Brazil. BMC Genomics, 2022, 23, 54.	2.8	4
3977	Identifying and testing marker-trait associations for growth and phenology in three pine species: Implications for genomic prediction. Evolutionary Applications, 2022, 15, 330-348.	3.1	4
3978	Aus rice root architecture variation contributing to grain yield under drought suggests a key role of nodal root diameter class. Plant, Cell and Environment, 2022, 45, 854-870.	5.7	10
3979	Genomic Analysis of Resistance to Fall Armyworm ( <i>Spodoptera frugiperda</i> ) in CIMMYT Maize Lines. Genes, 2022, 13, 251.	2.4	13
3980	Genetic diversity and population structure of rice ( <i>Oryza sativa</i> L.) landraces from Kerala, India analyzed through genotyping-by-sequencing. Molecular Genetics and Genomics, 2022, 297, 169-182.	2.1	3
3981	A chromosome-scale reference genome assembly of yellow mangrove ( <i>Bruguiera parviflora</i> ) reveals a whole genome duplication event associated with the Rhizophoraceae lineage. Molecular Ecology Resources, 2022, 22, 1939-1953.	4.8	13

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3982	Comparative transcriptomics and eQTL mapping of response to <i>Melampsora americana</i> in selected <i>Salix purpurea</i> F2 progeny. BMC Genomics, 2022, 23, 71.	2.8	5
3983	Identification of source populations for reintroduction in extinct populations based on genome-wide SNPs and mtDNA sequence: a case study of the endangered subalpine grassland butterfly <i>Aporia hippia</i> (Lepidoptera; Pieridae) in Japan. Journal of Insect Conservation, 2022, 26, 121-130.	1.4	3
3984	Identification and Mapping of Quantitative Trait Loci Associated with Stripe Rust Resistance in Spring Club Wheat Cultivar JD. Plant Disease, 2022, , .	1.4	1
3985	Linkage Disequilibrium Statistics and Block Visualization. Methods in Molecular Biology, 2022, 2443, 483-496.	0.9	1
3986	A B73–Palomero Toluque mapping population reveals local adaptation in Mexican highland maize. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	11
3987	Unraveling the potential of phenomic selection within and among diverse breeding material of maize ( <i>Zea mays</i> L.). G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	9
3988	Pepper Fruit Elongation Is Controlled by <i>Capsicum annuum</i> Ovate Family Protein 20. Frontiers in Plant Science, 2021, 12, 815589.	3.6	12
3989	Identification of candidate genes for panicle length in <i>Oryza sativa</i> L. ssp. <i>japonica</i> via genome-wide association study and linkage mapping. Euphytica, 2022, 218, 1.	1.2	3
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3991	Perspectives and recent progress of genome-wide association studies (GWAS) in fruits. Molecular Biology Reports, 2022, 49, 5341-5352.	2.3	12
3992	Classification and Association Analysis of <i>Gerbera</i> ( <i>Gerbera hybrida</i> ) Flower Color Traits. Frontiers in Plant Science, 2021, 12, 779288.	3.6	10
3993	Genome-Wide Association Reveals Trait Loci for Seed Glucosinolate Accumulation in Indian Mustard ( <i>Brassica juncea</i> L.). Plants, 2022, 11, 364.	3.5	8
3994	Dissecting the Root Phenotypic and Genotypic Variability of the Iowa Mung Bean Diversity Panel. Frontiers in Plant Science, 2021, 12, 808001.	3.6	4
3996	Association Mapping for Yield Attributing Traits and Yellow Mosaic Disease Resistance in Mung Bean [ <i>Vigna radiata</i> (L.) Wilczek]. Frontiers in Plant Science, 2021, 12, 749439.	3.6	5
3997	Insights into opium poppy ( <i>Papaver</i> spp.) genetic diversity from genotyping-by-sequencing analysis. Scientific Reports, 2022, 12, 111.	3.3	16
3998	Tanned leather of the paiche <i>Arapaima gigas</i> Schinz, 1822 (Arapaimidae) with extracts of vegetable origin to replace chromium salts. PLoS ONE, 2022, 17, e0261781.	2.5	3
3999	Chromosome-level <i>Thlaspi arvense</i> genome provides new tools for translational research and for a newly domesticated cash cover crop of the cooler climates. Plant Biotechnology Journal, 2022, 20, 944-963.	8.3	18
4000	Genome-Wide Association Study of Grain Number in Common Wheat From Shanxi Under Different Water Regimes. Frontiers in Plant Science, 2021, 12, 806295.	3.6	7

#	ARTICLE	IF	CITATIONS
4001	Quantitative trait loci mapping of stem sugar content and stem diameter in sorghum recombinant inbred lines using genotyping-by-sequencing. <i>Molecular Biology Reports</i> , 2022, 49, 3045-3054.	2.3	1
4002	Genome-Wide Association Mapping for Seed Weight in Soybean with Black Seed Coats and Green Cotyledons. <i>Agronomy</i> , 2022, 12, 250.	3.0	7
4003	Pilot scale genome wide association mapping identified novel loci for grain yield traits in rice. <i>Plant Physiology Reports</i> , 2022, 27, 11-21.	1.5	1
4004	Merging genotyping-by-sequencing data from two ex situ collections provides insights on the pea evolutionary history. <i>Horticulture Research</i> , 2022, , .	6.3	3
4005	Phenotyping and Quantitative Trait Locus Analysis for the Limited Transpiration Trait in an Upper-Mid South Soybean Recombinant Inbred Line Population (â€œJacksonâ€— â€œKS4895â€œ): High Throughput Aquaporin Inhibitor Screening. <i>Frontiers in Plant Science</i> , 2021, 12, 779834.	3.6	7
4006	QTL mapping and colocalization analysis reveal novel candidate genes for multiple disease resistance in maize. <i>Crop Science</i> , 2022, 62, 624-636.	1.8	4
4007	A transcriptome-based association study of Âgrowth, wood quality, and oleoresin traits in a slash pine Âbreeding population. <i>PLoS Genetics</i> , 2022, 18, e1010017.	3.5	13
4008	CWAS identifies genetic loci underlying nitrogen responsiveness in the climate resilient C4 model <i>Setaria italica</i> (L.). <i>Journal of Advanced Research</i> , 2022, 42, 249-261.	9.5	6
4009	Phylogeography of a canopyâ€forming kelp, <i>Eisenia bicyclis</i> (Laminariales, Phaeophyceae), based on a genomeâ€wide sequencing analysis. <i>Journal of Phycology</i> , 2022, , .	2.3	1
4010	Genome-Wide Association Analysis Coupled With Transcriptome Analysis Reveals Candidate Genes Related to Salt Stress in Alfalfa ( <i>Medicago sativa</i> L.). <i>Frontiers in Plant Science</i> , 2021, 12, 826584.	3.6	18
4012	Genetic analysis of sucrose concentration in soybean seeds using a historical soybean genomic panel. <i>Theoretical and Applied Genetics</i> , 2022, 135, 1375-1383.	3.6	9
4013	Genomic regions controlling yield-related traits in spring wheat: a mini review and a case study for rainfed environments in Australia and China. <i>Genomics</i> , 2022, 114, 110268.	2.9	3
4014	Elucidation of drought tolerance potential of horsegram ( <i>Macrotyloma uniflorum</i> Var.) germplasm using genome wide association studies. <i>Gene</i> , 2022, 819, 146241.	2.2	8
4015	Genome-Wide Association Analyses to Identify SNPs Related to. <i>Methods in Molecular Biology</i> , 2022, 2462, 201-219.	0.9	0
4016	Genome Wide Association Study Uncovers the QTLome for Osmotic Adjustment and Related Drought Adaptive Traits in Durum Wheat. <i>Genes</i> , 2022, 13, 293.	2.4	12
4017	Deltapine 15 contributes to the genomic architecture of modern upland cotton cultivars. <i>Theoretical and Applied Genetics</i> , 2022, , 1.	3.6	4
4018	Temporal changes in pathogen diversity in a perennial plantâ€pathogenâ€hyperparasite system. <i>Molecular Ecology</i> , 2022, 31, 2073-2088.	3.9	7
4019	Genome-Wide Association Study for Resistance to Tan Spot in Synthetic Hexaploid Wheat. <i>Plants</i> , 2022, 11, 433.	3.5	8

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4020	Genetic Insight Into the Insect Resistance in Bread Wheat Exploiting the Untapped Natural Diversity. <i>Frontiers in Genetics</i> , 2022, 13, 828905.	2.3	16
4021	Genome-Wide Association Study and Post-genome-Wide Association Study Analysis for Spike Fertility and Yield Related Traits in Bread Wheat. <i>Frontiers in Plant Science</i> , 2021, 12, 820761.	3.6	11
4022	Quantitative Trait Loci for Heat Stress Tolerance in <i>Brassica rapa</i> L. Are Distributed across the Genome and Occur in Diverse Genetic Groups, Flowering Phenologies and Morphotypes. <i>Genes</i> , 2022, 13, 296.	2.4	1
4023	Association mapping, trait variation, interaction and population structure analysis in cucumber ( <i>Cucumis sativus</i> L.). <i>Genetic Resources and Crop Evolution</i> , 2022, 69, 1901-1917.	1.6	3
4024	QTL analysis in multiple sorghum mapping populations facilitates dissection of the genetic control of agronomic and yield-related traits in sorghum [ <i>Sorghum bicolor</i> (Moench)]. <i>Euphytica</i> , 2022, 218, 1.	1.2	4
4025	Identification of QTLs for Grain Protein Content in Russian Spring Wheat Varieties. <i>Plants</i> , 2022, 11, 437.	3.5	9
4026	Haplotype mapping uncovers unexplored variation in wild and domesticated soybean at the major protein locus <i>cqProt-003</i> . <i>Theoretical and Applied Genetics</i> , 2022, 135, 1443-1455.	3.6	13
4027	Genetic Evaluation of <i>Juniperus sabina</i> L. (Cupressaceae) in Arid and Semi-Arid Regions of China Based on SSR Markers. <i>Forests</i> , 2022, 13, 231.	2.1	5
4028	Population Structure and Genetic Diversity Analysis in Sugarcane ( <i>Saccharum</i> spp. hybrids) and Six Related <i>Saccharum</i> Species. <i>Agronomy</i> , 2022, 12, 412.	3.0	4
4029	Population genomics and geographic dispersal in Chagas disease vectors: Landscape drivers and evidence of possible adaptation to the domestic setting. <i>PLoS Genetics</i> , 2022, 18, e1010019.	3.5	4
4030	Association analysis of yellow rust, fusarium head blight, tan spot, powdery mildew, and brown rust horizontal resistance genes in wheat. <i>Physiological and Molecular Plant Pathology</i> , 2022, 118, 101808.	2.5	10
4031	Accumulation of somatic mutations leads to genetic mosaicism in cannabis. <i>Plant Genome</i> , 2022, 15, e20169.	2.8	16
4032	Genome-wide association study identifies variants of <i>GhSAD1</i> conferring cold tolerance in cotton. <i>Journal of Experimental Botany</i> , 2022, 73, 2222-2237.	4.8	9
4033	Bulk segregation analysis in the <i>NGS</i> era: a review of its teenage years. <i>Plant Journal</i> , 2022, 109, 1355-1374.	5.7	58
4034	Population structure and association mapping studies for important agronomic traits in soybean. <i>Journal of Genetics</i> , 2014, 93, 775-84.	0.7	9
4035	Genetic dissection of grain iron and zinc concentrations in lentil ( <i>Medik.</i> ). <i>Journal of Genetics</i> , 2019, 98, .	0.7	2
4036	Candidate screening of blast resistance donors for rice breeding. <i>Journal of Genetics</i> , 2019, 98, .	0.7	0
4037	Identification of genomewide single-nucleotide polymorphisms associated with presummer, summer and autumn bolls in upland cotton. <i>Journal of Genetics</i> , 2019, 98, .	0.7	1

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4038	Cataloguing of blast resistance genes in landraces and breeding lines of rice from India. <i>Journal of Genetics</i> , 2019, 98, .	0.7	3
4039	Variation of grain quality characters and marker-trait association in rice ( <i>L.</i> ). <i>Journal of Genetics</i> , 2020, 99, .	0.7	2
4040	Nutritional improvement of cereal crops to combat hidden hunger during COVID-19 pandemic: Progress and prospects. <i>Advances in Food Security and Sustainability</i> , 2022, , .	1.4	0
4042	Scanning the rice Global MAGIC population for dynamic genetic control of seed traits under vegetative drought. <i>The Plant Phenome Journal</i> , 2022, 5, .	2.0	3
4043	Genomics of Climate Adaptation in <i>Pinus Lambertiana</i> . <i>Compendium of Plant Genomes</i> , 2022, , 51-65.	0.5	1
4045	Genomic Designing for Biotic Stress Resistant Grapevine. , 2022, , 87-255.		11
4046	Stable QTL for malate levels in ripe fruit and their transferability across <i>Vitis</i> species. <i>Horticulture Research</i> , 2022, 9, uhac009.	6.3	6
4048	Identification of Candidate Genes for Salinity and Anaerobic Tolerance at the Germination Stage in Rice by Genome-Wide Association Analyses. <i>Frontiers in Genetics</i> , 2022, 13, 822516.	2.3	12
4049	Nucleotide Variation in <i>Drosophila</i> cryptochrome Is Linked to Circadian Clock Function: An Association Analysis. <i>Frontiers in Physiology</i> , 2022, 13, 781380.	2.8	3
4050	Identification and fine mapping of a major QTL (qRtsc8-1) conferring resistance to maize tar spot complex and validation of production markers in breeding lines. <i>Theoretical and Applied Genetics</i> , 2022, 135, 1551-1563.	3.6	4
4051	Genetic Variation in ZmPAT7 Contributes to Tassel Branch Number in Maize. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2586.	4.1	5
4052	Identification of Chilling Accumulation-Associated Genes for Litchi Flowering by Transcriptome-Based Genome-Wide Association Studies. <i>Frontiers in Plant Science</i> , 2022, 13, 819188.	3.6	1
4053	Classification and Regression Models for Genomic Selection of Skewed Phenotypes: A Case for Disease Resistance in Winter Wheat ( <i>Triticum aestivum</i> L.). <i>Frontiers in Genetics</i> , 2022, 13, 835781.	2.3	6
4054	Using an incomplete block design to allocate lines to environments improves sparse genome-based prediction in plant breeding. <i>Plant Genome</i> , 2022, 15, e20194.	2.8	4
4055	Genome-wide association study for yield-related traits in sesame ( <i>Sesamum Indicum</i> ) Tj ETQq0 0 0 rgBT /Overlo	1.9	1
4056	Identification of a candidate gene underlying qHKW3, a QTL for hundred-kernel weight in maize. <i>Theoretical and Applied Genetics</i> , 2022, 135, 1579-1589.	3.6	4
4057	Population genomics of <i>Zea</i> species identifies selection signatures during maize domestication and adaptation. <i>BMC Plant Biology</i> , 2022, 22, 72.	3.6	9
4058	Evaluation of Methods for Measuring Fusarium-Damaged Kernels of Wheat. <i>Agronomy</i> , 2022, 12, 532.	3.0	6



