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Citation Report

#	ARTICLE	IF	CITATIONS
1	Characterization of 37 Breed-Specific Single-Nucleotide Polymorphisms in Sheep. <i>Journal of Heredity</i> , 2006, 97, 531-534.	1.0	28
2	Linking the gaps between conservation research and conservation management of rare dipterocarps: A case study of <i>Shorea lumutensis</i> . <i>Biological Conservation</i> , 2006, 131, 72-92.	1.9	61
3	The dysbindin gene (DTNBP1) and schizophrenia: No support for an association in the Korean population. <i>Neuroscience Letters</i> , 2006, 407, 101-106.	1.0	31
4	Accuracy and Reliability of High-Throughput Microsatellite Genotyping for Cacao Clone Identification. <i>Crop Science</i> , 2006, 46, 2084-2092.	0.8	44
5	The risk of dialysis access thrombosis is related to the transforming growth factor- β 1 production haplotype and is modified by polymorphisms in the plasminogen activator inhibitor-1 type 1 gene. <i>Blood</i> , 2006, 108, 4052-4058.	0.6	30
6	Genetic Variation Within and Among Populations of Maize Inbred B37 Revealed By SSR Markers. <i>Biotechnology and Biotechnological Equipment</i> , 2006, 20, 37-44.	0.5	0
7	Newly developed polymorphic microsatellite markers in Job's tears (<i>Coix lacryma-jobi</i> L.). <i>Molecular Ecology Notes</i> , 2006, 6, 689-691.	1.7	4
8	Characterization of new microsatellite markers in mung bean, <i>Vigna radiata</i> (L.). <i>Molecular Ecology Notes</i> , 2006, 6, 1132-1134.	1.7	62
9	Isolation of 23 polymorphic microsatellite loci in the Neotropical palm <i>Oenocarpus bataua</i> Martius (Arecaceae). <i>Molecular Ecology Notes</i> , 2006, 7, 75-78.	1.7	11
10	Evidence for linkage to and association with type 1 diabetes at the 3q21 region in the Finnish population. <i>Genes and Immunity</i> , 2006, 7, 69-72.	2.2	3
11	A neuronal nitric oxide synthase (NOS-I) haplotype associated with schizophrenia modifies prefrontal cortex function. <i>Molecular Psychiatry</i> , 2006, 11, 286-300.	4.1	204
12	SSR mining in coffee tree EST databases: potential use of EST-SSRs as markers for the <i>Coffea</i> genus. <i>Molecular Genetics and Genomics</i> , 2006, 276, 436-449.	1.0	136
13	Segregation distortion in <i>Arabidopsis</i> C24/Col-0 and Col-0/C24 recombinant inbred line populations is due to reduced fertility caused by epistatic interaction of two loci. <i>Theoretical and Applied Genetics</i> , 2006, 113, 1551-1561.	1.8	71
14	Serotonin transporter gene promoter polymorphism predicts SSRI response in generalized social anxiety disorder. <i>Psychopharmacology</i> , 2006, 187, 68-72.	1.5	134
15	Association between two μ -opioid receptor gene (OPRM1) haplotype blocks and drug or alcohol dependence. <i>Human Molecular Genetics</i> , 2006, 15, 807-819.	1.4	155
16	SNP-Based Analysis of Genetic Substructure in the German Population. <i>Human Heredity</i> , 2006, 62, 20-29.	0.4	121
17	Contribution of the N-acetyltransferase 2 polymorphism NAT2*6A to age-related hearing impairment. <i>Journal of Medical Genetics</i> , 2007, 44, 570-578.	1.5	69
18	Association of interleukin-1 β and interleukin-1 receptor antagonist polymorphisms with bacterial vaginosis in non-pregnant Italian women. <i>Molecular Human Reproduction</i> , 2007, 13, 243-250.	1.3	23

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19	Genetic Variation and Population Structure in Native Americans. <i>PLoS Genetics</i> , 2007, 3, e185.	1.5	454
20	Major Regulatory Genes in Maize Contribute to Standing Variation in Teosinte (<i>Zea mays</i> ssp.) <i>Tj ETQq1 1 0.784314 1.25 67</i> <i>Overlock 10 107</i>	1.2	67
21	Haplotype diversity of preharvest sprouting QTLs in wheat. <i>Genome</i> , 2007, 50, 107-118.	0.9	31
22	Linkage Disequilibrium in Related Breeding Lines of Chickens. <i>Genetics</i> , 2007, 177, 2161-2169.	1.2	90
23	A Weak Effect of Background Selection on Trinucleotide Microsatellites in Maize. <i>Journal of Heredity</i> , 2007, 99, 45-55.	1.0	3
24	Large-Scale Zygosity Testing Using Single Nucleotide Polymorphisms. <i>Twin Research and Human Genetics</i> , 2007, 10, 604-625.	0.3	110
25	Human Genomic Association Studies: A Primer for the Infectious Diseases Specialist. <i>Journal of Infectious Diseases</i> , 2007, 195, 1737-1744.	1.9	11
26	The Genetic Structure of <i>Drosophila ananassae</i> Populations From Asia, Australia and Samoa. <i>Genetics</i> , 2007, 175, 1429-1440.	1.2	32
27	Isolation and characterization of Ty1-copia retrotransposon sequences in the blue agave (<i>Agave</i>) <i>Tj ETQq0 0 0 1.7 32</i> <i>Overlock 10 Tf 50 4</i> <i>Science</i> , 2007, 172, 291-298.	1.7	32
28	Dysbindin gene variants are associated with bipolar I disorder in a Korean population. <i>Neuroscience Letters</i> , 2007, 418, 272-275.	1.0	28
29	Development of genomic microsatellite markers in <i>Coffea canephora</i> and their transferability to other coffee species. <i>Genome</i> , 2007, 50, 1156-1161.	0.9	25
30	No association between the glutamate decarboxylase 67 gene (GAD1) and schizophrenia in the Japanese population. <i>Schizophrenia Research</i> , 2007, 91, 22-26.	1.1	10
31	The HapMap— A Haplotype Map of the Human Genome. , 0, , 33-58.		1
32	Molecular Characterization of the U.S. Peanut Mini Core Collection Using Microsatellite Markers. <i>Crop Science</i> , 2007, 47, 1718-1727.	0.8	48
33	Empirical Comparison of Simple Sequence Repeats and Single Nucleotide Polymorphisms in Assessment of Maize Diversity and Relatedness. <i>PLoS ONE</i> , 2007, 2, e1367.	1.1	204
34	Genetic Relatedness of Portuguese Rice Accessions from Diverse Origins as Assessed by Microsatellite Markers. <i>Crop Science</i> , 2007, 47, 879-884.	0.8	44
35	Intraspecific differentiation of Chilean isolates of the entomopathogenic fungi <i>Metarhizium anisopliae</i> var. <i>anisopliae</i> as revealed by RAPD, SSR and ITS markers. <i>Genetics and Molecular Biology</i> , 2007, 30, 89-99.	0.6	28
36	Polymorphisms within the Toll-like receptor (<i>TLR</i>)-2, -4, and -6 genes in cattle. <i>Italian Journal of Animal Science</i> , 2007, 6, 182-182.	0.8	0

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37	Evaluation of Genetic Diversity and Genome-wide Linkage Disequilibrium among U.S. Wheat (Triticum) Tj ETQq0 0.0 rgBT /Overlock 1	0.8	167
38	Evidence for heritable predisposition to epigenetic silencing of MLH1. <i>International Journal of Cancer</i> , 2007, 120, 1684-1688.	2.3	75
39	Allele frequency distribution for 21 autosomal STR loci in Bhutan. <i>Forensic Science International</i> , 2007, 170, 68-72.	1.3	27
40	DC-SIGN (CD209), pentraxin 3 and vitamin D receptor gene variants associate with pulmonary tuberculosis risk in West Africans. <i>Genes and Immunity</i> , 2007, 8, 456-467.	2.2	164
41	Kin structure provides no explanation for intruders in social aphids. <i>Molecular Ecology</i> , 2007, 16, 3659-3670.	2.0	10
42	The genetic structure of cattle populations (Bos taurus) in northern Eurasia and the neighbouring Near Eastern regions: implications for breeding strategies and conservation. <i>Molecular Ecology</i> , 2007, 16, 3839-3853.	2.0	58
43	Origins and population genetics of weedy red rice in the USA. <i>Molecular Ecology</i> , 2007, 16, 4523-4535.	2.0	167
44	Allelic diversity associated with aridity gradient in wild emmer wheat populations. <i>Plant, Cell and Environment</i> , 2008, 31, 39-49.	2.8	80
45	Evaluation and characterization of resistance to fusarium head blight caused by Fusarium culmorum in UK winter wheat cultivars. <i>Plant Pathology</i> , 2007, 56, 264-276.	1.2	45
46	The extent of linkage disequilibrium in a large cattle population of western Africa and its consequences for association studies. <i>Animal Genetics</i> , 2007, 38, 277-286.	0.6	23
47	Opioid Receptor Gene (OPRM1, OPRK1, and OPRD1) Variants and Response to Naltrexone Treatment for Alcohol Dependence: Results From the VA Cooperative Study. <i>Alcoholism: Clinical and Experimental Research</i> , 2007, 31, 070212174136005-???	1.4	178
48	Characterization of polymorphic microsatellite markers, isolated from ginger (Zingiber officinale) Tj ETQq1 1 0.784314 rgBT /Overlock 1	1.7	22
49	Development of microsatellite markers for bambara groundnut (Vigna subterranea L. Verdc.) an underutilized African legume crop species. <i>Molecular Ecology Notes</i> , 2007, 7, 1326-1328.	1.7	32
50	Characterization of 26 MiniSTR Loci for Improved Analysis of Degraded DNA Samples. <i>Journal of Forensic Sciences</i> , 2008, 53, 73-80.	0.9	122
51	A set of multiplex panels of microsatellite markers for rapid molecular characterization of rice accessions. <i>BMC Plant Biology</i> , 2007, 7, 23.	1.6	29
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53	Low-DensityLipoprotein Receptor-Related Protein 5(LRP5) Gene Polymorphisms Are Associated With Bone Mass in Both Chinese and Whites. <i>Journal of Bone and Mineral Research</i> , 2007, 22, 385-393.	3.1	37
54	Sex-Specific Association of the Glucocorticoid Receptor Gene With Extreme BMD. <i>Journal of Bone and Mineral Research</i> , 2008, 23, 247-252.	3.1	15