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4059	Genome-Wide Association Study Reveals Genetic Architecture and Candidate Genes for Yield and Related Traits under Terminal Drought, Combined Heat and Drought in Tropical Maize Germplasm. <i>Genes</i> , 2022, 13, 349.	2.4	7
4060	Identification of Novel Genomic Regions for Bacterial Leaf Pustule (BLP) Resistance in Soybean ( <i>Glycine max</i> L.) via Integrating Linkage Mapping and Association Analysis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2113.	4.1	2
4061	Genome Wide Association Study Identifies Candidate Genes Related to the Earlywood Tracheid Properties in <i>Picea crassifolia</i> Kom.. <i>Forests</i> , 2022, 13, 332.	2.1	2
4062	Genome wide association analysis of acid detergent fiber content of 206 forage sorghum ( <i>Sorghum</i> ) Tj ETQq1 1 0.784314 rgBT /Over	1.6	1
4063	High-density genetic map and genome-wide association studies of aesthetic traits in <i>Phalaenopsis</i> orchids. <i>Scientific Reports</i> , 2022, 12, 3346.	3.3	6
4064	Genetic characterization and genome-wide association mapping for stem rust resistance in spring bread wheat. <i>BMC Genomic Data</i> , 2022, 23, 11.	1.7	6
4065	High-LD SNP markers exhibiting pleiotropic effects on salt tolerance at germination and seedlings stages in spring wheat. <i>Plant Molecular Biology</i> , 2022, 108, 585-603.	3.9	14
4066	Genome-Wide Association Study Reveals Genetic Basis of Trace Elements Accumulation in Maize Kernels. <i>Agriculture (Switzerland)</i> , 2022, 12, 262.	3.1	2
4067	Identification of <i>OsPK5</i> involved in rice glycolytic metabolism and GA/ABA balance for improving seed germination via genome-wide association study. <i>Journal of Experimental Botany</i> , 2022, 73, 3446-3461.	4.8	19
4068	Identification of Genomic Regions Associated with Agronomic and Disease Resistance Traits in a Large Set of Multiple DH Populations. <i>Genes</i> , 2022, 13, 351.	2.4	3
4070	Genome-Wide Association Mapping Indicates Quantitative Genetic Control of Spot Blotch Resistance in Bread Wheat and the Favorable Effects of Some Spot Blotch Loci on Grain Yield. <i>Frontiers in Plant Science</i> , 2022, 13, 835095.	3.6	9
4071	High-Density Genetic Variation Map Reveals Key Candidate Loci and Genes Associated With Important Agronomic Traits in Peanut. <i>Frontiers in Genetics</i> , 2022, 13, 845602.	2.3	3
4072	Genome wide association study of frost tolerance in wheat. <i>Scientific Reports</i> , 2022, 12, 5275.	3.3	13
4073	Identification of New QTLs for Dietary Fiber Content in <i>Aegilops biuncialis</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 3821.	4.1	6
4074	Epigenomics as a paradigm to understand the nuances of phenotypes. <i>Journal of Experimental Biology</i> , 2022, 225, .	1.7	7
4075	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.	1.2	3
4076	Genetic diversity and population structure of an African yam bean ( <i>Sphenostylis stenocarpa</i> ) collection from IITA GenBank. <i>Scientific Reports</i> , 2022, 12, 4437.	3.3	2
4077	Association Analysis between Genetic Variants of <i>elovl5a</i> and <i>elovl5b</i> and Poly-Unsaturated Fatty Acids in Common Carp ( <i>Cyprinus carpio</i> ). <i>Biology</i> , 2022, 11, 466.	2.8	3

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4078	SoySNP618K array: A high-resolution single nucleotide polymorphism platform as a valuable genomic resource for soybean genetics and breeding. <i>Journal of Integrative Plant Biology</i> , 2022, 64, 632-648.	8.5	7
4079	Genetic and Phenotypic Characteristics of the <i>Salmo trutta</i> Complex in Italy. <i>Applied Sciences</i> (Switzerland), 2022, 12, 3219.	2.5	6
4080	Genomic Association Mapping of Apparent Amylose and Protein Concentration in Milled Rice. <i>Agronomy</i> , 2022, 12, 857.	3.0	7
4081	Cross compatibility in intraspecific and interspecific hybridization in yam ( <i>Dioscorea</i> spp.). <i>Scientific Reports</i> , 2022, 12, 3432.	3.3	14
4082	QTL Mapping for Haploid Inducibility Using Genotyping by Sequencing in Maize. <i>Plants</i> , 2022, 11, 878.	3.5	4
4083	Bulked Segregant Analysis and Association Analysis Identified the Polymorphisms Related to the Intermuscular Bones in Common Carp ( <i>Cyprinus carpio</i> ). <i>Biology</i> , 2022, 11, 477.	2.8	4
4084	Genome-wide association mapping of Hagberg falling number, protein content, test weight, and grain yield in U.K. wheat. <i>Crop Science</i> , 2022, 62, 965-981.	1.8	10
4085	Genetic Bases of Flow- and Sink-Related Traits in Rice Revealed by Genome-Wide Association Study. <i>Agronomy</i> , 2022, 12, 776.	3.0	1
4086	Harnessing the diversity of wild emmer wheat for genetic improvement of durum wheat. <i>Theoretical and Applied Genetics</i> , 2022, 135, 1671-1684.	3.6	7
4087	Identification of Quantitative Trait Loci Associated with Bacterial Leaf Spot Resistance in Baby Leaf Lettuce. <i>Plant Disease</i> , 2022, 106, 2583-2590.	1.4	4
4088	Genome-wide Association Study for Starch Pasting Properties in Chinese Spring Wheat. <i>Frontiers in Genetics</i> , 2022, 13, 830644.	2.3	3
4089	Genetic Diversity and Selection Footprints in the Genome of Brazilian Soybean Cultivars. <i>Frontiers in Plant Science</i> , 2022, 13, 842571.	3.6	3
4090	Genetic Diversity, Population Structure and Linkage Disequilibrium Analyses in Tropical Maize Using Genotyping by Sequencing. <i>Plants</i> , 2022, 11, 799.	3.5	11
4091	Linkage disequilibrium and population structure in a core collection of <i>Brassica napus</i> (L.). <i>PLoS ONE</i> , 2022, 17, e0250310.	2.5	9
4092	Breaking the limits - multichromosomal structure of an early eudicot <i>Pulsatilla patens</i> mitogenome reveals extensive RNA-editing, longest repeats and chloroplast derived regions among sequenced land plant mitogenomes. <i>BMC Plant Biology</i> , 2022, 22, 109.	3.6	10
4093	Relationships Among Arsenic-Related Traits, Including Rice Grain Arsenic Concentration and Straighthead Resistance, as Revealed by Genome-Wide Association. <i>Frontiers in Genetics</i> , 2021, 12, 787767.	2.3	4
4094	Deciphering Haplotypic Variation and Gene Expression Dynamics Associated with Nutritional and Cooking Quality in Rice. <i>Cells</i> , 2022, 11, 1144.	4.1	1
4095	Nucleotide polymorphisms of the maize <i>ZmCWINV3</i> gene and their association with ear-related traits. <i>Genetic Resources and Crop Evolution</i> , 2022, 69, 2115-2124.	1.6	1

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4096	Genome-wide association study and genomic prediction of white rust resistance in USDA GRIN spinach germplasm. Horticulture Research, 2022, 9, .	6.3	16
4097	Mapping of Nematode Resistance in Hexaploid Sweetpotato Using a Next-Generation Sequencing-Based Association Study. Frontiers in Plant Science, 2022, 13, 858747.	3.6	8
4098	Convergent selection of a WD40 protein that enhances grain yield in maize and rice. Science, 2022, 375, eabg7985.	12.6	110
4099	A new strategy for using historical imbalanced yield data to conduct genome-wide association studies and develop genomic prediction models for wheat breeding. Molecular Breeding, 2022, 42, 1.	2.1	0
4100	Mapping the sex determination region in the <i>Salix</i> F1 hybrid common parent population confirms a ZW system in six diverse species. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	9
4101	A multi-trait multi-locus stepwise approach for conducting GWAS on correlated traits. Plant Genome, 2022, 15, e20200.	2.8	4
4102	Genomic signatures of adaptive divergence in lacustrine copepods. Freshwater Biology, 2022, 67, 1045-1062.	2.4	3
4103	Screening of stable resistant accessions and identification of resistance loci to <i>Barley yellow mosaic virus</i> disease. PeerJ, 2022, 10, e13128.	2.0	5
4104	Multi-trait association study identifies loci associated with tolerance of low phosphorus in <i>Oryza sativa</i> and its wild relatives. Scientific Reports, 2022, 12, 4089.	3.3	2
4105	Unraveling the Genetic Basis of Key Agronomic Traits of Wrinkled Vining Pea ( <i>Pisum sativum</i> L.) for Sustainable Production. Frontiers in Plant Science, 2022, 13, 844450.	3.6	6
4106	GWAS for main effects and epistatic interactions for grain morphology traits in wheat. Physiology and Molecular Biology of Plants, 2022, 28, 651-668.	3.1	6
4107	Integration of GWAS and transcriptome analyses to identify SNPs and candidate genes for aluminum tolerance in rapeseed ( <i>Brassica napus</i> L.). BMC Plant Biology, 2022, 22, 130.	3.6	10
4108	Genome-Wide Association Analyses Reveal Candidate Genes Controlling Harvest Index and Related Agronomic Traits in <i>Brassica napus</i> L.. Agronomy, 2022, 12, 814.	3.0	2
4109	Genetic architecture of the high inorganic phosphate phenotype derived from a low phytate mutant in winter wheat ( <i>Triticum aestivum</i> L.). Crop Science, 0, , .	1.8	2
4110	Newly Developed MAGIC Population Allows Identification of Strong Associations and Candidate Genes for Anthocyanin Pigmentation in Eggplant. Frontiers in Plant Science, 2022, 13, 847789.	3.6	15
4111	Fine-scale genetic structure of the rice landrace population in Japan. Molecular Genetics and Genomics, 2022, 297, 711-718.	2.1	4
4112	Genome-Wide Development of Polymorphic Microsatellite Markers and Association Analysis of Major Agronomic Traits in Core Germplasm Resources of Tartary Buckwheat. Frontiers in Plant Science, 2022, 13, 819008.	3.6	9
4114	Genome-wide association study and genomic prediction for yield and grain quality traits of hybrid rice. Molecular Breeding, 2022, 42, 1.	2.1	4

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4115	Genome-Wide Association Study Reveals the Genetic Basis of Five Quality Traits in Chinese Wheat. <i>Frontiers in Plant Science</i> , 2022, 13, 835306.	3.6	8
4117	Genetic architecture of embryogenic callus induction in maize from the perspective of population genomics. <i>Plant Cell, Tissue and Organ Culture</i> , 2022, 150, 345-359.	2.3	4
4118	<i>Pythium insidiosum</i> complex hides a cryptic novel species: <i>Pythium periculosum</i> . <i>Fungal Biology</i> , 2022, 126, 366-374.	2.5	6
4119	Genome-Wide Association Mapping of Resistance to Powdery Mildew in Regional Trials of Wheat Mainly from China. <i>Plant Disease</i> , 2022, 106, 2701-2710.	1.4	2
4120	Genome-wide association mapping identifies an <i>SNF4</i> ortholog that impacts biomass and sugar yield in sorghum and sugarcane. <i>Journal of Experimental Botany</i> , 2022, 73, 3584-3596.	4.8	1
4121	Development and Cross-Species Transferability of Novel Genomic-SSR Markers and Their Utility in Hybrid Identification and Trait Association Analysis in Chinese Cherry. <i>Horticulturae</i> , 2022, 8, 222.	2.8	7
4122	Population Structure Analysis and Association Mapping for Turicum Leaf Blight Resistance in Tropical Maize Using SSR Markers. <i>Genes</i> , 2022, 13, 618.	2.4	9
4123	Development of Resistance in <i>Escherichia coli</i> Against Repeated Water Disinfection. <i>Frontiers in Environmental Science</i> , 0, 10, .	3.3	2
4124	LPL, FNDC5 and PPAR $\gamma$ gene polymorphisms related to body composition parameters and lipid metabolic profile in adolescents from Southern Italy. <i>Journal of Translational Medicine</i> , 2022, 20, 107.	4.4	4
4125	Nitrate-Induced MtCLE34 Gene Lacks the Ability to Reduce Symbiotic Nodule Number and Carries Nonsense Mutation in a Few Accessions of <i>Medicago truncatula</i> . <i>Agronomy</i> , 2022, 12, 842.	3.0	3
4126	Differential environmental and genomic architectures shape the natural diversity for trichome patterning and morphology in different <i>Arabidopsis</i> organs. <i>Plant, Cell and Environment</i> , 2022, 45, 3018-3035.	5.7	2
4127	Genomic Predictions for Common Bunt, FHB, Stripe Rust, Leaf Rust, and Leaf Spotting Resistance in Spring Wheat. <i>Genes</i> , 2022, 13, 565.	2.4	13
4128	Identification of QTLs/ Candidate Genes for Seed Mineral Contents in Common Bean ( <i>Phaseolus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2	2.3	6
4129	Genome-wide SNPs detect fine-scale genetic structure in threatened populations of squirrel glider <i>Petaurus norfolcensis</i> . <i>Conservation Genetics</i> , 2022, 23, 541-558.	1.5	3
4130	Genetic Diversity and Association Analysis for Carotenoid Content among Sprouts of Cowpea ( <i>Vigna</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2	4.1	8
4131	Genome-Wide Association Study of Salt Tolerance at the Seed Germination Stage in Flax ( <i>Linum</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 14	2.4	14
4132	Fixation of hybrid sterility genes and favorable alleles of key yield-related genes with dominance contribute to the high yield of the Yongyou series of intersubspecific hybrid rice. <i>Journal of Genetics and Genomics</i> , 2022, 49, 448-457.	3.9	2
4133	A population-level statistic for assessing Mendelian behavior of genotyping-by-sequencing data from highly duplicated genomes. <i>BMC Bioinformatics</i> , 2022, 23, 101.	2.6	5

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4134	Reactive Oxygen Species Partly Mediate DNA Methylation in Responses to Different Heavy Metals in Pokeweed. <i>Frontiers in Plant Science</i> , 2022, 13, 845108.	3.6	13
4136	Association mapping of autumn-seeded rye ( <i>Secale cereale</i> L.) reveals genetic linkages between genes controlling winter hardiness and plant development. <i>Scientific Reports</i> , 2022, 12, 5793.	3.3	3
4137	Genotyping-by-Sequencing Based Molecular Genetic Diversity of Pakistani Bread Wheat ( <i>Triticum</i> ) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	2.3	1
4139	Genetic similarity between donor and recurrent parents can reduce the number of backcross generation in marker-assisted backcross. <i>Euphytica</i> , 2022, 218, 1.	1.2	0
4142	Application of multi-locus GWAS for the detection of bruchid resistance loci in cowpea ( <i>Vigna unguiculata</i> ). <i>Plant Breeding</i> , 2022, 141, 439-450.	1.9	5
4143	Genome-wide association mapping of agronomic traits and grain characteristics in spring wheat under conventional and organic management systems. <i>Crop Science</i> , 0, , .	1.8	5
4144	The population genetics of adaptation through copy number variation in a fungal plant pathogen. <i>Molecular Ecology</i> , 2023, 32, 2443-2460.	3.9	14
4145	Epistatic interaction between Rhg1-a and Rhg2 in PI 90763 confers resistance to virulent soybean cyst nematode populations. <i>Theoretical and Applied Genetics</i> , 2022, 135, 2025-2039.	3.6	7
4146	Drought-Tolerance QTLs Associated with Grain Yield and Related Traits in Spring Bread Wheat. <i>Plants</i> , 2022, 11, 986.	3.5	4
4147	Combined GWAS and QTL mapping revealed candidate genes and SNP network controlling recovery and tolerance traits associated with drought tolerance in seedling winter wheat. <i>Genomics</i> , 2022, 114, 110358.	2.9	20
4150	Fine mapping qKRN5.04 provides a functional gene negatively regulating maize kernel row number. <i>Theoretical and Applied Genetics</i> , 2022, 135, 1997-2007.	3.6	5
4151	Detection of QTLs for Plant Height Architecture Traits in Rice ( <i>Oryza sativa</i> L.) by Association Mapping and the RSTEP-LRT Method. <i>Plants</i> , 2022, 11, 999.	3.5	3
4152	Quantitative Trait Loci Analysis Based on High-Density Mapping of Single-Nucleotide Polymorphisms by Genotyping-by-Sequencing Against Pine Wilt Disease in Japanese Black Pine ( <i>Pinus thunbergii</i> ). <i>Frontiers in Plant Science</i> , 2022, 13, 850660.	3.6	4
4154	Downregulation of a gibberellin 3 $\beta$ -hydroxylase enhances photosynthesis and increases seed yield in soybean. <i>New Phytologist</i> , 2022, 235, 502-517.	7.3	26
4155	Genetic control of barley phenology in South American environments. <i>Euphytica</i> , 2022, 218, 1.	1.2	2
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4159	Genomic analysis and finding of candidate genes for <i>Nilaparvata lugens</i> (stål) resistance in Indian pigmented and other indigenous rice genotypes. <i>Crop Protection</i> , 2022, 156, 105959.	2.1	4

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4173	Genome-Wide Association Analysis of Resistance to <i>Pseudoperonospora cubensis</i> in Citron Watermelon. <i>Plant Disease</i> , 2022, 106, 1952-1958.	1.4	6
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5163	Genetic architecture of seed glycerolipids in Asian cultivated rice. <i>Plant, Cell and Environment</i> , 0, , .	5.7	9
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5165	Genome-Wide Association Analysis and Gene Mining of Resistance to China Race 1 of Frogeye Leaf Spot in Soybean. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	1
5166	Genome-Wide Association Mapping Revealed SNP Alleles Associated with Spike Traits in Wheat. <i>Agronomy</i> , 2022, 12, 1469.	3.0	9
5167	Genome-Wide Association Mapping of Grain Metal Accumulation in Wheat. <i>Genes</i> , 2022, 13, 1052.	2.4	6

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5169	Genome-Wide Association Study of Blast Resistant in Korean Rice (<i>Oryza sativa</i> L.) Breed Lines. <i>Plant Breeding and Biotechnology</i> , 2022, 10, 139-144.	0.9	1
5171	An Analysis of Natural Variation Reveals That OsFLA2 Controls Flag Leaf Angle in Rice ( <i>Oryza sativa</i> L.). <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	3
5172	Molecular characterization of tall fescue germplasm using SNP markers: population structure, linkage disequilibrium, and association mapping of yield-related traits. <i>Plant Biotechnology Reports</i> , 0, , .	1.5	0
5173	Genetic relationships and genome selection signatures between soybean cultivars from Brazil and United States after decades of breeding. <i>Scientific Reports</i> , 2022, 12, .	3.3	4
5174	Discovery of a <scp><i>DFR</i></scp> gene that controls anthocyanin accumulation in the spiny <i>Solanum</i> group: roles of a natural promoter variant and alternative splicing. <i>Plant Journal</i> , 2022, 111, 1096-1109.	5.7	18
5175	Molecular and archaeological evidence on the geographical origin of domestication for <i>Camelina sativa</i>. <i>American Journal of Botany</i> , 2022, 109, 1177-1190.	1.7	10
5176	Expressed genes and their new alleles identification during fibre elongation reveal the genetic factors underlying improvements of fibre length in cotton. <i>Plant Biotechnology Journal</i> , 2022, 20, 1940-1955.	8.3	5
5177	Identification of Low-Light-Resistant Germplasm and Related Loci of Soybean. <i>Agronomy</i> , 2022, 12, 1483.	3.0	2
5178	Genetic architecture of end-use quality traits in soft white winter wheat. <i>BMC Genomics</i> , 2022, 23, .	2.8	2
5179	Genome-wide association mapping and genomic prediction for pre-harvest sprouting resistance, low $\alpha$ -amylase and seed color in Iranian bread wheat. <i>BMC Plant Biology</i> , 2022, 22, .	3.6	15
5180	Genome-Wide Association Studies Provide Insights Into the Genetic Architecture of Seed Germination Traits in Maize. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	4
5181	Identification of Putative SNP Markers Associated with Resistance to Egyptian Loose Smut Race(s) in Spring Barley. <i>Genes</i> , 2022, 13, 1075.	2.4	6
5182	Genetic diversity and marker trait association for phytophthora resistance in chilli. <i>Molecular Biology Reports</i> , 0, , .	2.3	4
5183	Genetic Diversity and Pedigree Analysis of Red Currant Germplasm. <i>Plants</i> , 2022, 11, 1623.	3.5	3
5184	Convergent loss of anthocyanin pigments is controlled by the same MYB gene in cereals. <i>Journal of Experimental Botany</i> , 2022, 73, 6089-6102.	4.8	6
5185	Analysis of genetic diversity and population structure among cultivated potato clones from Korea and global breeding programs. <i>Scientific Reports</i> , 2022, 12, .	3.3	4
5186	High-Altitude Genetic Selection and Genome-Wide Association Analysis of Yield-Related Traits in <i>Elymus sibiricus</i> L. Using SLAF Sequencing. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	4

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5187	Single trait versus principal component based association analysis for flowering related traits in pigeonpea. <i>Scientific Reports</i> , 2022, 12, .	3.3	7
5188	Genome-Wide Screening of Broad-Spectrum Resistance to Leaf Rust ( <i>Puccinia triticina</i> Eriks) in Spring Wheat ( <i>Triticum aestivum</i> L.). <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	7
5189	Genome wide association study and haplotype analysis reveals the role of HvHKT1;5 in potassium retention but not Na <sup>+</sup> exclusion in barley ( <i>Hordeum vulgare</i> L.). <i>Environmental and Experimental Botany</i> , 2022, 201, 104973.	4.2	2
5190	Identification of Candidate Genes and Genomic Selection for Seed Protein in Soybean Breeding Pipeline. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	9
5191	Network and Evolutionary Analysis Reveals Candidate Genes of Membrane Trafficking Involved in Maize Seed Development and Immune Response. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	0
5192	Genome-wide association study identifies novel candidate loci or genes affecting stalk strength in maize. <i>Crop Journal</i> , 2023, 11, 220-227.	5.2	5
5194	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.	3.7	11
5196	Genetic Diversity and Genome-Wide Association Study of Pumpkins ( <i>Cucurbita Moschata</i> ) Originating from East Asia. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
5197	Developing core marker sets for effective genomic-assisted selection in wheat and barley breeding programs. <i>Breeding Science</i> , 2022, 72, 257-266.	1.9	2
5198	Genetic architecture and QTL selection response for Kernza perennial grain domestication traits. <i>Theoretical and Applied Genetics</i> , 2022, 135, 2769-2784.	3.6	4
5199	Spanish Melon Landraces: Revealing Useful Diversity by Genomic, Morphological, and Metabolomic Analysis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7162.	4.1	2
5200	Identification of major genomic regions for soybean seed weight by genome-wide association study. <i>Molecular Breeding</i> , 2022, 42, .	2.1	4
5201	The autotetraploid potato genome provides insights into highly heterozygous species. <i>Plant Biotechnology Journal</i> , 2022, 20, 1996-2005.	8.3	22
5202	Genomic Prediction Accuracy of Stripe Rust in Six Spring Wheat Populations by Modeling Genotype by Environment Interaction. <i>Plants</i> , 2022, 11, 1736.	3.5	3
5203	A Nuclear Factor Y-B Transcription Factor, GmNFYB17, Regulates Resistance to Drought Stress in Soybean. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7242.	4.1	12
5204	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, .	3.6	3
5205	Genome-Wide Association Study With Growth-Related Traits and Secondary Metabolite Contents in Red- and White-Heart Chinese Fir. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	3
5206	Genome-Wide Association Study of Grain Quality Traits in Rice Detected Genomic Regions of High-Quality Rice for Increasing Rice Consumption. <i>Biosciences, Biotechnology Research Asia</i> , 2022, 19, 333-346.	0.5	1

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5207	A genome-wide association study of lateral root number for Asian cotton ( <i>Gossypium arboreum</i> L.). <i>Journal of Cotton Research</i> , 2022, 5, .	2.5	2
5208	Dissecting the Genetic Structure of Maize Leaf Sheaths at Seedling Stage by Image-Based High-Throughput Phenotypic Acquisition and Characterization. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	1
5209	Genomic Prediction Strategies for Dry-Down-Related Traits in Maize. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	0
5210	Genetic and molecular analysis reveals that two major loci and their interaction confer clubroot resistance in canola introgressed from rutabaga. <i>Plant Genome</i> , 2022, 15, .	2.8	5
5211	Genetic Diversity and Selection Signatures in Synthetic-Derived Wheats and Modern Spring Wheat. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	2
5212	Reference genome assemblies reveal the origin and evolution of allohexaploid oat. <i>Nature Genetics</i> , 2022, 54, 1248-1258.	21.4	45
5213	Genome sequence-based genome-wide association study of feed efficiency in Pacific abalone. <i>Aquaculture</i> , 2022, 561, 738630.	3.5	1
5214	Consequences of introgression and gene flow on the genetic structure and diversity of Lima bean ( <i>Phaseolus lunatus</i> L.) in its Mesoamerican diversity area. <i>PeerJ</i> , 0, 10, e13690.	2.0	5
5215	Epistasis Activation Contributes Substantially to Heterosis in Temperate by Tropical Maize Hybrids. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	4
5216	Contrasting Water Withholding Responses of Young Maize Plants Reveal Link Between Lipid Peroxidation and Osmotic Regulation Corroborated by Genetic Analysis. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	1
5217	Partial Least Squares Enhances Genomic Prediction of New Environments. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	12
5218	Multi-omics analyses of 398 foxtail millet accessions reveal genomic regions associated with domestication, metabolite traits, and anti-inflammatory effects. <i>Molecular Plant</i> , 2022, 15, 1367-1383.	8.3	30
5219	Comparative Genetic Analysis of Durum Wheat Landraces and Cultivars Widespread in Tunisia. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	7
5220	Linkage mapping combined with GWAS revealed the genetic structural relationship and candidate genes of maize flowering time-related traits. <i>BMC Plant Biology</i> , 2022, 22, .	3.6	6
5221	Identification of Genomic Regions Associated with Fusarium Wilt Resistance in Cowpea. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 6889.	2.5	5
5222	Genetic diversity of subtropical double-haploid maize lines selected for high oil content. <i>Agronomy Journal</i> , 2022, 114, 2715-2727.	1.8	0
5223	Genome-Wide Association Studies of Root-Related Traits in <i>Brassica napus</i> L. under Low-Potassium Conditions. <i>Plants</i> , 2022, 11, 1826.	3.5	3
5224	Identification of Genetic Diversity, Pyrrolic Acid-Producing Strains and Transmission Modes of Endophytic <i>Sarocladium zeae</i> Fungi from Zea Crops. <i>Microorganisms</i> , 2022, 10, 1415.	3.6	3

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5226	Whole-genome single nucleotide polymorphism analysis for typing the pandemic pathogen <i>Fusarium graminearum sensu stricto</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	4
5227	Empirical comparison of genomic and phenotypic selection for resistance to <i>Fusarium</i> ear rot and fumonisin contamination in maize. <i>Theoretical and Applied Genetics</i> , 2022, 135, 2799-2816.	3.6	2
5229	Genetic mapping of sorghum resistance to an Illinois isolate of <i>Colletotrichum sublineola</i> . <i>Plant Genome</i> , 0, , .	2.8	1
5230	Exploiting genetic variation from unadapted germplasm—An example from improvement of sorghum in Ethiopia. <i>Plants People Planet</i> , 2022, 4, 523-536.	3.3	1
5231	Fungicide Resistance and Host Influence on Population Structure in <i>Botrytis</i> spp. from Specialty Crops in California. <i>Phytopathology</i> , 2022, 112, 2549-2559.	2.2	2
5232	Genome-wide association study revealed <i>ABCD4</i> on <i>SSC7</i> and <i>GREB1L</i> and <i>MIB1</i> on <i>SSC6</i> as crucial candidate genes for rib number in Beijing Black pigs. <i>Animal Genetics</i> , 2022, 53, 690-695.	1.7	6
5233	Combined nature and human selections reshaped peach fruit metabolome. <i>Genome Biology</i> , 2022, 23, .	8.8	23
5234	SSR-based genome-wide association study in turkish durum wheat germplasms revealed novel QTL of accumulated platinum. <i>Molecular Biology Reports</i> , 2022, 49, 11289-11300.	2.3	4
5235	Genome-wide Association Study for Yield and Yield-Related Traits in Diverse Blackgram Panel (Vigna) Tj ETQq1 1 0.784314 rgBT /Overbo 0, 13, .	2.3	5
5236	Genome-wide association study for morphological traits and resistance to <i>Peryonella pinodes</i> in the USDA pea single plant plus collection. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	4
5237	SoyMAGIC: An Unprecedented Platform for Genetic Studies and Breeding Activities in Soybean. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	2
5238	Transcriptome analysis of the spleen of heterophils to lymphocytes ratio-selected chickens revealed their mechanism of differential resistance to <i>Salmonella</i> . <i>Journal of Integrative Agriculture</i> , 2022, 21, 2372-2383.	3.5	3
5239	Mining of candidate genes for grape berry cracking using a genome-wide association study. <i>Journal of Integrative Agriculture</i> , 2022, 21, 2291-2304.	3.5	8
5240	Genetic dissection of <i>Brassica napus</i> photosynthetic pigment content diversity and identification of loci associated with photoperiod and alkaline soil responses. <i>Industrial Crops and Products</i> , 2022, 186, 115294.	5.2	1
5241	Structural analysis of <i>Actinidia arguta</i> natural populations and preliminary application in association mapping of fruit traits. <i>Scientia Horticulturae</i> , 2022, 304, 111306.	3.6	4
5242	SNP Genotyping for Purity Assessment of a Forage Oat ( <i>Avena sativa</i> L.) Variety from Colombia. <i>Agronomy</i> , 2022, 12, 1710.	3.0	1
5243	Integrating multi-locus genome-wide association studies with transcriptomic data to identify genetic loci underlying adult root trait responses to drought stress in flax ( <i>Linum usitatissimum</i> L.). <i>Environmental and Experimental Botany</i> , 2022, 202, 105019.	4.2	4

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5245	Multi-Locus Genome-Wide Association Studies to Characterize Fusarium Head Blight (FHB) Resistance in Hard Winter Wheat. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	5
5246	Genetic dissection of grain iron and zinc, and thousand kernel weight in wheat ( <i>Triticum aestivum</i> L.) using genome-wide association study. <i>Scientific Reports</i> , 2022, 12, .	3.3	13
5247	Deciphering the Genetic Basis of Root and Biomass Traits in Rapeseed ( <i>Brassica napus</i> L.) through the Integration of GWAS and RNA-Seq under Nitrogen Stress. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7958.	4.1	12
5248	Dissecting the Genetic Architecture of Phenology Affecting Adaptation of Spring Bread Wheat Genotypes to the Major Wheat-Producing Zones in India. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	1
5249	GWAS and RNA-seq analysis uncover candidate genes associated with alkaline stress tolerance in maize ( <i>Zea mays</i> L.) seedlings. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	5
5250	Development of single nucleotide polymorphism markers and genetic diversity in guava ( <i>Psidium guajava</i> L.). <i>Plants People Planet</i> , 2023, 5, 58-69.	3.3	3
5251	Genetic diversity and population structure of pigeonpea ( <i>Cajanus cajan</i> [L.] Millspaugh) landraces grown in Benin revealed by Genotyping-By-Sequencing. <i>PLoS ONE</i> , 2022, 17, e0271565.	2.5	3
5252	Genome-wide association study (GWAS) of germination and post-germination related seedling traits in rice. <i>Euphytica</i> , 2022, 218, .	1.2	3
5253	cis-regulatory variation affecting gene expression contributes to the improvement of maize kernel size. <i>Plant Journal</i> , 0, , .	5.7	2
5254	Differential associations between nucleotide polymorphisms and physiological traits in Norway spruce ( <i>Picea abies</i> Karst.) plants under contrasting water regimes. <i>Forestry</i> , 0, , .	2.3	2
5255	Genetic diversity and population structure of the USDA collection of <i>Brassica juncea</i> L.. <i>Industrial Crops and Products</i> , 2022, 187, 115379.	5.2	6
5256	QTL mapping of bud break in apple aimed at facilitating breeding of cultivars resilient to climate change. <i>Acta Horticulturae</i> , 2022, , 49-54.	0.2	2
5257	Transcriptome and association mapping revealed functional genes respond to drought stress in <i>Populus</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	2
5258	Preliminary Dissection of Grain Yield and Related Traits at Differential Nitrogen Levels in Diverse Pre-Breeding Wheat Germplasm Through Association Mapping. <i>Molecular Biotechnology</i> , 0, , .	2.4	2
5259	Genetic variation of seed oil characteristics in native Korean germplasm of Perilla crop ( <i>Perilla</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	1.4	4
5260	Genome-wide association study of Senegalese sorghum seedlings responding to a Texas isolate of <i>Colletotrichum sublineola</i> . <i>Scientific Reports</i> , 2022, 12, .	3.3	5
5261	High-quality reference genome sequences of two Cannaceae species provide insights into the evolution of Cannaceae. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	4