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56	Genetic diversity analysis of traditional and improved Indonesian rice (<i>Oryza sativa</i> L.) germplasm using microsatellite markers. Theoretical and Applied Genetics, 2007, 114, 559-568.	1.8	171
57	Development and characterization of new microsatellite markers for ginseng (<i>Panax ginseng</i> C. A.) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	0.8	39
58	Genetic ancestry, population sub-structure, and cardiovascular disease-related traits among African-American participants in the CARDIA Study. Human Genetics, 2007, 121, 565-575.	1.8	79
59	Association study of the oestrogen signalling pathway genes in relation to age at natural menopause. Journal of Genetics, 2007, 86, 269-276.	0.4	28
60	Characterization of microsatellite loci developed for <i>Amaranthus hypochondriacus</i> and their cross-amplifications in wild species. Conservation Genetics, 2008, 9, 243-246.	0.8	50
61	Microsatellite variation and population structure in the "Refractario" cacao of Ecuador. Conservation Genetics, 2008, 9, 327-337.	0.8	29
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63	Molecular diversity and genome-wide linkage disequilibrium patterns in a worldwide collection of <i>Oryza sativa</i> and its wild relatives. Euphytica, 2008, 160, 339-355.	0.6	78
64	Phenotypic and marker-assisted evaluation of spring and winter wheat germplasm for resistance to fusarium head blight. Euphytica, 2008, 164, 803-819.	0.6	35
65	Evaluation of genetic diversity and relationships within an on-farm collection of <i>Perilla frutescens</i> (L.) Britt. using microsatellite markers. Genetic Resources and Crop Evolution, 2008, 55, 523-535.	0.8	41
66	Genic SSRs for European and North American hop (<i>Humulus lupulus</i> L.). Genetic Resources and Crop Evolution, 2008, 55, 959-969.	0.8	25
67	Genetic diversity of Swiss maize (<i>Zea mays</i> L. ssp. <i>mays</i>) assessed with individuals and bulks on agarose gels. Genetic Resources and Crop Evolution, 2008, 55, 971-983.	0.8	19
68	Genetic diversity of ICARDA's worldwide barley landrace collection. Genetic Resources and Crop Evolution, 2008, 55, 1221-1230.	0.8	24
69	Ethnic differences in cytokine gene polymorphisms: potential implications for cancer development. Cancer Immunology, Immunotherapy, 2008, 57, 107-114.	2.0	55
70	Identification and characterization of simple sequence repeat markers for <i>Pythium aphanidermatum</i> , <i>P. cryptoirregulare</i> , and <i>P. irregulare</i> and the potential use in <i>Pythium</i> population genetics. Current Genetics, 2008, 53, 81-93.	0.8	21
71	The genetic diversity of UK, US and Australian cultivars of <i>Triticum aestivum</i> measured by DArT markers and considered by genome. Theoretical and Applied Genetics, 2008, 116, 439-453.	1.8	111
72	Association mapping of iron deficiency chlorosis loci in soybean (<i>Glycine max</i> L. Merr.) advanced breeding lines. Theoretical and Applied Genetics, 2008, 116, 777-787.	1.8	111

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73	Evaluation of genetic diversity of Fusarium head blight resistance in European winter wheat. <i>Theoretical and Applied Genetics</i> , 2008, 117, 813-828.	1.8	39
74	Population structure and linkage disequilibrium of a mini core set of maize inbred lines in China. <i>Theoretical and Applied Genetics</i> , 2008, 117, 1141-1153.	1.8	83
75	Minimising inter-laboratory variation when constructing a unified molecular database of plant varieties in an allogamous crop. <i>Theoretical and Applied Genetics</i> , 2008, 117, 1335-1344.	1.8	9
76	Characterization of AT-rich microsatellites in common bean (<i>Phaseolus vulgaris</i> L.). <i>Theoretical and Applied Genetics</i> , 2008, 118, 91-103.	1.8	39
77	Bin mapping of genomic and EST-derived SSRs in melon (<i>Cucumis melo</i> L.). <i>Theoretical and Applied Genetics</i> , 2008, 118, 139-150.	1.8	115
78	Population Structure and Diversity in Finger Millet (<i>Eleusine coracana</i>) Germplasm. <i>Tropical Plant Biology</i> , 2008, 1, 131-141.	1.0	122
79	Association of SLC22A4/5 Polymorphisms with Steroid Responsiveness of Inflammatory Bowel Disease in Japan. <i>Diseases of the Colon and Rectum</i> , 2008, 51, 598-603.	0.7	10
80	Genetic regulation of amniotic fluid TNF-alpha and soluble TNF receptor concentrations affected by race and preterm birth. <i>Human Genetics</i> , 2008, 124, 243-253.	1.8	52
81	Disentangling genetic vs. environmental causes of sex determination in the common frog, <i>Rana temporaria</i> . <i>BMC Genetics</i> , 2008, 9, 3.	2.7	28
82	Population substructure in Finland and Sweden revealed by the use of spatial coordinates and a small number of unlinked autosomal SNPs. <i>BMC Genetics</i> , 2008, 9, 54.	2.7	31
83	Single nucleotide polymorphisms of the <i>KIT</i> and <i>KITLG</i> genes in pigs. <i>Animal Science Journal</i> , 2008, 79, 303-313.	0.6	22
84	Diversité et structuration génétiques dans des populations naturelles de cacaoyers (<i>Theobroma</i>) Tj ETQq1 1,0,784314,rgBT /Ove	0.8	22
85	Genetic regulation of cervical antiinflammatory cytokine concentrations during pregnancy. <i>American Journal of Obstetrics and Gynecology</i> , 2008, 199, 163.e1-163.e11.	0.7	12
86	Maternal and fetal Toll-like receptor 4 genotype and chorionic plate inflammatory lesions. <i>American Journal of Obstetrics and Gynecology</i> , 2008, 199, 400.e1-400.e4.	0.7	22
87	Comparison of different methods to construct a core germplasm collection in woody perennial species with simple sequence repeat markers. A case study in cherimoya (<i>Annona cherimola</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.8	10
88	Genetic Diversity and Association Analysis for Salinity Tolerance, Heading Date and Plant Height of Barley Germplasm Using Simple Sequence Repeat Markers. <i>Journal of Integrative Plant Biology</i> , 2008, 50, 1004-1014.	4.1	37
89	An assessment of the Irish population for large-scale genetic mapping studies involving epilepsy and other complex diseases. <i>European Journal of Human Genetics</i> , 2008, 16, 176-183.	1.4	5
90	The OPRD1 and OPRK1 loci in alcohol or drug dependence: OPRD1 variation modulates substance dependence risk. <i>Molecular Psychiatry</i> , 2008, 13, 531-543.	4.1	143

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91	Association of cytokine gene polymorphisms and liver fibrosis in chronic hepatitis B. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2008, 23, 783-789.	1.4	22
92	Habitat and management affect genetic structure of <i>Festuca pratensis</i> but not <i>Lolium multiflorum</i> ecotype populations. <i>Plant Breeding</i> , 2008, 127, 510-517.	1.0	30
93	Outcrossing between an agroforestry plantation and remnant native populations of <i>Eucalyptus loxophleba</i> . <i>Molecular Ecology</i> , 2008, 17, 2769-2781.	2.0	56
94	Genetic structure, diversity, and allelic richness in composite collection and reference set in chickpea (<i>Cicer arietinum</i> L.). <i>BMC Plant Biology</i> , 2008, 8, 106.	1.6	170
95	Association of vitamin D receptor gene 3 polymorphisms with Hashimoto's thyroiditis in the Croatian population. <i>International Journal of Immunogenetics</i> , 2008, 35, 125-131.	0.8	57
96	Interaction between interleukin 3 and dystrobrevin-binding protein 1 in schizophrenia. <i>Schizophrenia Research</i> , 2008, 106, 208-217.	1.1	19
97	Development and evaluation of a high-throughput, low-cost genotyping platform based on oligonucleotide microarrays in rice. <i>Plant Methods</i> , 2008, 4, 13.	1.9	37
98	Diversity in coffee assessed with SSR markers: structure of the genus <i>Coffea</i> and perspectives for breeding. <i>Genome</i> , 2008, 51, 50-63.	0.9	68
99	Lack of association between the serotonin transporter promoter polymorphism (5-HTTLPR) and personality traits in asymptomatic patients with panic disorder. <i>Neuroscience Letters</i> , 2008, 431, 173-178.	1.0	15
100	Lack of association between TNF polymorphisms and Alzheimer's disease in an Italian cohort. <i>Neuroscience Letters</i> , 2008, 446, 139-142.	1.0	20
101	Interpopulation linkage disequilibrium patterns of GABRA2 and GABRG1 genes at the GABA cluster locus on human chromosome 4. <i>Genomics</i> , 2008, 91, 61-69.	1.3	18
102	Molecular diversity and association mapping of fiber quality traits in exotic <i>G. hirsutum</i> L. germplasm. <i>Genomics</i> , 2008, 92, 478-487.	1.3	179
103	Association mapping of yellow pigment in an elite collection of durum wheat cultivars and breeding lines. <i>Genome</i> , 2008, 51, 1016-1025.	0.9	57
104	Technical Note: Detection of the C Allele of β -Casein (CSN2) in Czech Dairy Goat Breeds Using LightCycler Analysis. <i>Journal of Dairy Science</i> , 2008, 91, 4053-4057.	1.4	7
105	Genetic Determinants of Response to Warfarin during Initial Anticoagulation. <i>New England Journal of Medicine</i> , 2008, 358, 999-1008.	13.9	516
106	Genetic structure of wild emmer wheat populations as reflected by transcribed versus anonymous SSR markers. <i>Genome</i> , 2008, 51, 187-195.	0.9	19
107	SSR Analysis on Diversity of AA Genome <i>Oryza</i> Species in the Southeast and South Asia. <i>Rice Science</i> , 2008, 15, 289-294.	1.7	4
108	Assessment of molecular diversity at QTLs for preharvest sprouting resistance in wheat using microsatellite markers. <i>Genome</i> , 2008, 51, 375-386.	0.9	16

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109	Genetic diversity of the azuki bean (<i>Vigna angularis</i> (Willd.) Ohwi & Ohashi) gene pool as assessed by SSR markers. <i>Genome</i> , 2008, 51, 728-738.	0.9	37
110	Genetic Differences in Human Circadian Clock Genes among Worldwide Populations. <i>Journal of Biological Rhythms</i> , 2008, 23, 330-340.	1.4	108
111	Molecular Characterization of Maize Inbreds with Expired U.S. Plant Variety Protection. <i>Crop Science</i> , 2008, 48, 1673-1685.	0.8	66
112	Selection Mapping of Loci for Quantitative Disease Resistance in a Diverse Maize Population. <i>Genetics</i> , 2008, 180, 583-599.	1.2	35
113	Heat Shock Protein A1B 1267 Polymorphism Is Highly Associated With Risk and Prognosis of Hepatocellular Carcinoma. <i>Medicine (United States)</i> , 2008, 87, 87-98.	0.4	20
114	Haplotype Diversity in Four Genes &i>(CLCNKA, CLCNKB, BSND, NEDD4L)</i> Involved in Renal Salt Reabsorption. <i>Human Heredity</i> , 2008, 65, 33-46.	0.4	16
115	Population structure and genetic diversity of New World maize races assessed by DNA microsatellites. <i>American Journal of Botany</i> , 2008, 95, 1240-1253.	0.8	251
116	Broccoli "Fiolaro"™ (<i>Brassica oleracea</i>) an endangered typical Italian cultivar. A genetic analysis by SSR markers. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2008, 6, 215-221.	0.4	3
117	CCL3L1 gene-containing segmental duplications and polymorphisms in CCR5 affect risk of systemic lupus erythaematosus. <i>Annals of the Rheumatic Diseases</i> , 2008, 67, 1076-1083.	0.5	83
118	Interleukin-6 (IL-6) and receptor (IL6-R) gene haplotypes associate with amniotic fluid protein concentrations in preterm birth. <i>Human Molecular Genetics</i> , 2008, 17, 1619-1630.	1.4	49
119	C3 R102G polymorphism increases risk of age-related macular degeneration. <i>Human Molecular Genetics</i> , 2008, 17, 1821-1824.	1.4	120
120	Retroelement Insertional Polymorphisms, Diversity and Phylogeography within Diploid, D-genome <i>Aegilops tauschii</i> (Triticeae, Poaceae) Sub-taxa in Iran. <i>Annals of Botany</i> , 2008, 101, 855-861.	1.4	49
121	Population-Based Resequencing Reveals That the Flowering Time Adaptation of Cultivated Barley Originated East of the Fertile Crescent. <i>Molecular Biology and Evolution</i> , 2008, 25, 2211-2219.	3.5	219
122	The Genetic Architecture of Complex Traits in Teosinte (<i>Zea mays</i> ssp. <i>parviglumis</i>): New Evidence From Association Mapping. <i>Genetics</i> , 2008, 180, 1221-1232.	1.2	73
123	Single nucleotide polymorphisms in ANKK1 and the dopamine D2 receptor gene affect cognitive outcome shortly after traumatic brain injury: A replication and extension study. <i>Brain Injury</i> , 2008, 22, 705-714.	0.6	75
124	Variation in cytosine methylation in Clementine mandarin cultivars. <i>Journal of Horticultural Science and Biotechnology</i> , 2008, 83, 833-839.	0.9	10
125	Community Resources and Strategies for Association Mapping in Sorghum. <i>Crop Science</i> , 2008, 48, 30-40.	0.8	305
126	Comparison of microsatellite and blood group diversity among different genotypes of cattle. <i>Acta Veterinaria Hungarica</i> , 2008, 56, 323-333.	0.2	1