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5262	Genomic characterization of polyextremotolerant black yeasts isolated from food and food production environments. <i>Frontiers in Fungal Biology</i> , 0, 3, .	2.0	0
5263	Multi-locus genome-wide association studies reveal novel alleles for flowering time under vernalisation and extended photoperiod in a barley MAGIC population. <i>Theoretical and Applied Genetics</i> , 0, , .	3.6	4
5264	Genome-Wide Association Studies Reveal Novel Loci for Herbivore Resistance in Wild Soybean (Glycine) Tj ETQq0 0.0 rgBT /Overlock 10	4.1	7
5265	The brassinosteroid biosynthesis gene TaD11-2A controls grain size and its elite haplotype improves wheat grain yields. <i>Theoretical and Applied Genetics</i> , 2022, 135, 2907-2923.	3.6	17
5266	Linkage analysis and residual heterozygotes derived near isogenic lines reveals a novel protein quantitative trait loci from a Glycine soja accession. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	5
5267	DARtseq molecular markers associated with the piping leaf margin phenotype in pineapple (Ananas) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.9	2
5268	Phenotypic and Genotypic Diversity of the Tomato Germplasm From the Lazio Region in Central Italy, With a Focus on Landrace Distinctiveness. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	5
5269	Exploiting Wild Emmer Wheat Diversity to Improve Wheat A and B Genomes in Breeding for Heat Stress Adaptation. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	5
5271	Mining Candidate Genes and Favorable Haplotypes for Flag Leaf Shape in Rice (Oryza sativa L.) Based on a Genome-Wide Association Study. <i>Agronomy</i> , 2022, 12, 1814.	3.0	7
5272	Genomic regions associated with resistance to soybean rust (Phakopsora pachyrhizi) under field conditions in soybean germplasm accessions from Japan, Indonesia and Vietnam. <i>Theoretical and Applied Genetics</i> , 0, , .	3.6	2
5274	Genome-wide association study and metabolic pathway prediction of barrenness in maize as a response to high planting density. <i>Journal of Integrative Agriculture</i> , 2022, 21, 3514-3523.	3.5	5
5275	A small chromosomal inversion mediated by MITE transposons confers cleistogamy in <i>Brassica napus</i>. <i>Plant Physiology</i> , 0, , .	4.8	1
5277	Genome-wide association mapping for component traits of drought and heat tolerance in wheat. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	14
5278	Genetic networks underlying salinity tolerance in wheat uncovered with genome-wide analyses and selective sweeps. <i>Theoretical and Applied Genetics</i> , 2022, 135, 2925-2941.	3.6	7
5279	A gain-of-function allele of a DREB transcription factor gene ameliorates drought tolerance in wheat. <i>Plant Cell</i> , 2022, 34, 4472-4494.	6.6	36
5280	Harnessing the potential of bulk segregant analysis sequencing and its related approaches in crop breeding. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	7
5281	Marker-Trait Associations for Total Carotenoid Content and Individual Carotenoids in Durum Wheat Identified by Genome-Wide Association Analysis. <i>Plants</i> , 2022, 11, 2065.	3.5	4
5282	rTASSEL: An R interface to TASSEL for analyzing genomic diversity. <i>Journal of Open Source Software</i> , 2022, 7, 4530.	4.6	4

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5284	Genome wide association mapping of yield and various desirable agronomic traits in Rice. <i>Molecular Biology Reports</i> , 0, , .	2.3	1
5287	Genetic diversity and population structure of Tongcheng pigs in China using whole-genome SNP chip. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	7
5288	A genome-wide association and fine-mapping study of white rust resistance in hexaploid chrysanthemum cultivars with a wild diploid reference genome. <i>Horticulture Research</i> , 2022, 9, .	6.3	5
5289	Genome-Wide Identification of Candidate Genes Underlying Soluble Sugar Content in Vegetable Soybean ( <i>Glycine max</i> L.) via Association and Expression Analysis. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	8
5290	Three types of genes underlying the Gametophyte factor1 locus cause unilateral cross incompatibility in maize. <i>Nature Communications</i> , 2022, 13, .	12.8	9
5292	A Survey of Genome-Wide Genetic Characterizations of Crossbred Dairy Cattle in Local Farms in Cambodia. <i>Animals</i> , 2022, 12, 2072.	2.3	1
5294	A Comparison of Three Machine Learning Methods for Multivariate Genomic Prediction Using the Sparse Kernels Method (SKM) Library. <i>Genes</i> , 2022, 13, 1494.	2.4	5
5295	Fine-mapping and association analysis of candidate genes for papilla number in sea cucumber, <i>Apostichopus japonicus</i> . <i>Marine Life Science and Technology</i> , 2022, 4, 343-355.	4.6	2
5296	Genetic dissection of nitrogen induced changes in the shoot and root biomass of spinach. <i>Scientific Reports</i> , 2022, 12, .	3.3	2
5297	Genotyping by Sequencing Advancements in Barley. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	3
5298	Genome-wide association study and genomic prediction of resistance to stripe rust in current Central and Northern European winter wheat germplasm. <i>Theoretical and Applied Genetics</i> , 2022, 135, 3583-3595.	3.6	13
5299	Association Analysis for Some Biochemical Traits in Wild Relatives of Wheat under Drought Stress Conditions. <i>Genes</i> , 2022, 13, 1491.	2.4	7
5300	Descriptive Genomic Analysis and Sequence Genotyping of the Two Papaya Species ( <i>Vasconcellea</i> ) Tj ETQq1 1 0.784314 rgBT <sub>2</sub> /Overlook	3.5	2
5301	A reference-anchored oat linkage map reveals quantitative trait loci conferring adult plant resistance to crown rust ( <i>Puccinia coronata</i> f. sp. <i>avenae</i> ). <i>Theoretical and Applied Genetics</i> , 2022, 135, 3307-3321.	3.6	4
5302	Identification and validation of novel loci associated with wheat quality through a genome-wide association study. <i>Journal of Integrative Agriculture</i> , 2022, 21, 3131-3147.	3.5	6
5303	Genome-Wide Association Study for Spot Blotch Resistance in Synthetic Hexaploid Wheat. <i>Genes</i> , 2022, 13, 1387.	2.4	5
5304	Genome-wide association mapping for root traits associated with frost tolerance in faba beans using KASP-SNP markers. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	1

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5305	Genome-wide marker effect heterogeneity is associated with a large effect dormancy locus in winter malting barley. <i>Plant Genome</i> , 0, , .	2.8	1
5306	Whole-genome analysis of hard winter wheat germplasm identifies genomic regions associated with spike and kernel traits. <i>Theoretical and Applied Genetics</i> , 2022, 135, 2953-2967.	3.6	7
5307	Genome-wide association mapping of nutritional traits for designing superior chickpea varieties. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	4
5308	Association mapping for abiotic stress tolerance using heat- and drought-related syntenic markers in okra. <i>Molecular Biology Reports</i> , 2022, 49, 11409-11419.	2.3	4
5310	Genome-wide association study reveals that GhTRL1 and GhPIN8 affect cotton root development. <i>Theoretical and Applied Genetics</i> , 2022, 135, 3161-3176.	3.6	3
5311	DRR Dhan 58, a Seedling Stage Salinity Tolerant NIL of Improved Samba Mahsuri Shows Superior Performance in Multi-location Trials. <i>Rice</i> , 2022, 15, .	4.0	4
5314	A genome-wide association study investigating fumonisin contamination in a panel of tropical maize elite lines. <i>Euphytica</i> , 2022, 218, .	1.2	3
5315	Genomics reveals the history of a complex plant invasion and improves the management of a biological invasion from the South African–Australian biotic exchange. <i>Ecology and Evolution</i> , 2022, 12, .	1.9	4
5316	A pan-Zea genome map for enhancing maize improvement. <i>Genome Biology</i> , 2022, 23, .	8.8	21
5317	Genome-wide association study for grain yield and component traits in bread wheat ( <i>Triticum</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 107	2.35	16
5318	Genetic dissection of lutein content in common wheat via association and linkage mapping. <i>Theoretical and Applied Genetics</i> , 2022, 135, 3127-3141.	3.6	2
5319	Population genomics reveal deep divergence and strong geographical structure in gentians in the Hengduan Mountains. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	3
5320	Molecular insights into high-altitude adaption and acclimatisation of <i>Aporrectodea caliginosa</i> . <i>Life Science Alliance</i> , 2022, 5, e202201513.	2.8	1
5325	Design and validation of a codominant molecular marker for fruit acidity in muskmelon ( <i>Cucumis</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 107	1.9	1
5326	Genotyping-by-sequencing of Canada’s apple biodiversity collection. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	2
5327	Morpho-physiological, biochemical and molecular characterization of coastal rice landraces to identify novel genetic sources of salinity tolerance. <i>Plant Physiology and Biochemistry</i> , 2022, 187, 50-66.	5.8	1
5328	Genome-wide association mapping for isolate-specific resistance to <i>Ascochyta rabiei</i> in chickpea ( <i>Cicer</i> ) Tj ETQq0 0.0 rgBT /Overlock 107	2.5	6
5329	ASSOCIATIVE MAPPING FOR EXOTIC SOYBEAN GERMPASM GRAIN YIELD IN HIGH TEMPERATURES. <i>Revista Caatinga</i> , 2022, 35, 567-573.	0.7	0

#	ARTICLE	IF	CITATIONS
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5331	SSR and GBS based GWAS study for identification of QTLs associated with nutritional elemental in common bean ( <i>Phaseolus vulgaris</i> L.). <i>Scientia Horticulturae</i> , 2022, 306, 111470.	3.6	6
5332	Identification of Loci Governing Agronomic Traits and Mutation Hotspots via a GBS-Based Genome-Wide Association Study in a Soybean Mutant Diversity Pool. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10441.	4.1	5
5334	Differentially expressed genes against <i>Colletotrichum lindemuthianum</i> in a bean genotype carrying the Co-2 gene revealed by RNA-sequencing analysis. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	1
5336	Identification of stable quantitative trait loci for grain yield in rice. <i>Pesquisa Agropecuaria Brasileira</i> , 0, 57, .	0.9	0
5337	Genomic and Bioinformatic Resources for Next-Generation Breeding Approaches Towards Enhanced Stress Tolerance in Cereals. , 2022, , 453-493.		2
5338	Genome-wide association and linkage mapping strategies reveal genetic loci and candidate genes of phosphorus utilization in soybean. <i>Journal of Integrative Agriculture</i> , 2022, 21, 2521-2537.	3.5	1
5339	Omics in tuber crops: Cassava and sweet potato. , 2022, , 527-543.		0
5340	Genetic diversity analysis and core collection construction for <i>Amaranthus tricolor</i> germplasm based on genome-wide single-nucleotide polymorphisms. <i>Scientia Horticulturae</i> , 2023, 307, 111428.	3.6	10
5341	Multi-Omics Data Reveal Amino Acids Related Genes in the Common Carp <i>Cyprinus carpio</i> . <i>Fishes</i> , 2022, 7, 225.	1.7	1
5342	Development of diagnostic SNP markers for identification of rye 1RS translocations in wheat. <i>Crop Science</i> , 0, , .	1.8	0
5343	A Combination of a Genome-Wide Association Study and a Transcriptome Analysis Reveals circRNAs as New Regulators Involved in the Response to Salt Stress in Maize. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9755.	4.1	12
5344	Sigma factor binding protein 1 (CsSIB1) is a putative candidate of the major-effect QTL dm5.3 for downy mildew resistance in cucumber ( <i>Cucumis sativus</i> ). <i>Theoretical and Applied Genetics</i> , 2022, 135, 4197-4215.	3.6	4
5345	Population transcriptomic analysis identifies the comprehensive lncRNAs landscape of spike in wheat ( <i>Triticum aestivum</i> L.). <i>BMC Plant Biology</i> , 2022, 22, .	3.6	6
5346	Uncovering anthocyanin diversity in potato landraces ( <i>Solanum tuberosum</i> L. Phureja) using RNA-seq. <i>PLoS ONE</i> , 2022, 17, e0273982.	2.5	2
5347	Genome-Wide Association Study Reveals Candidate Genes for Root-Related Traits in Rice. <i>Current Issues in Molecular Biology</i> , 2022, 44, 4386-4405.	2.4	3
5348	Genetic diversity and population structure of some Nigerian accessions of Bambara groundnut ( <i>Vigna</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.6	3
5349	A recessive mutation in muscadine grapes causes berry color-loss without influencing anthocyanin pathway. <i>Communications Biology</i> , 2022, 5, .	4.4	5

#	ARTICLE	IF	CITATIONS
5351	Utility of anthesis–silking interval information to predict grain yield under water and nitrogen limited conditions. <i>Crop Science</i> , 2023, 63, 151-163.	1.8	2
5352	The evening complex promotes maize flowering and adaptation to temperate regions. <i>Plant Cell</i> , 2023, 35, 369-389.	6.6	16
5353	Genome-wide association studies of seedling quantitative trait loci against salt tolerance in wheat. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	2
5354	Genome-wide association studies of grain yield and quality traits under optimum and low-nitrogen stress in tropical maize ( <i>Zea mays</i> L.). <i>Theoretical and Applied Genetics</i> , 2022, 135, 4351-4370.	3.6	10
5355	Population-level transcriptomes reveal gene expression and splicing underlying cadmium accumulation in barley. <i>Plant Journal</i> , 2022, 112, 847-859.	5.7	6
5356	The Germin-like protein <scp>OsGER4</scp> is involved in promoting crown root development under exogenous jasmonic acid treatment in rice. <i>Plant Journal</i> , 2022, 112, 860-874.	5.7	6
5357	Evidence of Asexual Overwintering of <i>Melampsora paradoxa</i> and Mapping of Stem Rust Host Resistance in <i>Salix</i> . <i>Plants</i> , 2022, 11, 2385.	3.5	1
5359	Resequencing worldwide spinach germplasm for identification of field resistance QTLs to downy mildew and assessment of genomic selection methods. <i>Horticulture Research</i> , 2022, 9, .	6.3	2
5360	A soybean sodium/hydrogen exchanger GmNHX6 confers plant alkaline salt tolerance by regulating Na <sup>+</sup> /K <sup>+</sup> homeostasis. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	10
5361	Genetic factors underlying anaerobic germination in rice: Genome-wide association study and transcriptomic analysis. <i>Plant Genome</i> , 0, , .	2.8	7
5362	Genome-wide association study identifies candidate genes and favorable haplotypes for seed yield in <i>Brassica napus</i> . <i>Molecular Breeding</i> , 2022, 42, .	2.1	3
5363	Population and conservation genetics using RAD sequencing in four endemic conifers from South America. <i>Biodiversity and Conservation</i> , 0, , .	2.6	0
5364	Association mapping and candidate genes for physiological non-destructive traits: Chlorophyll content, canopy temperature, and specific leaf area under normal and saline conditions in wheat. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	5
5365	Genetic sources and loci for <i>Fusarium</i> head blight resistance in bread wheat. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	2
5366	Genome wide association analysis for yield related traits in maize. <i>BMC Plant Biology</i> , 2022, 22, .	3.6	11
5367	Patterns of genetic variation and QTLs controlling grain traits in a collection of global wheat germplasm revealed by high-quality SNP markers. <i>BMC Plant Biology</i> , 2022, 22, .	3.6	1
5368	Genotyping-by-Sequencing Defines Genetic Structure within the “Acquaviva” Red Onion Landrace. <i>Plants</i> , 2022, 11, 2388.	3.5	1
5369	Genome-wide association mapping of septoria nodorum blotch resistance in Nordic winter and spring wheat collections. <i>Theoretical and Applied Genetics</i> , 2022, 135, 4169-4182.	3.6	8

#	ARTICLE	IF	CITATIONS
5370	Improved pea reference genome and pan-genome highlight genomic features and evolutionary characteristics. <i>Nature Genetics</i> , 2022, 54, 1553-1563.	21.4	46
5371	SNP discovery in proso millet ( <i>Panicum miliaceum</i> L.) using low-pass genome sequencing. <i>Plant Direct</i> , 2022, 6, .	1.9	4
5372	Genome-wide association study identifies new loci for 1000-seed weight in <i>Brassica napus</i> . <i>Euphytica</i> , 2022, 218, .	1.2	0
5373	Species and population genomic differentiation in <i>Pocillopora</i> corals (Cnidaria, Hexacorallia). <i>Genetica</i> , 2022, 150, 247-262.	1.1	0
5374	Phenotypic variability and genetic diversity analysis of cultivated potatoes in China. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	3
5376	Assessment of Genetic Diversity and Discovery of Molecular Markers in Durian ( <i>Durio zibethinus</i> L.) in China. <i>Diversity</i> , 2022, 14, 769.	1.7	1
5378	Genomic and Molecular Identification of Genes Contributing to the Caspofungin Paradoxical Effect in <i>Aspergillus fumigatus</i> . <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	1
5379	QTL mapping and identification of candidate genes using a genome-wide association study for heat tolerance at anthesis in rice ( <i>Oryza sativa</i> L.). <i>Frontiers in Genetics</i> , 0, 13, .	2.3	9
5380	Genomic surveillance unfolds the SARS-CoV-2 transmission and divergence dynamics in Bangladesh. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	3
5381	A genome-wide association study of folates in sweet corn kernels. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	2
5382	The Association of Grain Yield and Agronomical Traits with Genes of Plant Height, Photoperiod Sensitivity and Plastid Glutamine Synthetase in Winter Bread Wheat ( <i>Triticum aestivum</i> L.) Collection. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11402.	4.1	0
5383	Marker - trait association analysis for yield related traits in rice ( <i>Oryza sativa</i> L.). <i>Oryza</i> , 2022, 59, 269-280.	0.4	0
5384	A GBS-based genome-wide association study reveals the genetic basis of salinity tolerance at the seedling stage in bread wheat ( <i>Triticum aestivum</i> L.). <i>Frontiers in Genetics</i> , 0, 13, .	2.3	7
5385	A GBS-Based GWAS Analysis of Leaf and Stripe Rust Resistance in Diverse Pre-Breeding Germplasm of Bread Wheat ( <i>Triticum aestivum</i> L.). <i>Plants</i> , 2022, 11, 2363.	3.5	4
5386	Association mapping of resistance to tar spot complex in maize. <i>Plant Breeding</i> , 2022, 141, 745-755.	1.9	5
5387	Genome-wide association mapping of <i>Fusarium</i> crown rot resistance in <i>Aegilops tauschii</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	2
5388	Diverged subpopulations in tropical <i>Urochloa</i> ( <i>Brachiaria</i> ) forage species indicate a role for facultative apomixis and varying ploidy in their population structure and evolution. <i>Annals of Botany</i> , 2022, 130, 657-669.	2.9	6
5389	Multi-trait genome prediction of new environments with partial least squares. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	7



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5391	QTL mapping of seedling and field resistance to stem rust in DAKIYE/Reichenbachii durum wheat population. <i>PLoS ONE</i> , 2022, 17, e0273993.	2.5	1
5392	Genome-wide association studies and genomic selection assays made in a large sample of cacao ( <i>Theobroma cacao</i> L.) germplasm reveal significant marker-trait associations and good predictive value for improving yield potential. <i>PLoS ONE</i> , 2022, 17, e0260907.	2.5	4
5393	Rapid identification of a major locus <i>qPRL-C06</i> affecting primary root length in <i>Brassica napus</i> by QTL-seq. <i>Annals of Botany</i> , 2023, 131, 569-583.	2.9	2
5394	Mapping and selection of downy mildew resistance in spinach cv. whale by low coverage whole genome sequencing. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	5
5395	Genetic diversity and marker trait association for yield attributing traits in accessions of common bean ( <i>Phaseolus vulgaris</i> L.) in India. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 0, , 1-10.	0.8	1
5396	Linking pathogen-microbiome-host interactions to explain amphibian population dynamics. <i>Molecular Ecology</i> , 2022, 31, 5784-5794.	3.9	6
5397	Genome-wide association study reveals the genetic basis of brace root angle and diameter in maize. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	4
5398	Genetic variability for resistance to fungal pathogens in bread wheat. <i>Czech Journal of Genetics and Plant Breeding</i> , 2022, 59, 23-32.	0.8	4
5399	Unraveling the hierarchical genetic structure of tea green leafhopper, <i>Matsumurasca onukii</i> , in East Asia based on SSRs and SNPs. <i>Ecology and Evolution</i> , 2022, 12, .	1.9	3
5400	A teosinte-derived allele of an <i>HKT1</i> family sodium transporter improves salt tolerance in maize. <i>Plant Biotechnology Journal</i> , 2023, 21, 97-108.	8.3	23
5401	Designing Tobacco Genomes for Resistance to Biotic Stresses. , 2022, , 441-581.		1
5402	Abiotic Stress Resistance in Tobacco: Advances and Strategies. , 2022, , 329-427.		0
5403	Genetic Analysis of Agronomic and Quality Traits from Multi-Location white Yam Trials using Mixed Model with Genomic Relationship Matrix. <i>Global Journal of Botanical Science</i> , 0, 10, 8-22.	0.4	4
5404	Deep learning-based phenotyping for genome wide association studies of sudden death syndrome in soybean. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	7
5405	Identification and Genome-Wide Association Analysis for Fusarium Crown Rot Resistance in Wheat. <i>Plant Disease</i> , 2023, 107, 1151-1158.	1.4	4
5406	Integrating genome-wide association study with <i>RNA-seq</i> revealed <i>DBI</i> as a good candidate gene for intramuscular fat content in Beijing black pigs. <i>Animal Genetics</i> , 2023, 54, 24-34.	1.7	5
5407	Genome-wide association mapping reveals genes underlying population-level metabolome diversity in a fungal crop pathogen. <i>BMC Biology</i> , 2022, 20, .	3.8	7

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5408	Development of an inclusive 580K SNP array and its application for genomic selection and genome-wide association studies in rice. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	6
5409	QTL mapping and genomic prediction of resistance to wheat head blight caused by <i>Fusarium verticillioides</i> . <i>Frontiers in Genetics</i> , 0, 13, .	2.3	3
5410	Comparative Analysis of Multiple GWAS Results Identifies Metabolic Pathways Associated with Resistance to <i>A. flavus</i> Infection and Aflatoxin Accumulation in Maize. <i>Toxins</i> , 2022, 14, 738.	3.4	2
5411	A family of methyl esterases converts methyl salicylate to salicylic acid in ripening tomato fruit. <i>Plant Physiology</i> , 2023, 191, 110-124.	4.8	4
5413	RNA-Seq combined with population-level analysis reveals important candidate genes related to seed size in flax ( <i>Linum usitatissimum</i> L.). <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	1
5414	Identification of Disease Resistance Parents and Genome-Wide Association Mapping of Resistance in Spring Wheat. <i>Plants</i> , 2022, 11, 2905.	3.5	3
5416	Genetic dissection of fruit maturity date in apricot ( <i>P. armeniaca</i> L.) through a Single Primer Enrichment Technology (SPET) approach. <i>BMC Genomics</i> , 2022, 23, .	2.8	2
5417	Genome-wide association study for resistance to <i>Pseudomonas syringae</i> pv. <i>garcae</i> in <i>Coffea arabica</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	1
5418	Genome-wide association study of rice leaf metabolites and volatiles. <i>International Journal of Biological Macromolecules</i> , 2022, 222, 2479-2485.	7.5	0
5419	Identification of Candidate Genes for Salt Tolerance at the Germination Stage in Japonica Rice by Genome-Wide Association Analysis. <i>Agriculture (Switzerland)</i> , 2022, 12, 1588.	3.1	2
5420	The emergence of a cryptic lineage and cytonuclear discordance through past hybridization in the Japanese fire-bellied newt, <i>Cynops pyrrhogaster</i> (Amphibia: Urodela). <i>Biological Journal of the Linnean Society</i> , 0, , .	1.6	0
5422	Genomic prediction of drought tolerance during seedling stage in maize using low-cost molecular markers. <i>Euphytica</i> , 2022, 218, .	1.2	3
5423	Genome-wide association analysis identified consistent QTL for seed yield in a soybean diversity panel tested across multiple environments. <i>Plant Genome</i> , 2022, 15, .	2.8	6
5424	Mapping of Candidate Genes in Response to Low Nitrogen in Rice Seedlings. <i>Rice</i> , 2022, 15, .	4.0	6
5425	Genome-wide association study reveals distinct genetic associations related to leaf hair density in two lineages of wheat-wild relative <i>Aegilops tauschii</i> . <i>Scientific Reports</i> , 2022, 12, .	3.3	1
5426	Identification of Glu-D1 Alleles and Novel Marker-Trait Associations for Flour Quality and Grain Yield Traits under Heat-Stress Environments in Wheat Lines Derived from Diverse Accessions of <i>Aegilops tauschii</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 12034.	4.1	5
5427	Identification and genomic characterization of major effect bacterial blight resistance locus (BB-13) in Upland cotton ( <i>Gossypium hirsutum</i> L.). <i>Theoretical and Applied Genetics</i> , 2022, 135, 4421-4436.	3.6	2
5428	Discovery of DNA polymorphisms via genome-resequencing and development of molecular markers between two barley cultivars. <i>Plant Cell Reports</i> , 2022, 41, 2279-2292.	5.6	1

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5431	Response of Southeast Asian rice root architecture and anatomy phenotypes to drought stress. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	0
5432	Identification and Investigation of the Genetic Variations and Candidate Genes Responsible for Seed Weight via GWAS in Paper Mulberry. <i>International Journal of Molecular Sciences</i> , 2022, 23, 12520.	4.1	2
5433	Natural polymorphism of ZmICE1 contributes to amino acid metabolism that impacts cold tolerance in maize. <i>Nature Plants</i> , 2022, 8, 1176-1190.	9.3	23
5435	Genome-wide association mapping for field and seedling resistance to the emerging <i>Puccinia graminis</i> f. sp. <i>tritici</i> race TTRTF in wheat. <i>Plant Genome</i> , 2022, 15, .	2.8	1
5437	Genomic consequences and selection efficacy in sympatric sexual versus asexual kelps. <i>Frontiers in Marine Science</i> , 0, 9, .	2.5	2
5438	Genome sequencing reveals evidence of adaptive variation in the genus <i>Zea</i> . <i>Nature Genetics</i> , 2022, 54, 1736-1745.	21.4	29
5439	Development of genome-specific SSR markers for the identification of introgressed segments of <i>Sinapis alba</i> in the <i>Brassica juncea</i> background. <i>3 Biotech</i> , 2022, 12, .	2.2	4
5440	Phylogeographic structure of <i>Heteroplexis</i> (Asteraceae), an endangered endemic genus in the limestone karst regions of southern China. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	3
5441	Mutations in the SmAPRR2 transcription factor suppressing chlorophyll pigmentation in the eggplant fruit peel are key drivers of a diversified colour palette. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	9
5442	Breeding and selection of taro ( <i>Colocasia esculenta</i> ) for improved disease-resistance in Hawai'i. <i>Plants People Planet</i> , 0, , .	3.3	1
5443	Natural variation and domestication selection of ZmSULTR3;4 is associated with maize lateral root length in response to salt stress. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	1
5444	A Chromosome-Scale Genome Assembly of <i>Mitragyna speciosa</i> (Kratom) and the Assessment of Its Genetic Diversity in Thailand. <i>Biology</i> , 2022, 11, 1492.	2.8	2
5445	Genome-wide association studies reveal novel QTLs, QTL-by-environment interactions and their candidate genes for tocopherol content in soybean seed. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	4
5446	Identification of Molecular Markers and Candidate Genes Associated with Time to Flowering and Length of Reproductive Period in Soybean Through Association Mapping. <i>Plant Molecular Biology Reporter</i> , 2023, 41, 229-241.	1.8	1
5447	QTL mapping for early root and shoot vigor of upland rice ( <i>Oryza sativa</i> L.) under P deficient field conditions in Japan and Madagascar. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	4
5448	Genome-wide association mapping for wheat morphometric seed traits in Iranian landraces and cultivars under rain-fed and well-watered conditions. <i>Scientific Reports</i> , 2022, 12, .	3.3	9
5450	Regional association and transcriptome analysis revealed candidate genes controlling plant height in <i>Brassica napus</i> . <i>Molecular Breeding</i> , 2022, 42, .	2.1	1
5453	Genome-Wide Association Study Based on Plant Height and Drought-Tolerance Indices Reveals Two Candidate Drought-Tolerance Genes in Sweet Sorghum. <i>Sustainability</i> , 2022, 14, 14339.	3.2	5

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5454	Association mapping for important agronomic traits in wild and cultivated <i>Vigna</i> species using cross-species and cross-genera simple sequence repeat markers. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	3
5455	A Genome-Wide Scan Divulges Key Loci Involved in Resistance to Aphids ( <i>Aphis craccivora</i> ) in Cowpea ( <i>Vigna unguiculata</i> ). <i>Genes</i> , 2022, 13, 2002.	2.4	2
5456	The 4R QTLs pollen fertility restoration in triticale with CMS <i>Triticum timopheevii</i> . <i>Crop Science</i> , 0, , .	1.8	0
5457	Genome-Wide Association Study of Leaf Rust Resistance at Seedling and Adult Plant Stages in a Global Barley Panel. <i>Agriculture (Switzerland)</i> , 2022, 12, 1829.	3.1	3
5458	Candidate gene discovery for salt tolerance in rice ( <i>Oryza sativa</i> L.) at the germination stage based on genome-wide association study. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	2
5459	Genetic associations with resistance to <i>Meloidogyne enterolobii</i> in guava ( <i>Psidium</i> sp.) using cross-genera SNPs and comparative genomics to <i>Eucalyptus</i> highlight evolutionary conservation across the Myrtaceae. <i>PLoS ONE</i> , 2022, 17, e0273959.	2.5	0
5460	Leaf physiology variations are modulated by natural variations that underlie stomatal morphology in <i>Populus</i> . <i>Plant, Cell and Environment</i> , 2023, 46, 150-170.	5.7	6
5461	Genetic Analyses for Leaf Variegation in Hybrid Grape Populations ( <i>Vitis</i> spp.) Reveals Two Loci, Lvar1 and Lvar2. <i>Hortscience: A Publication of the American Society for Horticultural Science</i> , 2022, 57, 1416-1423.	1.0	1
5462	Utilization of Genotyping-by-Sequencing (GBS) for Rice Pre-Breeding and Improvement: A Review. <i>Life</i> , 2022, 12, 1752.	2.4	9
5463	Application of multi-layer neural network and hyperspectral reflectance in genome-wide association study for grain yield in bread wheat. <i>Field Crops Research</i> , 2022, 289, 108730.	5.1	6
5464	Genome-wide association study, haplotype analysis, and genomic prediction reveal the genetic basis of yield-related traits in soybean ( <i>Glycine max</i> L.). <i>Frontiers in Genetics</i> , 0, 13, .	2.3	6
5465	Development of the maize 5.5K loci panel for genomic prediction through genotyping by target sequencing. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	3
5467	Characterization of Mexican wheat landraces for drought and salt stress tolerance potential for future breeding. <i>Cereal Research Communications</i> , 0, , .	1.6	2
5468	A Genome-Wide Association Study of Senegalese Sorghum Seedlings Responding to Pathotype 5 of <i>Sporisorium reilianum</i> . <i>Plants</i> , 2022, 11, 2999.	3.5	3
5469	Transcriptome and Regional Association Analyses Reveal the Effects of Oleosin Genes on the Accumulation of Oil Content in <i>Brassica napus</i> . <i>Plants</i> , 2022, 11, 3140.	3.5	5
5470	Identification of Genetic Variations and Candidate Genes Responsible for Stalk Sugar Content and Agronomic Traits in Fresh Corn via GWAS across Multiple Environments. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13490.	4.1	3
5471	Rice Pangenome Array ( <i>sc</i> > RPGA < /sc > ): an efficient genotyping solution for pangenome-based accelerated crop improvement in rice. <i>Plant Journal</i> , 0, , .	5.7	5
5472	Genetic analysis of pungency deficiency in Japanese chili pepper "Shishito"™ ( <i>Capsicum annuum</i> ) revealed its unique heredity and brought the discovery of two genetic loci involved with the reduction of pungency. <i>Molecular Genetics and Genomics</i> , 2023, 298, 201-212.	2.1	1

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5473	Genome-wide association analysis reveals 6 copy number variations associated with the number of cervical vertebrae in Pekin ducks. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	3.7	3
5475	Watermelon domestication was shaped by stepwise selection and regulation of the metabolome. <i>Science China Life Sciences</i> , 2023, 66, 579-594.	4.9	4
5476	Genomic confirmation of <i>Gossypium barbadense</i> introgression into <i>G. hirsutum</i> and a subsequent MAGIC population. <i>Molecular Genetics and Genomics</i> , 2023, 298, 143-152.	2.1	1
5477	Low-Density Reference Fingerprinting SNP Dataset of CIMMYT Maize Lines for Quality Control and Genetic Diversity Analyses. <i>Plants</i> , 2022, 11, 3092.	3.5	1
5478	Genome-wide association studies for soybean epicotyl length in two environments using 3VmrMLM. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	3
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5484	ddRADseq-mediated detection of genetic variants in sugarcane. <i>Plant Molecular Biology</i> , 0, , .	3.9	2
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5490	Candidate loci for leaf angle in maize revealed by a combination of genome-wide association study and meta-analysis. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	3
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5499	Association mapping for common bacterial blight in carioca beans. Crop Breeding and Applied Biotechnology, 2022, 22, .	0.4	0
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5512	Genetic characterization of downy mildew resistance from the hop ( <i>Humulus lupulus</i> L.) line USDA 64035M. Crop Science, 2023, 63, 1082-1091.	1.8	2