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127	Genetic Diversity of Wild Soybean (<i>Glycine soja</i> Sieb. and Zucc.) Accessions from South Korea and Other Countries. <i>Crop Science</i> , 2008, 48, 606-616.	0.8	51
128	Characterization of the Inosine Triphosphatase (ITPA) Gene: Haplotype Structure, Haplotype-Phenotype Correlation and Promoter Function. <i>Therapeutic Drug Monitoring</i> , 2008, 30, 16-22.	1.0	25
129	Beta-1-adrenoceptor genetic variants and ethnicity independently affect response to beta-blockade. <i>Pharmacogenetics and Genomics</i> , 2008, 18, 895-902.	0.7	48
130	Effect of Advanced Cycle Breeding on Genetic Diversity in Barley Breeding Germplasm. <i>Crop Science</i> , 2008, 48, 1027-1036.	0.8	36
131	Genetic polymorphism at the CSN1S1 gene in two Czech goat breeds. <i>Czech Journal of Animal Science</i> , 2007, 52, 199-202.	0.5	4
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133	Application of Association Mapping to Understanding the Genetic Diversity of Plant Germplasm Resources. <i>International Journal of Plant Genomics</i> , 2008, 2008, 1-18.	2.2	221
134	Sweet Sorghum Genetic Diversity and Association Mapping for Brix and Height. <i>Plant Genome</i> , 2009, 2, .	1.6	168
135	Microsatellite-Based Analysis of Tobacco (<i>Nicotiana tabacum</i> L.) Genetic Resources. <i>Crop Science</i> , 2009, 49, 2149-2159.	0.8	38
136	Changes in Genetic Diversity of U.S. Flue-Cured Tobacco Germplasm over Seven Decades of Cultivar Development. <i>Crop Science</i> , 2009, 49, 498-508.	0.8	39
137	Development of new microsatellite markers and their application in the analysis of genetic diversity in lentils. <i>Breeding Science</i> , 2009, 59, 77-86.	0.9	89
138	Genetic variability of Brazilian rice landraces determined by SSR markers. <i>Pesquisa Agropecuaria Brasileira</i> , 2009, 44, 706-712.	0.9	19
139	Polymorphisms within the Toll-Like Receptor (TLR)-2, -4, and -6 Genes in Cattle. <i>Diversity</i> , 2009, 1, 7-18.	0.7	18
140	Molecular diversity assessment of AVRDC-The World Vegetable Center elite-parental mungbeans. <i>Breeding Science</i> , 2009, 59, 149-157.	0.9	19
141	Genetic Population Structure Analysis in New Hampshire Reveals Eastern European Ancestry. <i>PLoS ONE</i> , 2009, 4, e6928.	1.1	4
142	Combining Ability, Genetic Distances, and Heterosis among Elite CIMMYT and IITA Tropical Maize Inbred Lines. <i>Crop Science</i> , 2009, 49, 1201-1210.	0.8	54
143	Microsatellite Diversity Delineates Genetic Relationships of Shia and Sunni Muslim Populations of Uttar Pradesh, India. <i>Human Biology</i> , 2009, 81, 427-445.	0.4	9
144	Genetic structure of lake whitefish (<i>Coregonus clupeaformis</i>) in Lake Michigan. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2009, 66, 382-393.	0.7	34

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145	Three Novel CFTR Polymorphic Repeats Improve Segregation Analysis for Cystic Fibrosis. <i>Clinical Chemistry</i> , 2009, 55, 1372-1379.	1.5	36
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288	Genetic structure and ecogeographical adaptation in wild barley (<i>Hordeum chilense</i> Roemer et Tj ETQq1 1 0.784314 rgBT /Overlock 10 T5	1.6	37

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428	Biodiversity of <i>Secale strictum</i> in Iran measured using microsatellites. <i>Genetic Resources and Crop Evolution</i> , 2011, 58, 497-505.	0.8	8
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547	Genetic Diversity of Tropical Hybrid Rice Germplasm Measured by Molecular Markers. <i>Rice Science</i> , 2012, 19, 193-201.	1.7	22
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704	De Novo Characterization of Leaf Transcriptome Using 454 Sequencing and Development of EST-SSR Markers in Tea (<i>Camellia sinensis</i>). <i>Plant Molecular Biology Reporter</i> , 2013, 31, 524-538.	1.0	57
705	Identification of Major QTL for Waterlogging Tolerance Using Genome-Wide Association and Linkage Mapping of Maize Seedlings. <i>Plant Molecular Biology Reporter</i> , 2013, 31, 594-606.	1.0	43
706	Microsatellite markers of genetic diversity and population structure of <i>Carica papaya</i> . <i>Annals of Applied Biology</i> , 2013, 163, 298-310.	1.3	13
707	Use of genomic and genic SSR markers for assessing genetic diversity and population structure in Indian and African finger millet (<i>Eleusine coracana</i> (L.) Gaertn.) germplasm. <i>Plant Systematics and Evolution</i> , 2013, 299, 1395-1401.	0.3	31
708	A microsatellite-based genome-wide analysis of genetic diversity and linkage disequilibrium in Upland cotton (<i>Gossypium hirsutum</i> L.) cultivars from major cotton-growing countries. <i>Euphytica</i> , 2013, 191, 391-401.	0.6	85
709	Genetic diversity and population structure of the selected core set in <i>Amaranthus</i> using SSR markers. <i>Plant Breeding</i> , 2013, 132, 165-173.	1.0	25
710	Isolation, characterization and cross-species amplification of polymorphic microsatellite markers for <i>Oxytenanthera abyssinica</i> (A. Rich.) Munro (Poaceae). <i>Conservation Genetics Resources</i> , 2013, 5, 799-802.	0.4	2
711	High-density SNP-based genetic map development and linkage disequilibrium assessment in <i>Brassica napus</i> L. <i>BMC Genomics</i> , 2013, 14, 120.	1.2	198
712	Development and validation of microsatellite markers for <i>Brachiaria ruziziensis</i> obtained by partial genome assembly of Illumina single-end reads. <i>BMC Genomics</i> , 2013, 14, 17.	1.2	48
713	An initial assessment of linkage disequilibrium (LD) in coffee trees: LD patterns in groups of <i>Coffea canephora</i> Pierre using microsatellite analysis. <i>BMC Genomics</i> , 2013, 14, 10.	1.2	21
714	Identification of Traits, Genes, and Crops of the Future. , 2013, , 27-177.		1
715	Genetic structure and association mapping of cold tolerance in improved japonica rice germplasm at the booting stage. <i>Euphytica</i> , 2013, 193, 369-382.	0.6	38
716	Genome-wide association mapping for five major pest resistances in wheat. <i>Molecular Breeding</i> , 2013, 32, 943-960.	1.0	73
717	New microsatellite markers classifying nontoxic and toxic <i>Jatropha curcas</i> . <i>Journal of Genetics</i> , 2013, 92, 76-78.	0.4	4
718	Strategy for exploiting exotic germplasm using genetic, morphological, and environmental diversity: the <i>Aegilops tauschii</i> Coss. example. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1793-1808.	1.8	62
719	Association mapping combined with linkage analysis for aluminum tolerance among soybean cultivars released in Yellow and Changjiang River Valleys in China. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1659-1675.	1.8	59
720	SNP genotyping in melons: genetic variation, population structure, and linkage disequilibrium. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1285-1303.	1.8	85

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722	Morphological and genetic characterization of off-type rice plants collected from farm fields in Korea. <i>Journal of Plant Biology</i> , 2013, 56, 160-167.	0.9	2
723	Genetic data confirms field evidence for natural breeding in a wild taro population (<i>Colocasia</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 667 1695-1707.	0.8	14
724	Genetic diversity and population structure of a common bean (<i>Phaseolus vulgaris</i> L.) collection from Calabria (Italy). <i>Genetic Resources and Crop Evolution</i> , 2013, 60, 839-852.	0.8	27
725	Microsatellite-aided detection of genetic redundancy improves management of the International Cocoa Genebank, Trinidad. <i>Tree Genetics and Genomes</i> , 2013, 9, 1395-1411.	0.6	22
726	Insights into drought adaptation of two European oak species revealed by nucleotide diversity of candidate genes. <i>Tree Genetics and Genomes</i> , 2013, 9, 1179-1192.	0.6	24
727	EST-SNP genotyping of citrus species using high-resolution melting curve analysis. <i>Tree Genetics and Genomes</i> , 2013, 9, 1271-1281.	0.6	29
728	Genetic relationships, structure and parentage simulation among the olive tree (<i>Olea europaea</i> L.) Tj ETQq1 1 0.784314 rgBT /Overlock 9, 961-973.	0.6	81
729	Genetic structure and diversity of indigenous rice (<i>Oryza sativa</i>) varieties in the Eastern Himalayan region of Northeast India. <i>SpringerPlus</i> , 2013, 2, 228.	1.2	77
730	<sc>GABA</sc> Receptors, Alcohol Dependence and Criminal Behavior. <i>Journal of Forensic Sciences</i> , 2013, 58, 1227-1232.	0.9	12
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732	Analysis of genetic diversity and structure of eggplant populations (<i>Solanum melongena</i> L.) in China using simple sequence repeat markers. <i>Scientia Horticulturae</i> , 2013, 162, 71-75.	1.7	34
733	Parallel and nonparallel genome-wide divergence among replicate population pairs of freshwater and anadromous <sc>A</sc>tantic salmon. <i>Molecular Ecology</i> , 2013, 22, 5577-5593.	2.0	71
734	Transferability of SSR markers derived from <i>Dendrobium nobile</i> expressed sequence tags (ESTs) and their utilization in <i>Dendrobium</i> phylogeny analysis. <i>Scientia Horticulturae</i> , 2013, 158, 8-15.	1.7	13
735	Genetic diversity of the Australian National Mango Genebank. <i>Scientia Horticulturae</i> , 2013, 150, 213-226.	1.7	46
736	Analysis of genetic variability within and among Italian sheep breeds reveals population stratification and suggests the presence of a phylogeographic gradient. <i>Small Ruminant Research</i> , 2013, 112, 21-27.	0.6	29
737	Detection of molecular signatures of selection at microsatellite loci in the South African abalone (<i>Haliotis midae</i>) using a population genomic approach. <i>Marine Genomics</i> , 2013, 10, 27-36.	0.4	12
738	Genotyping serotonin transporter polymorphisms 5-HTTLPR and rs25531 in European- and African-American subjects from the National Institute of Mental Healthâ€™s Collaborative Center for Genomic Studies. <i>Translational Psychiatry</i> , 2013, 3, e307-e307.	2.4	49