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5515	Genetic and epigenetic variation separately contribute to range expansion and local metalliferous habitat adaptation during invasions of <i>Chenopodium ambrosioides</i> into China. <i>Annals of Botany</i> , 2022, 130, 1041-1056.	2.9	2
5516	Genome-wide analysis-based single nucleotide polymorphism marker sets to identify diverse genotypes in cabbage cultivars ( <i>Brassica oleracea</i> var. <i>capitata</i> ). <i>Scientific Reports</i> , 2022, 12, .	3.3	0
5517	In-depth understanding of the genetic control of stripe rust resistance ( <i>Puccinia striiformis</i> f. sp.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 5	1.4	12
5518	Characterization and genetic dissection of maize ear leaf midrib acquired by 3D digital technology. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	2
5519	Identification of new resistance loci against wheat sharp eyespot through genome-wide association study. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	1
5520	Association analysis revealed loci linked to post-drought recovery and traits related to persistence of smooth brome grass ( <i>Bromus inermis</i> ). <i>PLoS ONE</i> , 2022, 17, e0278687.	2.5	0
5521	Measurements of Antibacterial Activity of Seed Crude Extracts in Cultivated Rice and Wild Oryza Species. <i>Rice</i> , 2022, 15, .	4.0	0
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5524	Association study of SNP locus for color related traits in herbaceous peony ( <i>Paeonia lactiflora</i> Pall.) using SLAF-seq. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	0
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5528	Analysis of Genetic Diversity and Resistance to Foliar Pathogens Based on Genotyping-by-Sequencing of a Para Rubber Diversity Panel and Progeny of an Interspecific Cross. <i>Plants</i> , 2022, 11, 3418.	3.5	0
5529	Graph-based pangenomics maximizes genotyping density and reveals structural impacts on fungal resistance in melon. <i>Nature Communications</i> , 2022, 13, .	12.8	7
5531	Genetic Variation and Population Structure of <i>Oryza sativa</i> Accessions in the AfricaRice Collection and Development of the AfricaRice <i>O. sativa</i> Core Collection. <i>Crop Science</i> , 0, , .	1.8	1
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5535	Identifying the Genetic Basis of Mineral Elements in Rice Grain Using Genome-Wide Association Mapping. <i>Genes</i> , 2022, 13, 2330.	2.4	5
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5537	Single nucleotide polymorphism (SNP) in the doublesex ( <i>dsx</i> ) gene splice sites and relevance for its alternative splicing in the malaria vector <i>Anopheles gambiae</i> . <i>Wellcome Open Research</i> , 0, 7, 31.	1.8	1
5538	Effects of fruit dimorphism on genetic structure and gene flow in the coastal shrub <i>Scaevola taccada</i> . <i>Annals of Botany</i> , 2022, 130, 1029-1040.	2.9	0
5539	Marker-trait association analysis for grain shape traits in rice ( <i>Oryza sativa</i> L.). <i>Israel Journal of Plant Sciences</i> , 2022, 70, 47-56.	0.5	0
5540	Genetic variation of the candidate loci controlling twinning in the beef and dairy cattle breeds in Indonesia. <i>Asia-Pacific Journal of Molecular Biology and Biotechnology</i> , 0, , 55-64.	0.1	0
5544	Characterization of <i>Rsg3</i> , a novel greenbug resistance gene from the Chinese barley landrace PI 565676. <i>Plant Genome</i> , 2023, 16, .	2.8	7
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5546	A superior gene allele involved in abscisic acid signaling enhances drought tolerance and yield in chickpea. <i>Plant Physiology</i> , 2023, 191, 1884-1912.	4.8	8
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5548	Brown midrib mutant and genome-wide association analysis uncover lignin genes for disease resistance in maize. <i>Plant Genome</i> , 2023, 16, .	2.8	3
5550	Genome-wide association mapping and genomic prediction of agronomical traits and breeding values in Iranian wheat under rain-fed and well-watered conditions. <i>BMC Genomics</i> , 2022, 23, .	2.8	6
5551	The genomic analysis of a wide peach germplasm collection revealed genetic relationships between European landraces and American ferals and landraces. <i>Acta Horticulturae</i> , 2022, , 81-88.	0.2	0
5552	Genetic diversity analysis of drought tolerant flax varieties based on genome-wide SNP. , 2022, , .		1
5553	Genomics-based assembly of a sorghum bicolor (L.) moench core collection in the Uganda national genebank as a genetic resource for sustainable sorghum breeding. <i>Genetic Resources and Crop Evolution</i> , 0, , .	1.6	0
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5556	Large genomic introgression blocks of <i>Phaseolus parvifolius</i> Freytag bean into the common bean enhance the crossability between tepary and common beans. <i>Plant Direct</i> , 2022, 6, .	1.9	3

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5558	Ancient vicariance is reinforced by adaptive divergence in the southern beech: Contributions from geogenomics. <i>Journal of Biogeography</i> , 0, , .	3.0	0
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5562	Genetic analysis for detection of genes associated to drought tolerance in rice accessions belonging to north east India. <i>Molecular Biology Reports</i> , 0, , .	2.3	0
5563	Genome-wide association studies of viral infectionsâ”‘A short guide to a successful experimental and statistical analysis. <i>Frontiers in Systems Biology</i> , 0, 2, .	0.7	1
5564	Chromosome-scale genome assembly of a Japanese chili pepper landrace, <i>Capsicum annuum</i> â”‘Takanotsumeâ”‘™. <i>DNA Research</i> , 2023, 30, .	3.4	7
5565	Genomes of the cosmopolitan fruit pest <i>Bactrocera dorsalis</i> (Diptera: Tephritidae) reveal its global invasion history and thermal adaptation. <i>Journal of Advanced Research</i> , 2023, 53, 61-74.	9.5	15
5566	Chromosome-scale genome assembly of <i>Eustoma grandiflorum</i>, the first complete genome sequence in the genus <i>Eustoma</i>. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	1.8	2
5567	Construction of high density genetic map and quantitative trait locus mapping in a sorghum Tx623Aâ”‘%Aâ”‘â”‘%sudangrass S722 population. <i>Grassland Science</i> , 0, , .	1.1	0
5568	Genome-Wide Association Studies of Salt Tolerance at the Seed Germination Stage and Yield-Related Traits in <i>Brassica napus</i> L.. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15892.	4.1	3
5569	Multi-locus genome-wide association studies reveal genomic regions and putative candidate genes associated with leaf spot diseases in African groundnut ( <i>Arachis hypogaea</i> L.) germplasm. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	2
5570	Genetic dissection of marker trait associations for grain micro-nutrients and thousand grain weight under heat and drought stress conditions in wheat. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	2
5571	Association Mapping of Amylose Content in Maize RIL Population Using SSR and SNP Markers. <i>Plants</i> , 2023, 12, 239.	3.5	2
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5573	Genomeâ”‘wide association analysis of spike and kernel traits in the U.S. hard winter wheat. <i>Plant Genome</i> , 2023, 16, .	2.8	6
5574	Genome-wide association and RNA-seq analyses identify loci for pod orientation in rapeseed ( <i>Brassica</i> ) Tj ETQq1 1 0.784314 rgBT /Overl	3.6	6

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5576	Scion/Rootstock Interaction Studies for Quality Traits in Mango ( <i>Mangifera indica</i> L.) Varieties. <i>Agronomy</i> , 2023, 13, 204.	3.0	2
5577	Association mapping for broomrape resistance in sunflower. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	4
5578	An integrated genomic and biochemical approach to investigate the potentiality of heirloom tomatoes: Breeding resources for food quality and sustainable agriculture. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	2
5579	Analysis of genotype × environment interactions for agronomic traits of soybean ( <i>Glycine max</i> [L.] Tj ETQq0 0 0 rgBT /Overlock 10 Tf	2.8	9
5580	The genomic and bioclimatic characterization of Ethiopian barley ( <i>Hordeum vulgare</i> L.) unveils challenges and opportunities to adapt to a changing climate. <i>Global Change Biology</i> , 0, , .	9.5	1
5581	Development of a MAGIC population and high-resolution quantitative trait mapping for nicotine content in tobacco. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	0
5582	Transcriptome-referenced association study provides insights into the regulation of oil and fatty acid biosynthesis in <i>Torreyia grandis</i> kernel. <i>Journal of Advanced Research</i> , 2023, , .	9.5	0
5583	Genetic Basis of Resistance to Warrior (-) Yellow Rust Race at the Seedling Stage in Current Central and Northern European Winter Wheat Germplasm. <i>Plants</i> , 2023, 12, 420.	3.5	0
5584	Association analysis and evaluation of genetic diversity of <i>Teucrium stocksianum</i> Boiss. populations using ISSR markers. <i>Genetic Resources and Crop Evolution</i> , 0, , .	1.6	0
5585	Genome-wide association study of yield-related traits in common wheat ( <i>Triticum aestivum</i> L.) under normal and drought treatment conditions. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	5
5586	Genome-Wide Association Study and Genomic Prediction on Plant Architecture Traits in Sweet Corn and Waxy Corn. <i>Plants</i> , 2023, 12, 303.	3.5	2
5587	Discovering Loci for Breeding Prospective and Phenology in Wheat Mediterranean Landraces by Environmental and eigenGWAS. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1700.	4.1	3
5588	Characterization of a host-specific toxic activity produced by <i>Bipolaris cookei</i> , causal agent of Target Leaf Spot of Sorghum. <i>Phytopathology</i> , 0, , .	2.2	0
5589	The influence of habitat characteristics on the occupancy and dispersal of two headwater fishes in a dendritic network. <i>Ecosphere</i> , 2023, 14, .	2.2	0
5590	Genome-wide association study reveals novel loci and a candidate gene for resistance to frogeye leaf spot ( <i>Cercospora sojina</i> ) in soybean. <i>Molecular Genetics and Genomics</i> , 2023, 298, 441-454.	2.1	3
5591	A receptor-like kinase controls the amplitude of secondary cell wall synthesis in rice. <i>Current Biology</i> , 2023, 33, 498-506.e6.	3.9	9
5592	Resistance of QYm.nau-2D to wheat yellow mosaic virus was derived from an alien introgression into common wheat. <i>Theoretical and Applied Genetics</i> , 2023, 136, 1-16.	3.6	0

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5594	Genome-Wide Association Study Reveals the Genetic Basis of Seed Germination in Japonica Rice. <i>Agriculture (Switzerland)</i> , 2023, 13, 118.	3.1	0
5595	Molecular and Physiological Variability in Bread Wheat and Its Wild Relative ( <i>Aegilops tauschii</i> Coss.) Species under Water-Deficit Stress Conditions. <i>BioTech</i> , 2023, 12, 3.	2.6	0
5596	Identification of Genomic Regions Associated with High Grain Zn Content in Polished Rice Using Genotyping-by-Sequencing (GBS). <i>Plants</i> , 2023, 12, 144.	3.5	2
5597	Validation of Novel spot blotch disease resistance alleles identified in unexplored wheat ( <i>Triticum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	3.6	2
5598	Association mapping for protein, total soluble sugars, starch, amylose and chlorophyll content in rice. <i>BMC Plant Biology</i> , 2022, 22, .	3.6	9
5599	GWAS and functional studies suggest a role for altered DNA repair in the evolution of drug resistance in <i>Mycobacterium tuberculosis</i> . <i>ELife</i> , 0, 12, .	6.0	3
5600	Combined linkage mapping and association analysis uncovers candidate genes for 25 leaf-related traits across three environments in maize. <i>Theoretical and Applied Genetics</i> , 2023, 136, .	3.6	1
5601	Genetic approaches to exploit landraces for improvement of <i>Triticum turgidum</i> ssp. <i>durum</i> in the age of climate change. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	5
5602	Uncovering the genetic basis for quality traits in the Mediterranean old wheat germplasm and phenotypic and genomic prediction assessment by cross-validation test. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	1
5605	Dissecting the genetic architecture of leaf morphology traits in mungbean ( <i>Vigna radiata</i> (L.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.8	7
5606	Yield prediction through integration of genetic, environment, and management data through deep learning. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	1.8	10
5607	Genetic Analysis and Physical Mapping of Oat Adult Plant Resistance Loci Against <i>Puccinia coronata</i> f. sp. <i>avenae</i> . <i>Phytopathology</i> , 2023, 113, 1307-1316.	2.2	1
5608	High-density linkage maps and chromosome level genome assemblies unveil direction and frequency of extensive structural rearrangements in wood white butterflies ( <i>Leptidea</i> spp.). <i>Chromosome Research</i> , 2023, 31, .	2.2	18
5609	A major genetic locus in neighbours controls changes of gene expression and susceptibility in intraspecific rice mixtures. <i>New Phytologist</i> , 2023, 238, 835-844.	7.3	2
5613	Wild barley ( <i>Hordeum spontaneum</i> ) and landraces ( <i>Hordeum vulgare</i> ) from Turkey contain an abundance of novel <i>Rhynchosporium commune</i> resistance loci. <i>Theoretical and Applied Genetics</i> , 2023, 136, .	3.6	0
5614	Genetic analyses of tropical maize lines under artificial infestation of fall armyworm and foliar diseases under optimum conditions. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	2
5615	Marker-trait association analyses revealed major novel QTLs for grain yield and related traits in durum wheat. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	7

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5616	Genome-wide association and genomic prediction for resistance to southern corn rust in DH and testcross populations. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	1
5617	Genome-wide association analyses of leaf rust resistance in cultivated emmer wheat. <i>Theoretical and Applied Genetics</i> , 2023, 136, .	3.6	1
5618	Evaluating Introgression Sorghum Germplasm Selected at the Population Level While Exploring Genomic Resources as a Screening Method. <i>Plants</i> , 2023, 12, 444.	3.5	3
5619	Flame resistant cotton lines generated by synergistic epistasis in a MAGIC population. <i>PLoS ONE</i> , 2023, 18, e0278696.	2.5	2
5620	Detection of the local adaptive and genome-wide associated loci in southeast Nigerian taro ( <i>Colocasia esculenta</i> (L.) Schott) populations. <i>BMC Genomics</i> , 2023, 24, .	2.8	0
5621	Initiation of genomics-assisted breeding in Virginia-type peanuts through the generation of a de novo reference genome and informative markers. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	3
5622	Combining datasets to routinely predict fusarium head blight resistance in a wheat breeding program. <i>Crop Science</i> , 2023, 63, 1197-1208.	1.8	0
5623	Development of Ripening Gene-Specific Markers and their Association with Shelf-Life in Mango ( <i>Mangifera indica</i> L.) varieties. <i>The National Academy of Sciences, India</i> , 2023, 46, 179-184.	1.3	1
5624	Candidate genes affecting stomatal density in rice ( <i>Oryza sativa</i> L.) identified by genome-wide association. <i>Plant Science</i> , 2023, 330, 111624.	3.6	3
5625	Genome-wide association study identifies 12 new genetic loci associated with growth traits in pigs. <i>Journal of Integrative Agriculture</i> , 2024, 23, 217-227.	3.5	1
5626	Estimates of Genomic Heritability and the Marker-Derived Gene for Re(Production) Traits in Xinggao Sheep. <i>Genes</i> , 2023, 14, 579.	2.4	1
5627	Single nucleotide polymorphism (SNP) in the doublesex (dsx) gene splice sites and relevance for its alternative splicing in the malaria vector <i>Anopheles gambiae</i> . <i>Wellcome Open Research</i> , 0, 7, 31.	1.8	0
5629	SNP Diversity and Genetic Structure of “Rogosija”, an Old Western Balkan Durum Wheat Collection. <i>Plants</i> , 2023, 12, 1157.	3.5	0
5630	Genome-wide association study for the extractable phenolic profile and coat color of common bean seeds ( <i>Phaseolus vulgaris</i> L.). <i>BMC Plant Biology</i> , 2023, 23, .	3.6	2
5631	The Relationship between Cadmium-Related Gene Sequence Variations in Rice and Cadmium Accumulation. <i>Agronomy</i> , 2023, 13, 800.	3.0	1
5633	Genome-wide association study of leaf-related traits in tea plant in Guizhou based on genotyping-by-sequencing. <i>BMC Plant Biology</i> , 2023, 23, .	3.6	6
5634	Integrated multi-locus genome-wide association studies and transcriptome analysis for seed yield and yield-related traits in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	1
5635	Genome-wide association study of alkylresorcinols content in 161 wheat cultivars. <i>Journal of Cereal Science</i> , 2023, 111, 103679.	3.7	2