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740	Evaluation of genetic diversity in <i>Magnaporthe grisea</i> populations adapted to finger millet using simple sequence repeats (SSRs) markers. <i>Physiological and Molecular Plant Pathology</i> , 2013, 84, 10-18.	1.3	36
741	Assessment of molecular diversity and population structure of the Ethiopian sorghum [<i>Sorghum bicolor</i> (L.) Moench] germplasm collection maintained by the USDA-ARS National Plant Germplasm System using SSR markers. <i>Genetic Resources and Crop Evolution</i> , 2013, 60, 1817-1830.	0.8	28
742	Phylogeography and niche modelling of the relict plant <i>Amborella trichopoda</i> (<i>Amborellaceae</i>) reveal multiple Pleistocene refugia in New Caledonia. <i>Molecular Ecology</i> , 2013, 22, 6163-6178.	2.0	35
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744	Korean population genetic data and concordance for the PowerPlex® ESX 17, AmpFISTR Identifiler®, and PowerPlex® 16 systems. <i>Forensic Science International: Genetics</i> , 2013, 7, e47-e51.	1.6	15
745	Pathogenic and genetic diversity of <i>Didymella rabiei</i> affecting chickpea in Syria. <i>Crop Protection</i> , 2013, 46, 70-79.	1.0	18
746	Systems for making NIAS Core Collections, single-seed-derived germplasm, and plant photo images available to the research community. <i>Genetic Resources and Crop Evolution</i> , 2013, 60, 1945-1951.	0.8	7
747	Genome-wide copy number variations in <i>Oryza sativa</i> L.. <i>BMC Genomics</i> , 2013, 14, 649.	1.2	26
748	Peach genetic resources: diversity, population structure and linkage disequilibrium. <i>BMC Genetics</i> , 2013, 14, 84.	2.7	78
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751	Pharmacogenomics of cisplatin-based chemotherapy in ovarian-cancer patients from Yakutia. <i>Molecular Genetics, Microbiology and Virology</i> , 2013, 28, 137-140.	0.0	8
752	Development and characterization of microsatellite markers for <i>Morus</i> spp. and assessment of their transferability to other closely related species. <i>BMC Plant Biology</i> , 2013, 13, 194.	1.6	46
753	SNP genotyping reveals genetic diversity between cultivated landraces and contemporary varieties of tomato. <i>BMC Genomics</i> , 2013, 14, 835.	1.2	49
754	Genotyping a large collection of pepper (<i>Capsicum</i> spp.) with SSR loci brings new evidence for the wild origin of cultivated <i>C. annuum</i> and the structuring of genetic diversity by human selection of cultivar types. <i>Genetic Resources and Crop Evolution</i> , 2013, 60, 2375-2390.	0.8	110
755	Genetic diversity and gene flow dynamics revealed in the rare mixed populations of wild soybean (<i>Glycine soja</i>) and semi-wild type (<i>Glycine gracilis</i>) in China. <i>Genetic Resources and Crop Evolution</i> , 2013, 60, 2303-2318.	0.8	9
756	Conservation management of rare and predominantly selfing tropical trees: an example using <i>Hopea biltonensis</i> (<i>Dipterocarpaceae</i>). <i>Biodiversity and Conservation</i> , 2013, 22, 2989-3006.	1.2	5

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758	GENETIC DIVERGENCE ALONG THE SPECIATION CONTINUUM: THE TRANSITION FROM HOST RACE TO SPECIES IN <i>RHAGOLETIS</i> (DIPTERA: TEPHRITIDAE). <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 2561-2576.	1.1	70
759	Genome-Wide Association Analysis of Ten Chilling Tolerance Indices at the Germination and Seedling Stages in Maize. <i>Journal of Integrative Plant Biology</i> , 2013, 55, 735-744.	4.1	63
760	Genetic diversity of the rice bean (<i>Vigna umbellata</i>) gene pool as assessed by SSR markers. <i>Genome</i> , 2013, 56, 717-727.	0.9	37
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762	Molecular characterization and assessment of genetic diversity of inbred lines showing variability for drought tolerance in maize. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2013, 22, 71-79.	0.9	20
763	A study of the relationships of cultivated peanut (<i>Arachis hypogaea</i>) and its most closely related wild species using intron sequences and microsatellite markers. <i>Annals of Botany</i> , 2013, 111, 113-126.	1.4	166
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765	SNP array reveals genome-wide patterns of geographical and potential adaptive divergence across the natural range of Atlantic salmon (<i>Salmo salar</i>). <i>Molecular Ecology</i> , 2013, 22, 532-551.	2.0	212
766	Genetic diversity analysis of elite European maize (<i>Zea mays</i> L.) inbred lines using AFLP, SSR, and SNP markers reveals ascertainment bias for a subset of SNPs. <i>Theoretical and Applied Genetics</i> , 2013, 126, 133-141.	1.8	97
767	A high-throughput SNP marker system for parental polymorphism screening, and diversity analysis in common bean (<i>Phaseolus vulgaris</i> L.). <i>Theoretical and Applied Genetics</i> , 2013, 126, 535-548.	1.8	139
768	Genetic analysis and phenotypic associations for drought tolerance in <i>Hordeum spontaneum</i> introgression lines using SSR and SNP markers. <i>Euphytica</i> , 2013, 189, 9-29.	0.6	42
769	Presence of phylogeographic structure among wild diploid alfalfa accessions (<i>Medicago sativa</i> L.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2013, 60, 23-31.	0.8	13
770	Population structure of the primary gene pool of <i>Oryza sativa</i> in Thailand. <i>Genetic Resources and Crop Evolution</i> , 2013, 60, 335-353.	0.8	41
771	Remnant genetic diversity detected in an ancient crop: <i>Triticum dicoccon</i> Schrank landraces from Asturias, Spain. <i>Genetic Resources and Crop Evolution</i> , 2013, 60, 355-365.	0.8	3
772	Global analysis of <i>Coffea canephora</i> Pierre ex Froehner (Rubiaceae) from the Guineo-Congolese region reveals impacts from climatic refuges and migration effects. <i>Genetic Resources and Crop Evolution</i> , 2013, 60, 483-501.	0.8	54
773	Genetic diversity assessment of Ethiopian tetraploid wheat landraces and improved durum wheat varieties using microsatellites and markers linked with stem rust resistance. <i>Genetic Resources and Crop Evolution</i> , 2013, 60, 513-527.	0.8	24
774	Nuclear and chloroplast microsatellite markers to assess genetic diversity and evolution in hazelnut species, hybrids and cultivars. <i>Genetic Resources and Crop Evolution</i> , 2013, 60, 543-568.	0.8	48

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777	Genetic diversity and relationships among Italian and foreign almond germplasm as revealed by microsatellite markers. <i>Scientia Horticulturae</i> , 2013, 162, 305-312.	1.7	19
778	Population genetic structure of <i>Schistosoma mansoni</i> and <i>Schistosoma haematobium</i> from across six sub-Saharan African countries: Implications for epidemiology, evolution and control. <i>Acta Tropica</i> , 2013, 128, 261-274.	0.9	69
779	Genetic Structure and Indica/Japonica Component Changes in Major Inbred Rice Varieties in China. <i>Rice Science</i> , 2013, 20, 39-44.	1.7	2
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781	Microsatellite markers uncover cryptic species of <i>Odontotermes</i> (Termitoidea: Termitidae) from Peninsular Malaysia. <i>Gene</i> , 2013, 518, 412-418.	1.0	6
782	Insight into the biology, genetics and evolution of the <i>Centella asiatica</i> polyploid complex in Madagascar. <i>Industrial Crops and Products</i> , 2013, 47, 118-125.	2.5	22
783	Development of simple sequence repeat (SSR) markers from <i>Paeonia ostii</i> to study the genetic relationships among tree peonies (Paeoniaceae). <i>Scientia Horticulturae</i> , 2013, 164, 58-64.	1.7	35
784	Genome-wide association of 10 horticultural traits with expressed sequence tag-derived SNP markers in a collection of lettuce lines. <i>Crop Journal</i> , 2013, 1, 25-33.	2.3	22
785	Associations of acetyl-coenzyme A carboxylase α , stearoyl-coenzyme A desaturase, and lipoprotein lipase genes with dairy traits in Alpine goats. <i>Journal of Dairy Science</i> , 2013, 96, 1856-1864.	1.4	10
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788	Development and Application of Microsatellites in Candidate Genes Related to Wood Properties in the Chinese White Poplar (<i>Populus tomentosa</i> Carr.). <i>DNA Research</i> , 2013, 20, 31-44.	1.5	29
789	Introgression and selection shaping the genome and adaptive loci of weedy rice in northern China. <i>New Phytologist</i> , 2013, 197, 290-299.	3.5	61
790	Genetic diversity of cassava (<i>Manihot esculenta</i> Crantz) landraces and cultivars from southern, eastern and central Africa. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2013, 11, 170-181.	0.4	32
791	Use of multiple markers demonstrates a cryptic western refugium and postglacial colonisation routes of Atlantic salmon (<i>Salmo salar</i> L.) in northwest Europe. <i>Heredity</i> , 2013, 111, 34-43.	1.2	27
792	Outlier Loci and Selection Signatures of Simple Sequence Repeats (SSRs) in Flax (<i>Linum usitatissimum</i>) Tj ETQq1 1 0,784314,rgBT /Over 1.0 16	1.0	16

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794	Genetic diversity and population structure of cotton (<i>Gossypium</i> spp.) of the New World assessed by SSR markers. <i>Botany</i> , 2013, 91, 251-259.	0.5	37
795	Haplotype dictionary for the Rht-1 loci in wheat. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1733-1747.	1.8	50
796	Genetic diversity and population structure of <i>Musa</i> accessions in ex situ conservation. <i>BMC Plant Biology</i> , 2013, 13, 41.	1.6	61
797	U.S. population data for 29 autosomal STR loci. <i>Forensic Science International: Genetics</i> , 2013, 7, e82-e83.	1.6	135
798	Genetic structure and domestication of carrot (<i>Daucus carota</i> subsp. <i>sativus</i>) (Apiaceae). <i>American Journal of Botany</i> , 2013, 100, 930-938.	0.8	167
799	Assessment of genetic diversity in the sorghum reference set using EST-SSR markers. <i>Theoretical and Applied Genetics</i> , 2013, 126, 2051-2064.	1.8	73
800	Efficacy of pyramiding elite alleles for dynamic development of plant height in common wheat. <i>Molecular Breeding</i> , 2013, 32, 327-338.	1.0	26
801	EST-SSR markers from five sequenced cDNA libraries of common bean (<i>Phaseolus vulgaris</i> L.) comparing three bioinformatic algorithms. <i>Molecular Ecology Resources</i> , 2013, 13, 688-695.	2.2	16
802	Genetic diversity of two Indian common bean germplasm collections based on morphological and microsatellite markers. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2013, 11, 121-130.	0.4	28
803	Association mapping for soilborne pathogen resistance in synthetic hexaploid wheat. <i>Molecular Breeding</i> , 2013, 31, 299-311.	1.0	57
804	Association analysis of physicochemical traits on eating quality in rice (<i>Oryza sativa</i> L.). <i>Euphytica</i> , 2013, 191, 9-21.	0.6	38
805	Genetic characterization of a core collection of flax (<i>Linum usitatissimum</i> L.) suitable for association mapping studies and evidence of divergent selection between fiber and linseed types. <i>BMC Plant Biology</i> , 2013, 13, 78.	1.6	101
806	Genetic diversity among summer and winter <i>Beauveria bassiana</i> populations as revealed by AFLP analysis. <i>Journal of Asia-Pacific Entomology</i> , 2013, 16, 269-273.	0.4	5
807	Association Mapping of Starch Physicochemical Properties with Starch Biosynthesizing Genes in Waxy Rice (<i>Oryza sativa</i> L.). <i>Journal of Agricultural and Food Chemistry</i> , 2013, 61, 10110-10117.	2.4	37
808	SNP-revealed genetic diversity in wild emmer wheat correlates with ecological factors. <i>BMC Evolutionary Biology</i> , 2013, 13, 169.	3.2	36
809	Genetic analysis of population differentiation and adaptation in <i>Leuciscus waleckii</i> . <i>Genetica</i> , 2013, 141, 417-429.	0.5	11
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811	Efficacy of population structure analysis with breeding populations and inbred lines. <i>Genetica</i> , 2013, 141, 389-399.	0.5	27
812	Microsatellite-based analysis of genetic diversity in 91 commercial <i>Brassica oleracea</i> L. cultivars belonging to six varietal groups. <i>Genetic Resources and Crop Evolution</i> , 2013, 60, 1967-1986.	0.8	45
813	Genetic structure and diversity of coffee (<i>Coffea</i>) across Africa and the Indian Ocean islands revealed using microsatellites. <i>Annals of Botany</i> , 2013, 111, 229-248.	1.4	30
814	Genetic Diversity Revealed by Single Nucleotide Polymorphism Markers in a Worldwide Germplasm Collection of Durum Wheat. <i>International Journal of Molecular Sciences</i> , 2013, 14, 7061-7088.	1.8	111
815	Retrospective View of North American Potato (<i>Solanum tuberosum</i> L.) Breeding in the 20th and 21st Centuries. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1003-1013.	0.8	171
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817	Waxy Phenotype Evolution in the Allotetraploid Cereal Broomcorn Millet: Mutations at the GBSSI Locus in Their Functional and Phylogenetic Context. <i>Molecular Biology and Evolution</i> , 2013, 30, 109-122.	3.5	31
818	Population structure in Japanese rice population. <i>Breeding Science</i> , 2013, 63, 49-57.	0.9	31
819	Functionally Relevant Microsatellite Markers From Chickpea Transcription Factor Genes for Efficient Genotyping Applications and Trait Association Mapping. <i>DNA Research</i> , 2013, 20, 355-374.	1.5	115
820	Allele frequencies for 40 autosomal SNP loci typed for US population samples using electrospray ionization mass spectrometry. <i>Croatian Medical Journal</i> , 2013, 54, 225-231.	0.2	5
821	Human Platelet Antigen Alleles in 998 Taiwanese Blood Donors Determined by Sequence-Specific Primer Polymerase Chain Reaction. <i>BioMed Research International</i> , 2013, 2013, 1-5.	0.9	13
822	Molecular diversity and population structure of Chinese green foxtail [<i>Setaria viridis</i> (L.) Beauv.] revealed by microsatellite analysis. <i>Journal of Experimental Botany</i> , 2013, 64, 3645-3656.	2.4	40
823	The genetic diversity of strawberry (<i>Fragaria ananassa</i> Duch.) hybrids based on ISSR markers - doi: 10.4025/actasciagron.v35i4.16737. <i>Acta Scientiarum - Agronomy</i> , 2013, 35, .	0.6	13
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825	Evaluation of genetic diversity and linkage disequilibrium in Korean-bred rice varieties using SSR markers. <i>Electronic Journal of Biotechnology</i> , 2013, 16, .	1.2	2
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827	Citrus (Rutaceae) SNP Markers Based on Competitive Allele-Specific PCR; Transferability Across the Aurantioideae Subfamily. <i>Applications in Plant Sciences</i> , 2013, 1, 1200406.	0.8	24
828	Isolation and Characterization of Novel EST-Derived Genic Markers in <i>Pisum sativum</i> (Fabaceae). <i>Applications in Plant Sciences</i> , 2013, 1, 1300026.	0.8	3

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830	Polymorphic Alu insertions in human populations of Bosnia and Herzegovina. <i>Annals of Human Biology</i> , 2013, 40, 181-185.	0.4	7
831	Microsatellite-based genetic diversity among accessions of maize landraces from Sinaloa in México. <i>Hereditas</i> , 2013, 150, 53-59.	0.5	28
832	Association Analysis for Quality Traits in a Diverse Panel of Chinese Sesame (<i>Sesamum indicum</i> L.) Germplasm. <i>Journal of Integrative Plant Biology</i> , 2013, 55, 745-758.	4.1	41
833	Identification of QTL in Spring Wheat Associated with Resistance to a Novel Isolate of <i>Pyrenophora tritici-repentis</i> . <i>Crop Science</i> , 2013, 53, 842-852.	0.8	32
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904	Genetic structure of <i>Korean</i> populations of bumblebees <i>Bombus ignitus</i> (<i>Hymenoptera: Apidae</i>) as revealed by microsatellite markers. <i>Entomological Research</i> , 2014, 44, 262-270.	0.6	3
905	Analysis of molecular genetic diversity and population structure in <i>Amaranthus</i> germplasm using SSR markers. <i>Plant Biosystems</i> , 2014, 148, 635-644.	0.8	30
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914	Genetic diversity and population structure of wild soybean (<i>Glycine soja</i> Sieb. and Zucc.) accessions in Korea. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2014, 12, S45-S48.	0.4	5
915	Application of <i>indica</i> – <i>japonica</i> single-nucleotide polymorphism markers for diversity analysis of <i>Oryza</i> AA genome species. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2014, 12, S36-S40.	0.4	2
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925	Association mapping of yield-related traits and SSR markers in wild soybean (<i>Glycine) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 502	0.9	47
926	Development of EST-SSR markers and construction of a linkage map in faba bean (<i>Vicia) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 502	0.9	30
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947	An analysis of genetic differentiation and geographical variation of spinach germplasm using SSR markers. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2014, 12, 185-190.	0.4	19
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958	Morphological Characteristics and SSR profilings of Soybean Landraces by collecting sites of Korea. <i>Han'guk Yukchong Hakhoe Chi</i> , 2014, 46, 353-363.	0.2	2
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972	Distribution and genetic status of brown bears in FYR Macedonia: implications for conservation. <i>Acta Theriologica</i> , 2014, 59, 119-128.	1.1	12

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973	Genetic diversity, population structure and differentiation of rice species from Niger and their potential for rice genetic resources conservation and enhancement. <i>Genetic Resources and Crop Evolution</i> , 2014, 61, 199-213.	0.8	16
974	The domestication and dispersal of the cultivated ramie (<i>Boehmeria nivea</i> (L.) Gaud. in Freyc.) determined by nuclear SSR marker analysis. <i>Genetic Resources and Crop Evolution</i> , 2014, 61, 55-67.	0.8	9
975	Synchronous evidence from both phenotypic and molecular signatures for the natural occurrence of sympatric hybridization between cultivated soybean (<i>Glycine max</i>) and its wild progenitor (<i>G. soja</i>). <i>Genetic Resources and Crop Evolution</i> , 2014, 61, 235-246.	0.8	2
976	Isolation and Characterization of 14 Polymorphic Microsatellite Loci in the Big-Headed Turtle (<i>Platysternon megacephalum</i>). <i>Biochemical Genetics</i> , 2014, 52, 203-208.	0.8	6
977	QTLs conferring FOV 7 resistance detected by linkage and association mapping in Upland cotton. <i>Euphytica</i> , 2014, 197, 237-249.	0.6	42
978	Characterization of the genetic changes in a multi-generational pedigree of an elite Canadian soybean cultivar. <i>Theoretical and Applied Genetics</i> , 2014, 127, 211-229.	1.8	15
979	Transforming growth factor beta1 (TGF β 1) polymorphisms and breast cancer risk. <i>Tumor Biology</i> , 2014, 35, 4757-4764.	0.8	11
980	Population structure and association mapping of yield contributing agronomic traits in foxtail millet. <i>Plant Cell Reports</i> , 2014, 33, 881-893.	2.8	71
981	Genetic diversity and structure of <i>Lilium pumilum</i> DC. in southeast of Qinghai-Tibet plateau. <i>Plant Systematics and Evolution</i> , 2014, 300, 1453.	0.3	18
982	The possible origin of thick stem in Chinese wild soybean (<i>Glycine soja</i>). <i>Plant Systematics and Evolution</i> , 2014, 300, 1079-1087.	0.3	0
983	Microsatellite based analysis of the genetic structure and diversity of <i>Capsicum chinense</i> in the Neotropics. <i>Genetic Resources and Crop Evolution</i> , 2014, 61, 741-755.	0.8	25
984	Transferability of molecular markers from major legumes to <i>Lathyrus</i> spp. for their application in mapping and diversity studies. <i>Molecular Biology Reports</i> , 2014, 41, 269-283.	1.0	34
985	Population structure and genetic diversity analysis of Indian and exotic rice (<i>Oryza sativa</i> L.) accessions using SSR markers. <i>Molecular Biology Reports</i> , 2014, 41, 4329-4339.	1.0	45
986	Diversity among melon (<i>Cucumis melo</i> L.) landraces from the Indo-Gangetic plains of India and their genetic relationship with USA melon cultivars. <i>Genetic Resources and Crop Evolution</i> , 2014, 61, 1189-1208.	0.8	23
987	Development and molecular characterization of genic molecular markers for grain protein and calcium content in finger millet (<i>Eleusine coracana</i> (L.) Gaertn.). <i>Molecular Biology Reports</i> , 2014, 41, 1189-1200.	1.0	65
988	Development of highly polymorphic simple sequence repeat markers using genome-wide microsatellite variant analysis in Foxtail millet [<i>Setaria italica</i> (L.) P. Beauv.]. <i>BMC Genomics</i> , 2014, 15, 78.	1.2	95
989	Genetic variation and population genetic structure of <i>Rhizophora apiculata</i> (Rhizophoraceae) in the greater Sunda Islands, Indonesia using microsatellite markers. <i>Journal of Plant Research</i> , 2014, 127, 287-297.	1.2	28
990	Fine genetic characterization of elite maize germplasm using high-throughput SNP genotyping. <i>Theoretical and Applied Genetics</i> , 2014, 127, 621-631.	1.8	78