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5636	Association mapping identifies loci and candidate genes for grain-related traits in spring wheat in response to heat stress. <i>Plant Science</i> , 2023, 331, 111676.	3.6	6
5637	Identification of sex-linked codominant markers and development of a rapid LAMP-based genetic sex identification method in channel catfish ( <i>Ictalurus punctatus</i> ). <i>Aquaculture</i> , 2023, 572, 739556.	3.5	1
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5649	The contrary conservation situations of two local critically endangered species, <i>Vaccinium emarginatum</i> ( <i>Ericaceae</i> ) and <i>Elatostema platyphyllum</i> ( <i>Urticaceae</i> ), growing on the eastern edge of the distribution. <i>Frontiers in Ecology and Evolution</i> , 0, 11, .	2.2	1
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5672	Genome-wide assessment of genetic diversity and association mapping for salt tolerance traits in okra ( <i>Abelmoschus esculentus</i> L. Moench) using genotyping-by-sequencing. <i>Scientia Horticulturae</i> , 2023, 313, 111922.	3.6	1
5673	Identification of candidate genes for LepR1 resistance against <i>Leptosphaeria maculans</i> in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	1
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5704	Population Structure Analysis and Genome-Wide Association Study of Tea ( <i>Camellia sinensis</i> (L.) Tj ETQq1 1 0.784314 rgBT /Overloc	0.7	2
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5729	Deciphering the genetic basis of resistance to soybean cyst nematode combining IBD and association mapping. Theoretical and Applied Genetics, 2023, 136, .	3.6	1
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5761	OsCYBDOMG1, a cytochrome b561 domain-containing protein, regulates salt tolerance and grain yield in rice. <i>Theoretical and Applied Genetics</i> , 2023, 136, .	3.6	1
5764	Genome-Wide Association Study for Seed Dormancy Using Re-Sequenced Germplasm under Multiple Conditions in Rice. <i>International Journal of Molecular Sciences</i> , 2023, 24, 6117.	4.1	1
5765	Genetic variation in the glycine-rich protein gene <i>BnGRP1</i> contributes to low phosphorus tolerance in <i>Brassica napus</i> . <i>Journal of Experimental Botany</i> , 2023, 74, 3531-3543.	4.8	2
5766	Genetic Diversity and Population Structure of Ugandan Soybean ( <i>Glycine max</i> L.) Germplasm Based on DArTseq. <i>Plant Molecular Biology Reporter</i> , 2023, 41, 417-426.	1.8	3



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5768	Molecular and Technological Characterization of <i>Saccharomyces Cerevisiae</i> from Sourdough. <i>Fermentation</i> , 2023, 9, 329.	3.0	2
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5770	Discovery and genome-guided mapping of <i>REN12</i> from <i>Vitis amurensis</i> , conferring strong, rapid resistance to grapevine powdery mildew. <i>Horticulture Research</i> , 2023, 10, .	6.3	5
5771	Assessing Genetic Distinctness and Redundancy of Plant Germplasm Conserved Ex Situ Based on Published Genomic SNP Data. <i>Plants</i> , 2023, 12, 1476.	3.5	0
5773	Using genome wide association to assist new apple cultivar development in mitigating climate change. <i>Acta Horticulturae</i> , 2023, , 441-448.	0.2	0
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5778	Genome-wide association study for grain zinc concentration in bread wheat ( <i>Triticum aestivum</i> L.). <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	1
5779	SSR and SNP Marker-Based Investigation of Indian Rice Landraces in Relation to Their Genetic Diversity, Population Structure, and Geographical Isolation. <i>Agriculture (Switzerland)</i> , 2023, 13, 823.	3.1	6
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5781	Genotyping by Sequencing for SNP-Based Linkage Analysis and the Development of KASPar Markers for Male Sterility and Polyembryony in Citrus. <i>Plants</i> , 2023, 12, 1567.	3.5	2
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5785	Genome-wide association study of grain iron and zinc concentration in common bean ( <i>Phaseolus vulgaris</i> ). <i>Plant Breeding</i> , 2023, 142, 357-371.	1.9	2
5786	Meiotic Behaviors of Allotetraploid Citrus Drive the Interspecific Recombination Landscape, the Genetic Structures, and Traits Inheritance in Tetrazyg Progenies Aiming to Select New Rootstocks. <i>Plants</i> , 2023, 12, 1630.	3.5	1

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5788	<i>Medicago truncatula</i> quantitative resistance to a new strain of <i>Verticillium alfalfae</i> from Iran revealed by a genome-wide association study. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0
5789	Potential of publicly available <i>Beta vulgaris</i> germplasm for sustainable sugarbeet improvement indicated by combining analysis of genetic diversity and historic resistance evaluation. <i>Crop Science</i> , 0, , .	1.8	0
5790	Microsatellite markers-aided dissection of iron, zinc and cadmium accumulation potential in <i>Triticum aestivum</i> . <i>PeerJ</i> , 0, 11, e15229.	2.0	0
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5795	Identification of qBK2.1, a novel QTL controlling rice resistance against <i>Fusarium fujikuroi</i> . , 2023, 64, .		0
5796	Genome-wide association study reveals genomic loci influencing agronomic traits in Ethiopian sorghum ( <i>Sorghum bicolor</i> (L.) Moench) landraces. <i>Molecular Breeding</i> , 2023, 43, .	2.1	0
5797	Mapping the quantitative field resistance to stripe rust in a hard winter wheat population "Overlay" – "Overland". <i>Crop Science</i> , 0, , .	1.8	0
5798	Genome-Wide Association Study of Asian and European Common Wheat Accessions for Yield-Related Traits and Stripe Rust Resistance. <i>Plant Disease</i> , 2023, 107, 3085-3095.	1.4	1
5799	Identification of QTL, QTL-by-environment interactions, and their candidate genes for resistance HG Type 0 and HG Type 1.2.3.5.7 in soybean using 3VmrMLM. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	1
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5802	The inability of barley to germinate after submergence depends on hypoxia-induced secondary dormancy. <i>Journal of Experimental Botany</i> , 2023, 74, 4277-4289.	4.8	5
5803	Yield component QTLs identified by genome-wide association mapping validated in a diverse <i>tropical japonica</i> rice biparental mapping population. <i>Crop Science</i> , 0, , .	1.8	1
5804	Phylogeography of the temperate grassland plant <i>Tephrosia kirilowii</i> (Asteraceae) inferred from multiplexed inter-simple sequence repeat genotyping by sequencing (MIG-seq) data. <i>Journal of Plant Research</i> , 2023, 136, 437-452.	2.4	3
5805	Genome-wide SSR marker analysis to understand the genetic diversity and population sub-structure in <i>Akebia trifoliata</i> . <i>Genetic Resources and Crop Evolution</i> , 2023, 70, 2741-2754.	1.6	0

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5808	Comprehensive analysis of physiological and metabolomic responses to drought reveals specific modulation of acquired tolerance mechanisms in rice. <i>Physiologia Plantarum</i> , 2023, 175, .	5.2	5
5809	Genomic prediction of hybrid performance in grain sorghum ( <i>Sorghum bicolor</i> L.). <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	3
5810	Genetic Diversity and Population Structure of Sorghum ( <i>Sorghum bicolor</i> (L.) Moench) Landraces Using DArTseq-Derived Single-Nucleotide Polymorphism (SNP) Markers. <i>Journal of Molecular Evolution</i> , 2023, 91, 552-561.	1.8	3
5811	Environment as a limiting factor of the historical global spread of mungbean. <i>ELife</i> , 0, 12, .	6.0	4
5812	Genetic diversity and population structure among Ugandan Shea tree ( <i>Vitellaria paradoxa</i> Subsp.) Tj ETQq1 1 0.784314 rgBT <sub>1</sub> /Overl	1.8	1
5813	Identification of genomic regions linked to blast ( <i>Pyricularia grisea</i> ) resistance in pearl millet. <i>Plant Breeding</i> , 0, , .	1.9	0
5814	Genetic diversity, population structure, and genome-wide association study for the flowering trait in a diverse panel of 428 moth bean ( <i>Vigna aconitifolia</i> ) accessions using genotyping by sequencing. <i>BMC Plant Biology</i> , 2023, 23, .	3.6	0
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5816	Genome-wide association analysis of hyperspectral reflectance data to dissect the genetic architecture of growth-related traits in maize under plant growth-promoting bacteria inoculation. <i>Plant Direct</i> , 2023, 7, .	1.9	2
5818	Quantitative genetic analysis of floral traits shows current limits but potential evolution in the wild. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2023, 290, .	2.6	1
5819	Cytokinin signaling promotes salt tolerance by modulating shoot chloride exclusion in maize. <i>Molecular Plant</i> , 2023, 16, 1031-1047.	8.3	8
5821	A genome-wide association study of morphometric traits in dromedaries. <i>Veterinary Medicine and Science</i> , 0, , .	1.6	0
5823	Efficacy of plant breeding using genomic information. <i>Plant Genome</i> , 2023, 16, .	2.8	0
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5825	Hybrid allele-specific ChIP-seq analysis identifies variation in brassinosteroid-responsive transcription factor binding linked to traits in maize. <i>Genome Biology</i> , 2023, 24, .	8.8	3
5826	Historical Selection, Adaptation Signatures, and Ambiguity of Introgressions in Wheat. <i>International Journal of Molecular Sciences</i> , 2023, 24, 8390.	4.1	0
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5829	Genetic diversity and genome-scale population structure of wild Indian major carp, <i>Labeo catla</i> (Hamilton, 1822), revealed by genotyping-by-sequencing. <i>Frontiers in Genetics</i> , 0, 14, .	2.3	0
5830	Genetic Diversification of Starch Branching Enzymes during Maize Domestication and Improvement. <i>Genes</i> , 2023, 14, 1068.	2.4	0
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5833	Mapping of the bs5 and bs6 non-race-specific recessive resistances against bacterial spot of pepper. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0
5834	Validation and marker-assisted selection of DArT-genomic regions associated with wheat yield-related traits under normal and drought conditions. <i>Frontiers in Genetics</i> , 0, 14, .	2.3	2
5835	Genetic mapping identified three hotspot genomic regions and candidate genes controlling heat tolerance-related traits in groundnut. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	3
5836	Mixed infections of <i>Zymoseptoria tritici</i> lead to reduced <i>Septoria tritici</i> blotch disease symptoms. <i>Plant Pathology</i> , 0, , .	2.4	0
5838	Allelic variation in transcription factor <i>PtoWRKY68</i> contributes to drought tolerance in <i>Populus</i> . <i>Plant Physiology</i> , 0, , .	4.8	4
5839	A genome-wide association study and genomic prediction for <i>Phakopsora pachyrhizi</i> resistance in soybean. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	3
5840	Screening and validation of salt-stress responsive cg-SSR markers in wheat ( <i>Triticum aestivum</i> L.) germplasm of Pakistan. <i>Molecular Biology Reports</i> , 2023, 50, 5931-5940.	2.3	1
5841	Exploring the Genetic Variation of Stripe Rust Foliar and Head Infection in Egyptian Wheat as an Effect of Climate Change. <i>Agronomy</i> , 2023, 13, 1509.	3.0	1
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5843	Genome wide association studies and candidate gene mining for understanding the genetic basis of straw silica content in a set of <i>Oryza nivara</i> (Sharma et Shastry) accessions. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0
5845	Multi-Trait Genome-Wide Association Studies of <i>Sorghum bicolor</i> Regarding Resistance to Anthracnose, Downy Mildew, Grain Mold and Head Smut. <i>Pathogens</i> , 2023, 12, 779.	2.8	1
5846	Mining Salt Tolerance SNP Loci and Prediction of Candidate Genes in the Rice Bud Stage by Genome-Wide Association Analysis. <i>Plants</i> , 2023, 12, 2163.	3.5	2
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5848	Identification of Growth-Related SNPs and Genes in the Genome of the Pearl Oyster ( <i>Pinctada fucata</i> ) Using GWAS. <i>Fishes</i> , 2023, 8, 296.	1.7	0

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5850	Genome-wide identification and analysis of glyceraldehyde-3-phosphate dehydrogenase family reveals the role of GmGAPDH14 to improve salt tolerance in soybean ( <i>Glycine max</i> L.). <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	4
5852	Population genomic analysis reveals geographic structure and climatic diversification for <i>Macrophomina phaseolina</i> isolated from soybean and dry bean across the United States, Puerto Rico, and Colombia. <i>Frontiers in Genetics</i> , 0, 14, .	2.3	4
5853	Identification of SNPs Associated with Grain Quality Traits in Spring Barley Collection Grown in Southeastern Kazakhstan. <i>Agronomy</i> , 2023, 13, 1560.	3.0	4
5854	Four haplotype blocks linked to Ascochyta blight disease resistance in chickpea under Mediterranean conditions. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	1
5855	Genotype by environment interaction characterization and its modeling with random regression to climatic variables in two rice breeding populations. <i>Crop Science</i> , 2023, 63, 2220-2240.	1.8	1
5857	Genome-wide association study of multiyear dynamic growth traits in hybrid <i>Liriodendron</i> identifies robust genetic loci associated with growth trajectories. <i>Plant Journal</i> , 0, , .	5.7	1
5858	Genetic diversity and population structure of bermudagrass ( <i>Cynodon</i> spp.) revealed by genotyping-by-sequencing. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0
5860	ddRAD sequencing based genotyping of six indigenous dairy cattle breeds of India to infer existing genetic diversity and population structure. <i>Scientific Reports</i> , 2023, 13, .	3.3	5
5861	Genetic variation in <i>ZmWAX2</i> confers maize resistance to <i>Fusarium verticillioides</i> . <i>Plant Biotechnology Journal</i> , 2023, 21, 1812-1826.	8.3	2
5862	Phenomic data-driven biological prediction of maize through field-based high-throughput phenotyping integration with genomic data. <i>Journal of Experimental Botany</i> , 2023, 74, 5307-5326.	4.8	4
5863	Genomic signatures of local adaptation in recent invasive <i>Aedes aegypti</i> populations in California. <i>BMC Genomics</i> , 2023, 24, .	2.8	1
5864	QTL mapping and candidate gene prediction for the sensitivity of flag leaf angle to exogenous GA3 in rice ( <i>Oryza sativa</i> L.). <i>Euphytica</i> , 2023, 219, .	1.2	0
5865	Phenotypic and genotypic resources for the USDA quinoa ( <i>Chenopodium quinoa</i> ) genebank accessions. <i>Crop Science</i> , 2023, 63, 2685-2698.	1.8	2
5866	Identification of candidate genes for soybean seed coat-related traits using QTL mapping and GWAS. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	2
5867	Identification of Novel QTLs/Defense Genes in Spring Wheat Germplasm Panel for Seedling and Adult Plant Resistance to Stem Rust and Their Validation Through KASP Marker Assays. <i>Plant Disease</i> , 2023, 107, 1847-1860.	1.4	1
5868	Gene allele system of shade tolerance in southern China soybean germplasm revealed by genome-wide association study using gene allele sequence as markers. <i>Theoretical and Applied Genetics</i> , 2023, 136, .	3.6	4
5869	Key triggers of adaptive genetic variability of sessile oak [ <i>Q. petraea</i> (Matt.) Liebl.] from the Balkan refugia: outlier detection and association of SNP loci from ddRAD-seq data. <i>Heredity</i> , 2023, 131, 130-144.	2.6	2

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5873	Genetic diversity and selection signatures in a gene bank panel of maize inbred lines from Southeast Europe compared with two West European panels. <i>BMC Plant Biology</i> , 2023, 23, .	3.6	1
5874	Identification of quantitative trait loci associated with R1-mediated resistance to powdery mildew and sex determination in hop ( <i>Humulus lupulus</i> L.). <i>Theoretical and Applied Genetics</i> , 2023, 136, .	3.6	1
5875	Detection of reproducible QTL associated with bioenergy traits in sorghum across several growing environments. <i>Euphytica</i> , 2023, 219, .	1.2	0
5876	Genome-wide association studies identify OsWRKY53 as a key regulator of salt tolerance in rice. <i>Nature Communications</i> , 2023, 14, .	12.8	9
5877	Genome-Wide Association Study of Seed Morphology Traits in Senegalese Sorghum Cultivars. <i>Plants</i> , 2023, 12, 2344.	3.5	4
5878	Clonal Differentiation and Identification of Polyploids in <i>Juglans</i> hybrids. <i>Silvae Genetica</i> , 2023, 72, 72-80.	0.8	0
5879	Selective sweeps identification in distinct groups of cultivated rye ( <i>Secale cereale</i> L.) germplasm provides potential candidate genes for crop improvement. <i>BMC Plant Biology</i> , 2023, 23, .	3.6	0
5880	Accelerating gene discovery in climate-resilient and nutrient-rich major and minor millets through genome-wide association studies: Progress and prospects. <i>Plant Breeding</i> , 0, , .	1.9	0
5881	Interplay between tree genetic variation, plant community composition and environment in forest communities dominated by black alder ( <i>Alnus glutinosa</i> (L.) Gaertn.). <i>Perspectives in Plant Ecology, Evolution and Systematics</i> , 2023, 60, 125748.	2.7	1
5882	Genome-wide association mapping of resistance to the foliar diseases septoria nodorum blotch and tan spot in a global winter wheat collection. <i>Molecular Breeding</i> , 2023, 43, .	2.1	1
5883	Novel SNP based analysis of genetic diversity in <i>Polygonatum verticillatum</i> Linn. across Indian Himalayas. <i>3 Biotech</i> , 2023, 13, .	2.2	0
5884	Demographic history and distinct selection signatures of two domestication genes in mungbean. <i>Plant Physiology</i> , 2023, 193, 1197-1212.	4.8	4
5885	A novel QTL linked to asparagine synthetase gene for stem height increment in oil palm ( <i>E. guineensis</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.2	0
5886	Genetic variation and population differentiation in North American, central Asian and European isolates of <i>Venturia inaequalis</i> . <i>Plant Pathology</i> , 2023, 72, 1505-1516.	2.4	0
5887	Identification of novel putative alleles related to important agronomic traits of wheat using robust strategies in GWAS. <i>Scientific Reports</i> , 2023, 13, .	3.3	0
5888	Genome-wide association study unravels genomic regions associated with chlorophyll fluorescence parameters in wheat ( <i>Triticum aestivum</i> L.) under different sowing conditions. <i>Plant Cell Reports</i> , 2023, 42, 1453-1472.	5.6	6