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991	Genetic diversity and linkage disequilibrium analysis in elite sugar beet breeding lines and wild beet accessions. <i>Theoretical and Applied Genetics</i> , 2014, 127, 559-571.	1.8	18
992	Transcriptome sequencing for high throughput SNP development and genetic mapping in Pea. <i>BMC Genomics</i> , 2014, 15, 126.	1.2	104
993	Development of STS and CAPS markers for variety identification and genetic diversity analysis of tea germplasm in Taiwan. , 2014, 55, 12.		22
994	Assessment of genetic diversity in salt-tolerant rice and its wild relatives for ten SSR loci and one allele mining primer of salt gene located on 1st chromosome. <i>Plant Systematics and Evolution</i> , 2014, 300, 1741-1747.	0.3	30
995	An efficient and cost-effective approach for genic microsatellite marker-based large-scale trait association mapping: identification of candidate genes for seed weight in chickpea. <i>Molecular Breeding</i> , 2014, 34, 241-265.	1.0	35
996	Genetic diversity and population structure in the US Upland cotton (<i>Gossypium hirsutum</i> L.). <i>Theoretical and Applied Genetics</i> , 2014, 127, 283-295.	1.8	151
997	Microsatellite markers reveal genetic diversity of wild soybean in different habitats and implications for conservation strategies (<i>Glycine soja</i>) in China. <i>Conservation Genetics</i> , 2014, 15, 605-618.	0.8	6
998	Development of mapped simple sequence repeat markers from common bean (<i>Phaseolus vulgaris</i> L.) based on genome sequences of a Chinese landrace and diversity evaluation. <i>Molecular Breeding</i> , 2014, 33, 489-496.	1.0	16
999	Population structure and linkage disequilibrium of ICRISAT foxtail millet (<i>Setaria italica</i> (L.)ÂP. Beauv.) core collection. <i>Euphytica</i> , 2014, 196, 423-435.	0.6	16
1000	Genome-wide analysis of <sc>I</sc>talian sheep diversity reveals a strong geographic pattern and cryptic relationships between breeds. <i>Animal Genetics</i> , 2014, 45, 256-266.	0.6	84
1001	Microsatellite analysis of Icelandic populations of the poplar fungal pathogen <i>Melampsora larici-populina</i> shows evidence of repeated colonization events. <i>European Journal of Plant Pathology</i> , 2014, 139, 597-608.	0.8	2
1002	Characterization of <i>Pseudoperonospora cubensis</i> isolates from Europe and Asia using ISSR and SRAP molecular markers. <i>European Journal of Plant Pathology</i> , 2014, 139, 641-653.	0.8	23
1003	Association analysis of bacterial leaf spot resistance and SNP markers derived from expressed sequence tags (ESTs) in lettuce (<i>Lactuca sativa</i> L.). <i>Molecular Breeding</i> , 2014, 34, 997-1006.	1.0	11
1004	Genetic diversity revealed by EST-SSR markers in carob tree (<i>Ceratonia siliqua</i> L.). <i>Biochemical Systematics and Ecology</i> , 2014, 55, 205-211.	0.6	16
1005	Genetic diversity in <i>Vicia faba</i> L. populations cultivated in Tunisia revealed by simple sequence repeat analysis. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2014, 12, 278-285.	0.4	7
1006	Identification, characterisation and discriminatory power of microsatellite markers in the parasitic weed <i><sc>O</sc>robancha cumana</i>. <i>Weed Research</i> , 2014, 54, 120-132.	0.8	18
1007	Comparative genomics and association mapping approaches for opaque2 modifier genes in finger millet accessions using genic, genomic and candidate gene-based simple sequence repeat markers. <i>Molecular Breeding</i> , 2014, 34, 1261-1279.	1.0	61
1008	Genetic assessment of safflower (<i><sc>C</sc>arthamus tinctorius</i> <sc>L</sc>.) collection with microsatellite markers acquired via pyrosequencing method. <i>Molecular Ecology Resources</i> , 2014, 14, 69-78.	2.2	37

#	ARTICLE	IF	CITATIONS
1009	Development and characterization of a new set of 164 polymorphic <i>EST</i> and <i>SSR</i> markers for diversity and breeding studies in rubber tree (<i>Hevea brasiliensis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 11 50 737 T		
1010	Developing core collections to optimize the management and the exploitation of diversity of the coffee <i>Coffea canephora</i> . <i>Genetica</i> , 2014, 142, 185-199.	0.5	33
1011	Diversity characterization and association analysis of agronomic traits in a Chinese peanut (<i>Arachis hypogaea</i> L.) mini-core collection. <i>Journal of Integrative Plant Biology</i> , 2014, 56, 159-169.	4.1	53
1012	Population genetic parameters of brown bears in western Serbia: implications for research and conservation. <i>Ursus</i> , 2014, 25, 34-43.	0.3	3
1013	Pharmacogenomic assessment of cisplatin-based chemotherapy outcomes in ovarian cancer. <i>Pharmacogenomics</i> , 2014, 15, 329-337.	0.6	49
1014	Determination of heterotic groups for tropical <i>Indica</i> hybrid rice germplasm. <i>Theoretical and Applied Genetics</i> , 2014, 127, 407-417.	1.8	52
1015	Population genomic analyses from low-coverage <i>RAD</i> seq data: a case study on the non-model cucurbit bottle gourd. <i>Plant Journal</i> , 2014, 77, 430-442.	2.8	80
1016	Identification of the Worldwide Olive Germplasm Bank of C�rdoba (Spain) using <i>SSR</i> and morphological markers. <i>Tree Genetics and Genomes</i> , 2014, 10, 141-155.	0.6	163
1017	Development of Genomic <i>SSR</i> Markers and Molecular Characterization of <i>Magnaporthe oryzae</i> Isolates from Wheat in Brazil. <i>Biochemical Genetics</i> , 2014, 52, 52-70.	0.8	11
1018	Haplotype diversity and evolutionary history of the <i>Lr34</i> locus of wheat. <i>Molecular Breeding</i> , 2014, 33, 639-655.	1.0	13
1019	Molecular Epidemiology of Ascariasis: A Global Perspective on the Transmission Dynamics of <i>Ascaris</i> in People and Pigs. <i>Journal of Infectious Diseases</i> , 2014, 210, 932-941.	1.9	109
1020	Genetic diversity and association mapping of iron and zinc concentrations in chickpea (<i>Cicer</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 11 50 737 T	0.9	111
1021	Genetic structure of cherry fruit fly (<i>Rhagoletis cingulata</i>) populations across managed, unmanaged, and natural habitats. <i>Entomologia Experimentalis Et Applicata</i> , 2014, 150, 157-165.	0.7	9
1022	ISSR-Based Molecular Characterization of an Elite Germplasm Collection of Sweet Potato (<i>Ipomoea</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 11 50 737 T	1.7	9
1023	Allele and haplotype frequencies of <i>HLA-DPA1</i> and <i>DPB1</i> in the population of Guadeloupe. <i>Tissue Antigens</i> , 2014, 83, 147-153.	1.0	6
1024	Detecting genotypic changes associated with selective mortality at sea in Atlantic salmon: polygenic multilocus analysis surpasses genome scan. <i>Molecular Ecology</i> , 2014, 23, 4444-4457.	2.0	60
1025	Ecological adaptation and reproductive isolation in sympatry: genetic and phenotypic evidence for native host races of <i>Rhagoletis pomonella</i> . <i>Molecular Ecology</i> , 2014, 23, 688-704.	2.0	57
1026	Analysis of <i>ATP6</i> sequence diversity in the <i>Triticum</i> and <i>Aegilops</i> species group reveals the crucial role of rearrangement in mitochondrial genome evolution. <i>Genome</i> , 2014, 57, 279-288.	0.9	2

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1027	Genetic diversity and clonal variation within the main Sicilian olive cultivars based on morphological traits and microsatellite markers. <i>Scientia Horticulturae</i> , 2014, 180, 130-138.	1.7	43
1028	A Look into Genetic Diversity of Enset (<i>Ensete ventricosum</i> (Welw.) Cheesman) Using Transferable Microsatellite Sequences of Banana in Ethiopia. <i>Journal of Crop Improvement</i> , 2014, 28, 159-183.	0.9	17
1029	Polymorphic microsatellite markers for a wind-dispersed tropical tree species, <i>Triplaris cumingiana</i> (Polygonaceae). <i>Applications in Plant Sciences</i> , 2014, 2, 1400051.	0.8	2
1030	Genetic diversity of <i>Vicia faba</i> L. based on random amplified polymorphic DNA and simple sequence repeat markers. <i>Acta Botanica Gallica</i> , 2014, 161, 151-158.	0.9	5
1031	Highly efficient genomics-assisted development of a library of introgression lines of <i>Solanum pimpinellifolium</i> . <i>Molecular Breeding</i> , 2014, 34, 1817-1831.	1.0	34
1032	Molecular and phenotypic characterization of variation related to pea enation mosaic virus resistance in lentil (<i>Lens culinaris</i> Medik.). <i>Canadian Journal of Plant Science</i> , 2014, 94, 1333-1344.	0.3	2
1033	Genome-Wide Association Study Dissects the Genetic Architecture of Seed Weight and Seed Quality in Rapeseed (<i>Brassica napus</i> L.). <i>DNA Research</i> , 2014, 21, 355-367.	1.5	247
1034	Allelic Variation in Loci for Adaptive Response and Its Effect on Agronomical Traits in Chinese Wheat (<i>Triticum aestivum</i> L.). <i>Journal of Integrative Agriculture</i> , 2014, 13, 1469-1476.	1.7	2
1035	Genetic diversity and population structure study of drumstick (<i>Moringa oleifera</i> Lam.) using morphological and SSR markers. <i>Industrial Crops and Products</i> , 2014, 60, 316-325.	2.5	51
1036	Population data of 12 X-chromosome STR loci in Yanbian Korean samples from China. <i>Forensic Science International: Genetics</i> , 2014, 13, 143-144.	1.6	13
1037	Molecular characterization of olive (<i>Olea europaea</i> L.) Sicilian cultivars using SSR markers. <i>Biochemical Systematics and Ecology</i> , 2014, 57, 15-19.	0.6	28
1038	Exploiting EST databases for the development and characterization of EST-SSR markers in blueberry (<i>Vaccinium</i>) and their cross-species transferability in <i>Vaccinium</i> spp. <i>Scientia Horticulturae</i> , 2014, 176, 319-329.	1.7	30
1039	Genetic Diversity of Farmers' Preferred Sorghum Accessions and Improved Lines from ICRISAT Reveal a Disconnect Between Innovation and Technology Transfer. <i>Journal of Crop Science and Biotechnology</i> , 2014, 17, 97-102.	0.7	0
1040	Homoeologous duplicated regions are involved in quantitative resistance of <i>Brassica napus</i> to stem canker. <i>BMC Genomics</i> , 2014, 15, 498.	1.2	69
1041	Nuclear and chloroplast diversity and phenotypic distribution of rice (<i>Oryza sativa</i> L.) germplasm from the democratic people's republic of Korea (DPRK; North Korea). <i>Rice</i> , 2014, 7, 7.	1.7	14
1042	Molecular diversity of the entomopathogenic fungal <i>Metarhizium</i> community within an agroecosystem. <i>Journal of Invertebrate Pathology</i> , 2014, 123, 6-12.	1.5	60
1043	Potential of SNP markers for the characterization of Brazilian cassava germplasm. <i>Theoretical and Applied Genetics</i> , 2014, 127, 1423-1440.	1.8	34
1044	Development and characterization of a new 12-plex ChrX miniSTR system. <i>International Journal of Legal Medicine</i> , 2014, 128, 595-598.	1.2	8