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5889	Identification of Quantitative Trait Loci Associated with Powdery Mildew Resistance in Spring Barley under Conditions of Southeastern Kazakhstan. <i>Plants</i> , 2023, 12, 2375.	3.5	2
5890	Genomic Resequencing Unravels the Genetic Basis of Domestication, Expansion, and Trait Improvement in <i>Morus Atropurpurea</i> . <i>Advanced Science</i> , 2023, 10, .	11.2	0
5891	Genome-Wide Association Study of Lint Percentage in <i>Gossypium hirsutum</i> L. Races. <i>International Journal of Molecular Sciences</i> , 2023, 24, 10404.	4.1	1
5892	<i>ZmRPN1</i> confers quantitative variation in pollen number and boosts hybrid seed production in maize. <i>Plant Biotechnology Journal</i> , 2023, 21, 1978-1989.	8.3	0
5893	ZmAGO18b negatively regulates maize resistance against southern leaf blight. <i>Theoretical and Applied Genetics</i> , 2023, 136, .	3.6	0
5895	Comparative single nucleotide polymorphism analysis of maize Iodent and BSSS germplasms. <i>Biologia Plantarum</i> , 0, 67, 150-158.	1.9	0
5896	An application of vGWAS to differences in flowering time in maize across mega-environments. <i>Crop Science</i> , 0, , .	1.8	0
5897	Diversity and association mapping assessment of an untouched native grapevine genetic resource by iPBS retrotransposon markers. <i>Genetic Resources and Crop Evolution</i> , 2024, 71, 679-690.	1.6	5
5898	Increasing aleurone layer number and pericarp yield for elevated nutrient content in maize. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	1.8	0
5899	Population genomic analysis reveals key genetic variations and driving force for embryonic callus induction capability in maize. <i>Journal of Integrative Agriculture</i> , 2023, , .	3.5	1
5900	Genetic population structure of the precious coral <i>Corallium japonicum</i> in the Northwest Pacific. <i>Frontiers in Marine Science</i> , 0, 10, .	2.5	2
5901	Genome-wide association analysis of resistance to frogeye leaf spot China race 7 in soybean based on high-throughput sequencing. <i>Theoretical and Applied Genetics</i> , 2023, 136, .	3.6	0
5902	Revisiting the Genomic Approaches in the Cereals and the Path Forward. , 2023, , 1-40.		1
5904	Genome-wide association mapping in elite winter wheat breeding for yield improvement. <i>Journal of Applied Genetics</i> , 2023, 64, 377-391.	1.9	1
5905	Genome-Wide Association Study Using Genotyping by Sequencing for Bacterial Leaf Blight Resistance Loci in Local Thai Indica Rice. <i>Agronomy</i> , 2023, 13, 1286.	3.0	2
5907	SSR marker-based genetic diversity and marker-trait association analysis in aromatic rice ( <i>Oryza sativa</i> ) landraces. , 2023, 93, .		0
5909	Identification of a novel Pm65 allele conferring a wide spectrum of resistance to powdery mildew in wheat accession PI 351817. <i>Phytopathology</i> , 0, , .	2.2	1
5910	Novel genomic regions on chromosome 5B controlling wheat powdery mildew seedling resistance under Egyptian conditions. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	2

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5911	Exploring genetic diversity and population structure of a large grapevine ( <i>Vitis vinifera</i> L.) germplasm collection in Türkiye. <i>Frontiers in Plant Science</i> , 2023, 14, .	3.6	5
5912	Genetic analysis and QTL mapping of domestication-related traits in chili pepper ( <i>Capsicum annuum</i> L.). <i>Frontiers in Genetics</i> , 2023, 14, .	2.3	1
5913	Tissues and mechanisms associated with <i>Verticillium</i> wilt resistance in tomato using bi-grafted near-isogenic lines. <i>Journal of Experimental Botany</i> , 2023, 74, 4685-4706.	4.8	1
5914	Genome-Wide Association Mapping for Yield and Yield-Related Traits in Rice ( <i>Oryza Sativa</i> L.) Using SNPs Markers. <i>Genes</i> , 2023, 14, 1089.	2.4	1
5915	Population structure analysis to explore genetic diversity and geographical distribution characteristics of wild tea plant in Guizhou Plateau. <i>BMC Plant Biology</i> , 2023, 23, .	3.6	1
5916	Identification of candidate growth-related SNPs and genes using GWAS and transcriptome analyses in leopard coral grouper ( <i>Plectropomus leopardus</i> ). <i>Aquaculture</i> , 2023, 574, 739677.	3.5	5
5917	Multi-Environment Genome-Wide Association Studies of Yield Traits in Common Bean ( <i>Phaseolus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Colombian Caribbean Subregions. <i>Agronomy</i> , 2023, 13, 1396.	3.0	2
5918	Identification of novel loci for flowering time in mungbean [ <i>Vigna radiata</i> (L.) R. Wilczek] using genome-wide association study. <i>Genes and Genomics</i> , 2023, 45, 911-919.	1.4	0
5919	Genome-wide association mapping for component traits of drought tolerance in dry beans ( <i>Phaseolus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.5	1
5920	FHB resistance conferred by <i>Fhb1</i> is under inhibitory regulation of two genetic loci in wheat ( <i>Triticum</i> ) Tj ETQq1 1 0,784314 rgBT /Overlock 10 Tf 50	3.6	1
5922	Discovery of a key gene associated with fruit maturity date and analysis of its regulatory pathway in peach. <i>Plant Science</i> , 2023, 333, 111735.	3.6	1
5923	Validation of genes affecting rice mesocotyl length through candidate association analysis and identification of the superior haplotypes. <i>Frontiers in Plant Science</i> , 2023, 14, .	3.6	1
5924	Microsatellite marker assisted molecular diversity and population structure analysis of <i>Kaempferia galanga</i> Linn. germplasm collected from different parts of India. <i>Journal of Applied Research on Medicinal and Aromatic Plants</i> , 2023, 35, 100500.	1.5	0
5925	Genome-wide association study of ear tip barrenness in waxy maize. <i>Breeding Science</i> , 2023, 73, 261-268.	1.9	0
5926	Enhancing adaptation of tropical maize to temperate environments using genomic selection. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	1.8	0
5929	High-density DArTSeq SNP markers revealed wide genetic diversity and structured population in common bean ( <i>Phaseolus vulgaris</i> L.) germplasm in Ethiopia. <i>Molecular Biology Reports</i> , 2023, 50, 6739-6751.	2.3	3
5930	Multi-locus genome-wide association study of fusarium head blight in relation to days to anthesis and plant height in a spring wheat association panel. <i>Frontiers in Plant Science</i> , 2023, 14, .	3.6	1
5931	Population Genomics Unravels the Characteristic Relationship between Introgression and Geographical Distribution in Upland Cotton. <i>Agronomy</i> , 2023, 13, 1781.	3.0	1

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5933	A major yellow rust resistance QTL on chromosome 6A shows increased frequency in recent Norwegian spring wheat cultivars and breeding lines. <i>Theoretical and Applied Genetics</i> , 2023, 136, .	3.6	1
5934	Genetic dissection of grain morphology and yield components in a wheat line with defective grain filling. <i>Theoretical and Applied Genetics</i> , 2023, 136, .	3.6	1
5935	Genomic insights into selection for heterozygous alleles and woody traits in <i>Populus tomentosa</i> . <i>Plant Biotechnology Journal</i> , 2023, 21, 2002-2018.	8.3	5
5936	Identification of solvent retention capacity quantitative trait loci by combined linkage and association mapping in wheat ( <i>Triticum aestivum</i> L.). <i>Crop Science</i> , 0, , .	1.8	0
5938	Delineation of novel genomic loci and putative candidate genes associated with seed iron and zinc content in lentil ( <i>Lens culinaris</i> Medik.). <i>Plant Science</i> , 2023, 335, 111787.	3.6	1
5939	Genome-Wide Association Study of Xian Rice Grain Shape and Weight in Different Environments. <i>Plants</i> , 2023, 12, 2549.	3.5	1
5940	Comprehensive analysis of transcriptional data on seed germination of two maize inbred lines under low-temperature conditions. <i>Plant Physiology and Biochemistry</i> , 2023, 201, 107874.	5.8	3
5941	Transcriptomic, epigenomic and physiological comparisons reveal key factors for different manganese tolerances in three <i>Chenopodium ambrosioides</i> L. populations. <i>Plant Physiology and Biochemistry</i> , 2023, 201, 107883.	5.8	3
5943	High-density linkage mapping and genetic dissection of resistance to broomrape ( <i>Orobanche crenata</i> ) Tj ETQq1 1 0,784314 rgBT /Overl	3.6	3
5944	Advances in Eco-TILLING: In Search of Superior Natural Variants. , 2023, , 115-135.		0
5945	GWLD: an R package for genome-wide linkage disequilibrium analysis. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	1.8	3
5946	Adoption and impact of improved amaranth cultivars in TanzaniaÂusing DNA fingerprinting. <i>Food Security</i> , 0, , .	5.3	0
5947	Hybrid breeding for fall armyworm resistance: Combining ability and hybrid prediction. <i>Plant Breeding</i> , 2023, 142, 607-620.	1.9	1
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5951	Long-distance gene flow in <i>Acacia senegal</i> : Hope for disturbed and fragmented populations. <i>Ecology and Evolution</i> , 2023, 13, .	1.9	1
5953	k-mer-Based Genome-Wide Association Studies in Plants: Advances, Challenges, and Perspectives. <i>Genes</i> , 2023, 14, 1439.	2.4	2

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5955	<i>SNPscan breeder</i> – a computer program to test genomic tools in breeding programs. <i>Silvae Genetica</i> , 2023, 72, 126-131.	0.8	1
5956	Study of the Myb114 Gene Polymorphism in the Cole Crops ( <i>Brassica oleracea</i> L.) in Connection with Anthocyanin Biosynthesis Regulation Based on Comparison with the MYB Factors of Vegetable Nightshades ( <i>Solanaceae</i> ). <i>Russian Journal of Genetics</i> , 2023, 59, 30-39.	0.6	0
5957	Genetic characterization of FODMAPs and ATIs in heritage and modern spring wheat. <i>Crop Science</i> , 0, , .	1.8	0
5958	Comparison of the statistical methods for genome-wide association studies on simulated quantitative traits of domesticated goats ( <i>Capra hircus</i> L.). <i>Small Ruminant Research</i> , 2023, 227, 107053.	1.2	2
5959	Genetic structure analysis and identifying key founder inbred lines in diverse elite sub-tropical maize inbred lines. <i>Scientific Reports</i> , 2023, 13, .	3.3	0
5960	Major chromosome 5H haplotype switch structures the European two-rowed spring barley germplasm of the past 190 years. <i>Theoretical and Applied Genetics</i> , 2023, 136, .	3.6	2
5961	A Genome-Wide Association Study Reveals Region Associated with Seed Protein Content in Cowpea. <i>Plants</i> , 2023, 12, 2705.	3.5	2
5962	Harnessing genome-wide genetic diversity, population structure and linkage disequilibrium in Ethiopian durum wheat gene pool. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	1
5963	Genetic dissection and origin of pleiotropic loci underlying multi-level fiber quality traits in Upland cotton ( <i>Gossypium hirsutum</i> L.). <i>Journal of Integrative Agriculture</i> , 2023, , .	3.5	0
5964	Characterising a genetic stronghold amidst pervasive admixture: Morelet's crocodiles ( <i>Crocodylus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.5	0
5966	Natural variation in <i>Brachypodium distachyon</i> responses to combined abiotic stresses. <i>Plant Journal</i> , 2024, 117, 1676-1701.	5.7	1
5967	GWAS for Early-Establishment QTLs and Their Linkage to Major Phenology-Affecting Genes (Vrn, Ppd,) Tj ETQq0 0 0 rgBT /Overlock 10 T	2.4	0
5968	Genomic landscape of the OsTPP7 gene in its haplotype diversity and association with anaerobic germination tolerance in rice. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0
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5974	Identification of quantitative trait loci controlling nitrogen use efficiency-related traits in rice at the seedling stage under salt condition by genome-wide association study. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	1
5975	Identification of Markers Associated with Wheat Dwarf Virus (WDV) Tolerance/Resistance in Barley ( <i>Hordeum vulgare</i> ssp. <i>vulgare</i> ) Using Genome-Wide Association Studies. <i>Viruses</i> , 2023, 15, 1568.	3.3	0
5976	Evaluation of three sets of advanced backcrosses of eggplant with wild relatives from different gene pools under low N fertilization conditions. <i>Horticulture Research</i> , 2023, 10, .	6.3	0
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5979	Genome-wide association study reveals candidate genes controlling root system architecture under low phosphorus supply at seedling stage in <i>Brassica napus</i> . <i>Molecular Breeding</i> , 2023, 43, .	2.1	0
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5998	Genetic variation among elite inbred lines suggests potential to breed for BNI-capacity in maize. Scientific Reports, 2023, 13, .	3.3	1
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6025	Association Mapping of Candidate Genes Associated with Iron and Zinc Content in Rice ( <i>Oryza sativa</i> ) Tj ETQq1 1 0,784314 rgBT /Overl	2.4	0
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6037	Unravelling marker trait associations linking nutritional value with pigmentation in rice seed. <i>Plant Genome</i> , 2023, 16, .	2.8	1
6038	Association mapping in bambara groundnut [ <i>Vigna subterranea</i> (L.) Verdc.] reveals loci associated with agro-morphological traits. <i>BMC Genomics</i> , 2023, 24, .	2.8	1
6039	Genetic mapping of quantitative trait loci associated with drought tolerance in chickpea ( <i>Cicer</i> ) Tj ETQq1 1 0.784314 rgBT /Overlook 10	3.3	2
6040	The Development of Thematic Core Collections in Cassava Based on Yield, Disease Resistance, and Root Quality Traits. <i>Plants</i> , 2023, 12, 3474.	3.5	0
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6046	Uncovering microsatellite markers associated with agronomic traits of South Sudan landrace maize. <i>Genes and Genomics</i> , 0, , .	1.4	0
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6057	Genetic variation, correlation, and association mapping of seed yield and its component traits in sesame. <i>Genetic Resources and Crop Evolution</i> , 0, , .	1.6	0
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6063	Skim exome capture genotyping in wheat. <i>Plant Genome</i> , 0, , .	2.8	0
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6072	Development of cassava core collections based on morphological and agronomic traits and SNPs markers. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	1
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6090	Genetic Variation and Association Analysis of Elite Waxy Maize Inbred Lines in South Korea. Plant Molecular Biology Reporter, 0, , .	1.8	0
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6102	Analyzing genomic variation in cultivated pumpkins and identification of candidate genes controlling seed traits. <i>Plant Genome</i> , 2023, 16, .	2.8	0
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6104	Molecular characterization of stable QTL and putative candidate genes for grain zinc and iron concentrations in two related wheat populations. <i>Theoretical and Applied Genetics</i> , 2023, 136, .	3.6	0
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6106	Genetic characterization of root architectural traits in barley ( <i>Hordeum vulgare</i> L.) using SNP markers. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	1
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6116	Identifying QTLs involved in hybrid performance and heterotic group complementarity: new GWAS models applied to factorial and admixed diallel maize hybrid panels. <i>Theoretical and Applied Genetics</i> , 2023, 136, .	3.6	1
6117	Assessment of Indian wheat germplasm for <i>Septoria nodorum</i> blotch and tan spot reveals new QTLs conferring resistance along with recessive alleles of <i>Tsn1</i> and <i>Snn3</i> . <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0
6118	Genome-wide association mapping highlights candidate genes and immune genotypes for net blotch and powdery mildew resistance in barley. <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 4923-4932.	4.1	2

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6121	Importance of genetic architecture in marker selection decisions for genomic prediction. <i>Theoretical and Applied Genetics</i> , 2023, 136, .	3.6	0
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6131	Association Analysis of Tiller-Related Traits with EST-SSR Markers in <i>Psathyrostachys juncea</i> . <i>Genes</i> , 2023, 14, 1970.	2.4	0
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