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1045	Association analysis of seed longevity in rice under conventional and high-temperature germination conditions. <i>Plant Systematics and Evolution</i> , 2014, 300, 389-402.	0.3	13
1046	Selection of American hazelnut as a potential oilseed crop. <i>Agroforestry Systems</i> , 2014, 88, 449-459.	0.9	9
1047	Assessment of genetic diversity among sorghum landraces and their wild/weedy relatives in western Kenya using simple sequence repeat (SSR) markers. <i>Conservation Genetics</i> , 2014, 15, 1269-1280.	0.8	3
1048	Effect of the inbreeding depression in progeny fitness of runner bean (<i>Phaseolus coccineus</i> L.) and its implications for breeding. <i>Euphytica</i> , 2014, 200, 413-428.	0.6	11
1049	New cDNA-SSR markers in the narrow-leaved vetch (<i>Vicia sativa</i> subsp. <i>nigra</i>) using 454 pyrosequencing. <i>Molecular Breeding</i> , 2014, 33, 749-754.	1.0	10
1050	One-step reconstruction of multi-generation pedigree networks in apple (<i>Malus domestica</i> Borkh.) and the parentage of Golden Delicious. <i>Molecular Breeding</i> , 2014, 34, 511-524.	1.0	21
1051	F1 hybrid of cultivated apple (<i>Malus domestica</i>) and European pear (<i>Pyrus communis</i>) with fertile F2 offspring. <i>Molecular Breeding</i> , 2014, 34, 817-828.	1.0	14
1052	Association mapping of starch physicochemical properties with starch synthesis-related gene markers in nonwaxy rice (<i>Oryza sativa</i> L.). <i>Molecular Breeding</i> , 2014, 34, 1747-1763.	1.0	60
1053	Association mapping of agro-morphological characters among the global collection of finger millet genotypes using genomic SSR markers. <i>Molecular Biology Reports</i> , 2014, 41, 5287-5297.	1.0	51
1054	Single nucleotide polymorphisms in genes encoding toll-like receptors 7, 8 and 9 in Danish patients with systemic lupus erythematosus. <i>Molecular Biology Reports</i> , 2014, 41, 5755-5763.	1.0	54
1055	Analysis of in situ diversity and population structure in Ethiopian cultivated <i>Sorghum bicolor</i> (L.) landraces using phenotypic traits and SSR markers. <i>SpringerPlus</i> , 2014, 3, 212.	1.2	51
1056	Development of genic SSR markers from transcriptome sequencing of pear buds. <i>Journal of Zhejiang University: Science B</i> , 2014, 15, 303-312.	1.3	23
1057	Genome distribution and validation of novel microsatellite markers of <i>Fusarium verticillioides</i> and their transferability to other <i>Fusarium</i> species. <i>Journal of Microbiological Methods</i> , 2014, 101, 18-23.	0.7	19
1058	A footprint of past climate change on the diversity and population structure of <i>Miscanthus sinensis</i> . <i>Annals of Botany</i> , 2014, 114, 97-107.	1.4	87
1059	Characterization of masson pine (<i>Pinus massoniana</i> Lamb.) microsatellite DNA by 454 genome shotgun sequencing. <i>Tree Genetics and Genomes</i> , 2014, 10, 429-437.	0.6	14
1060	Genome-wide characterization and selection of expressed sequence tag simple sequence repeat primers for optimized marker distribution and reliability in peach. <i>Tree Genetics and Genomes</i> , 2014, 10, 1271-1279.	0.6	10
1061	Genetic Diversity and Population Structure Among Pea (<i>Pisum sativum</i> L.) Cultivars as Revealed by Simple Sequence Repeat and Novel Genic Markers. <i>Molecular Biotechnology</i> , 2014, 56, 925-938.	1.3	26
1062	Isolation and characterization of polymorphic microsatellites in the Tibetan cypress <i>Cupressus gigantea</i> using paired-end Illumina shotgun sequencing. <i>Conservation Genetics Resources</i> , 2014, 6, 795-797.	0.4	5

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1063	Genetic analysis and molecular characterization of Chinese sesame (<i>Sesamum indicum</i> L.) cultivars using Insertion-Deletion (InDel) and Simple Sequence Repeat (SSR) markers. <i>BMC Genetics</i> , 2014, 15, 35.	2.7	77
1064	Genomic regions involved in yield potential detected by genome-wide association analysis in Japanese high-yielding rice cultivars. <i>BMC Genomics</i> , 2014, 15, 346.	1.2	29
1065	Genome-wide association for grain morphology in synthetic hexaploid wheats using digital imaging analysis. <i>BMC Plant Biology</i> , 2014, 14, 128.	1.6	102
1066	Identification and validation of functional markers in a global rice collection by association mapping. <i>Genome</i> , 2014, 57, 355-362.	0.9	4
1067	Development of 5123 Intron-Length Polymorphic Markers for Large-Scale Genotyping Applications in Foxtail Millet. <i>DNA Research</i> , 2014, 21, 41-52.	1.5	109
1068	Molecular Diversity and Association Analysis of Drought and Salt Tolerance in <i>Gossypium hirsutum</i> L. Germplasm. <i>Journal of Integrative Agriculture</i> , 2014, 13, 1845-1853.	1.7	49
1069	Small-scale patterns in snowmelt timing affect gene flow and the distribution of genetic diversity in the alpine dwarf shrub <i>Salix herbacea</i> . <i>Heredity</i> , 2014, 113, 233-239.	1.2	101
1070	Development and characterization of microsatellites of an important medicinal plant <i>Orthosiphon stamineus</i> (misai kucing). <i>Biochemical Systematics and Ecology</i> , 2014, 55, 317-321.	0.6	3
1071	Structured diversity using EST-PCR and EST-SSR markers in a set of wild blueberry clones and cultivars. <i>Biochemical Systematics and Ecology</i> , 2014, 54, 337-347.	0.6	23
1072	Assessment of genetic diversity of Korean <i>Miscanthus</i> using morphological traits and SSR markers. <i>Biomass and Bioenergy</i> , 2014, 66, 81-92.	2.9	25
1073	Genetic Diversity of DXP Population Yield Component in Oil Palm's Paternal Half-sib Family based on Microsatellite Markers. <i>Energy Procedia</i> , 2014, 47, 196-203.	1.8	3
1074	Establishment of the integrated applied core collection and its comparison with mini core collection in soybean (<i>Glycine max</i>). <i>Crop Journal</i> , 2014, 2, 38-45.	2.3	23
1075	Evaluating an interspecific <i>Helianthus annuus</i> – <i>Helianthus tuberosus</i> population for use in a perennial sunflower breeding program. <i>Field Crops Research</i> , 2014, 155, 254-264.	2.3	21
1076	Genotyping and development of single-nucleotide polymorphism (SNP) markers associated with blast resistance genes in rice using GoldenGate assay. <i>Molecular Breeding</i> , 2014, 34, 1449-1463.	1.0	11
1077	Distribution of Weedy Red Rice (<i>Oryza sativa</i>) Resistant to Imidazolinone Herbicides and its Relationship to Rice Cultivars and Wild <i>Oryza</i> Species. <i>Weed Science</i> , 2014, 62, 280-293.	0.8	18
1078	Genetic relationships and structure among open-pollinated maize varieties adapted to eastern and southern Africa using microsatellite markers. <i>Molecular Breeding</i> , 2014, 34, 1423-1435.	1.0	21
1079	Natural and human-mediated selection in a landrace of Thai rice (<i>Oryza sativa</i>). <i>Annals of Applied Biology</i> , 2014, 165, 280-292.	1.3	14
1080	Target region amplification polymorphism (TRAP) for assessing genetic diversity and marker-trait associations in chickpea (<i>Cicer arietinum</i> L.) germplasm. <i>Genetic Resources and Crop Evolution</i> , 2014, 61, 965-977.	0.8	8

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1081	The first set of expressed sequence tags (EST) from the medicinal mushroom <i>Agaricus subrufescens</i> delivers resource for gene discovery and marker development. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 7879-7892.	1.7	13
1082	Genetic diversity and association mapping of seed vigor in rice (<i>Oryza sativa</i> L.). <i>Planta</i> , 2014, 239, 1309-1319.	1.6	93
1083	Exploration of presence/absence variation and corresponding polymorphic markers in soybean genome. <i>Journal of Integrative Plant Biology</i> , 2014, 56, 1009-1019.	4.1	21
1084	Development of polymorphic EST-SSR markers by sequence alignment in <i>Frankliniella occidentalis</i> (Pergande). <i>Journal of Asia-Pacific Entomology</i> , 2014, 17, 581-585.	0.4	3
1085	Genetic distribution on 20 STR loci from the Han population in Shanghai, China. <i>Forensic Science International: Genetics</i> , 2014, 9, e30-e31.	1.6	36
1086	Comparative assessment of genomic SSR, EST-SSR and EST-SNP markers for evaluation of the genetic diversity of wild and cultured Pacific oyster, <i>Crassostrea gigas</i> Thunberg. <i>Aquaculture</i> , 2014, 420-421, S85-S91.	1.7	25
1087	MOLECULAR DIVERSITY ASSESSMENT OF CUMIN ECOTYPES USING AFLP MARKERS. <i>Acta Horticulturae</i> , 2014, , 263-270.	0.1	0
1088	ANALYSIS OF PINOT CULTIVARS BY MICROSATELLITE MARKERS. <i>Acta Horticulturae</i> , 2014, , 627-638.	0.1	0
1089	BUILDING A QUALITY NICHE FOR CARIBBEAN HOT PEPPERS. <i>Acta Horticulturae</i> , 2014, , 109-118.	0.1	0
1090	Comprehensive Transcriptome Assembly of Chickpea (<i>Cicer arietinum</i> L.) Using Sanger and Next Generation Sequencing Platforms: Development and Applications. <i>PLoS ONE</i> , 2014, 9, e86039.	1.1	87
1091	Genetic Diversity for Stripe Rust Resistance in Wheat Landraces and Identification of Accessions with Resistance to Stem Rust and Stripe Rust. <i>Crop Science</i> , 2014, 54, 2131-2139.	0.8	22
1092	Phylogenetic relationships among Iranian and Spanish date palms (<i>Phoenix dactylifera</i> L.) revealed by microsatellite markers. <i>Journal of Horticultural Science and Biotechnology</i> , 2014, 89, 115-120.	0.9	2
1093	Assessment of genetic diversity and genetic relationships among 46 Iranian and non-Iranian dwarfing rootstocks of apple (<i>Malus domestica</i> Borkh.) using microsatellite markers. <i>Journal of Horticultural Science and Biotechnology</i> , 2014, 89, 121-129.	0.9	1
1094	Genetic and antigenic diversity of <i>Theileria parva</i> in cattle in Eastern and Southern zones of Tanzania. A study to support control of East Coast fever. <i>Parasitology</i> , 2015, 142, 698-705.	0.7	10
1095	Assessment of recent bottlenecks and estimation of effective population size in the Ethiopian wild sorghum using simple sequence repeat allele diversity and mutation models. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2015, 13, 274-281.	0.4	4
1096	Genome-wide genetic diversity, population structure and admixture analysis in African and Asian cattle breeds. <i>Animal</i> , 2015, 9, 218-226.	1.3	66
1097	Genetic Diversity of Main Inbred Indica Rice Varieties Applied in Guangdong Province as Revealed by Molecular Marker. <i>Rice Science</i> , 2015, 22, 1-8.	1.7	11
1098	Genetic variation and association mapping for 12 agronomic traits in indica rice. <i>BMC Genomics</i> , 2015, 16, 1067.	1.2	76

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1099	Isolation and Characterization of Microsatellite Loci and Genetic Diversity in Cassava (<i>Manihot</i>)	0.9	2
1100	Genetic diversity and DNA fingerprinting in jute (<i>Corchorus</i> spp.) based on SSR markers. <i>Crop Journal</i> , 2015, 3, 416-422.	2.3	32
1101	Hybridization and the spread of the apple maggot fly, <i>Rhagoletis pomonella</i> (Diptera)	1.5	20
1102	Population Structure of <i>Pythium irregulare</i> , <i>P. ultimum</i> , and <i>P. sylvaticum</i> in Forest Nursery Soils of Oregon and Washington. <i>Phytopathology</i> , 2015, 105, 684-694.	1.1	12
1103	Evaluation of a Diverse, Worldwide Collection of Wild, Cultivated, and Landrace Pepper (<i>Capsicum</i>)	1.1	21
1104	Drought susceptibility of modern rice varieties: an effect of linkage of drought tolerance with undesirable traits. <i>Scientific Reports</i> , 2015, 5, 14799.	1.6	145
1105	Example of the application the microsatellite DNA fragments in the study of farmed European catfish (<i>Silurus glanis</i> , L.) broodstock. <i>Archives of Polish Fisheries</i> , 2015, 23, 91-99.	0.6	1
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1119	<sc>EST</sc>â€‹<sc>SSR</sc> analysis provides insights about genetic relatedness, population structure and gene flow in grass pea (<i>Lathyrus sativus</i>). <i>Plant Breeding</i> , 2015, 134, 338-344.	1.0	15
1120	Development, characterization and mapping of microsatellite markers for lentil (<i>Lens culinaris</i>) Tj ETQq1 1 0,784314 rgBT /Overdell	1.0	27
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1125	Genetic characterization of red-colored heartwood genotypes of Chinese fir using simple sequence repeat (SSR) markers. <i>Genetics and Molecular Research</i> , 2015, 14, 18552-18561.	0.3	12
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1166	A Genome-wide Combinatorial Strategy Dissects Complex Genetic Architecture of Seed Coat Color in Chickpea. <i>Frontiers in Plant Science</i> , 2015, 6, 979.	1.7	25
1167	Association Analysis of Grain-setting Rates in Apical and Basal Spikelets in Bread Wheat (<i>Triticum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.7	13
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1202	Absence of Putative Artemisinin Resistance Mutations Among <i>Plasmodium falciparum</i> in Sub-Saharan Africa: A Molecular Epidemiologic Study. <i>Journal of Infectious Diseases</i> , 2015, 211, 680-688.	1.9	235
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1232	Association mapping of seed quality traits in <i>Brassica napus</i> L. using GWAS and candidate QTL approaches. <i>Molecular Breeding</i> , 2015, 35, 1.	1.0	51
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1242	SSR marker development, genetic diversity and population structure analysis of Bambara groundnut [<i>Vigna subterranea</i> (L.) Verdc.] landraces. <i>Genetic Resources and Crop Evolution</i> , 2015, 62, 1225-1243.	0.8	48

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1243	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.	1.8	14
1244	Novel Chloroplast Microsatellite (cpSSR) Markers for Genetic Diversity Assessment of Cultivated and Wild <i>Hevea</i> Rubber. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 1486-1498.	1.0	31
1245	Comparative Assessment of Synthetic-derived and Conventional Bread Wheat Advanced Lines Under Osmotic Stress and Implications for Molecular Analysis. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 1907-1917.	1.0	14
1246	Development and characterization of microsatellite markers in sawih tree (<i>Duabanga moluccana</i>) Tj ETQq1 1 0.784314 rgBT /Overlook 163-165.	1.4	2
1247	Genetic analysis of four European huchen (<i>Hucho hucho</i> Linnaeus, 1758) broodstocks from Poland, Germany, Slovakia, and Ukraine: implication for conservation. <i>Journal of Applied Genetics</i> , 2015, 56, 469-480.	1.0	12
1248	Development of Novel Microsatellite Markers in <i>Jatropha curcas</i> and Evaluation of Their Cross-Species Transferability. <i>Proceedings of the National Academy of Sciences India Section B - Biological Sciences</i> , 2015, 85, 1011-1016.	0.4	2
1249	Assessment of genetic diversity and population structure of mung bean (<i>Vigna radiata</i>) germplasm using EST-based and genomic SSR markers. <i>Gene</i> , 2015, 566, 175-183.	1.0	42
1250	Variability of candidate genes, genetic structure and association with sugar accumulation and climacteric behavior in a broad germplasm collection of melon (<i>Cucumis melo</i> L.). <i>BMC Genetics</i> , 2015, 16, 28.	2.7	72
1251	Population structure and genetic diversity characterization of a sunflower association mapping population using SSR and SNP markers. <i>BMC Plant Biology</i> , 2015, 15, 52.	1.6	91
1252	Genetic Diversity and Population Structure Analysis Between Indian Red Jungle Fowl and Domestic Chicken Using Microsatellite Markers. <i>Animal Biotechnology</i> , 2015, 26, 201-210.	0.7	13
1253	Genetic diversity and elite gene introgression reveal the japonica rice breeding in northern China. <i>Journal of Integrative Agriculture</i> , 2015, 14, 811-822.	1.7	6
1254	The AVRDC "The World Vegetable Center" mungbean (<i>Vigna radiata</i>) core and mini core collections. <i>BMC Genomics</i> , 2015, 16, 344.	1.2	95
1255	Genome-wide identification of SSR and SNP markers from the non-heading Chinese cabbage for comparative genomic analyses. <i>BMC Genomics</i> , 2015, 16, 328.	1.2	48
1256	Identification of a diverse mini-core panel of Indian rice germplasm based on genotyping using microsatellite markers. <i>Plant Breeding</i> , 2015, 134, 164-171.	1.0	36
1257	Genetic variability in trait-specific rice germplasm groups based on coefficient of parentage, SSR markers and fertility restoration. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2015, 13, 56-67.	0.4	1
1258	Genome-wide conserved non-coding microsatellite (CNMS) marker-based integrative genetical genomics for quantitative dissection of seed weight in chickpea. <i>Journal of Experimental Botany</i> , 2015, 66, 1271-1290.	2.4	46
1259	Population structure and genetic diversity of Brazilian popcorn germplasm inferred by microsatellite markers. <i>Electronic Journal of Biotechnology</i> , 2015, 18, 181-187.	1.2	19
1260	Development of SSR markers and genetic diversity analysis in enset (<i>Ensete ventricosum</i> (Welw.)) Tj ETQq1 1 0.784314 rgBT /Overlook 2.7	2.7	42

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1261	Genetic diversity and population structure in cultivated and weedy types of <i>Perilla</i> in East Asia and other countries as revealed by SSR markers. <i>Horticulture Environment and Biotechnology</i> , 2015, 56, 524-534.	0.7	17
1262	Genome-wide insertion-deletion (InDel) marker discovery and genotyping for genomics-assisted breeding applications in chickpea. <i>DNA Research</i> , 2015, 22, 377-386.	1.5	53
1263	Development of SSR markers and assessment of genetic diversity of adzuki bean in the Chinese germplasm collection. <i>Molecular Breeding</i> , 2015, 35, 1.	1.0	16
1264	Genetic diversity, population structure, and association mapping of biomass traits in maize with simple sequence repeat markers. <i>Genes and Genomics</i> , 2015, 37, 725-735.	0.5	16
1265	Genetic relationships among diverse spray- and standard-type chrysanthemum varieties and their derived radio-mutants determined using AFLPs. <i>Horticulture Environment and Biotechnology</i> , 2015, 56, 498-505.	0.7	2
1266	Identification of EST-SSRs and molecular diversity analysis in <i>Mentha piperita</i> . <i>Crop Journal</i> , 2015, 3, 335-342.	2.3	31
1267	Seeds morpho-colourimetric analysis as complementary method to molecular characterization of melon diversity. <i>Scientia Horticulturae</i> , 2015, 192, 441-452.	1.7	23
1268	Soft computing model on genetic diversity and pathotype differentiation of pathogens: A novel approach. <i>Electronic Journal of Biotechnology</i> , 2015, 18, 347-354.	1.2	1
1269	Genetic diversity of 15 autosomal STR loci in the population of Southern Punjab Pakistan. <i>Forensic Science International: Genetics</i> , 2015, 19, e1-e2.	1.6	7
1270	Assessment of wheat variety distinctness using SSR markers. <i>Journal of Integrative Agriculture</i> , 2015, 14, 1923-1935.	1.7	30
1271	Simple sequence repeat analysis of genetic diversity among <i>Acyrtosiphon pisum</i> carboxylase inhibitor-resistant and susceptible <i>Echinochloa crusgalli</i> and <i>Aoryzicola</i> populations in <i>Korea</i> . <i>Weed Research</i> , 2015, 55, 90-100.	0.8	10
1272	Molecular Characterization of Exotic and Indigenous Maize Inbreds for Biofortification with Kernel Carotenoids. <i>Food Biotechnology</i> , 2015, 29, 276-295.	0.6	19
1273	HRM analysis of chloroplast and mitochondrial DNA revealed additional genetic variability in <i>Prunus</i> . <i>Scientia Horticulturae</i> , 2015, 197, 124-129.	1.7	5
1274	Screening for simple sequence repeat markers in <i>Puccinia striiformis tritici</i> based on genomic sequence. <i>Journal of Zhejiang University: Science B</i> , 2015, 16, 727-732.	1.3	14
1275	Discrimination of the commercial Korean native chicken population using microsatellite markers. <i>Journal of Animal Science and Technology</i> , 2015, 57, 5.	0.8	18
1276	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.	2.3	63
1277	Genetic structure, linkage disequilibrium and association mapping of salt tolerance in japonica rice germplasm at the seedling stage. <i>Molecular Breeding</i> , 2015, 35, 1.	1.0	26
1278	CNMS: The preferred genic markers for comparative genomic, molecular phylogenetic, functional genetic diversity and differential gene regulatory expression analyses in chickpea. <i>Journal of Biosciences</i> , 2015, 40, 579-592.	0.5	0

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1279	Mitochondrial SSRs and their utility in distinguishing wild species, CMS lines and maintainer lines in pigeonpea (<i>Cajanus cajan</i> L.). <i>Euphytica</i> , 2015, 206, 737-746.	0.6	14
1280	Mapping quantitative trait loci associated with soybean resistance to common cutworm and soybean compensatory growth after defoliation using SNP marker-based genome-wide association analysis. <i>Molecular Breeding</i> , 2015, 35, 1.	1.0	10
1281	Mediterranean basin <i>Ficus carica</i> L.: from genetic diversity and structure to authentication of a Protected Designation of Origin cultivar using microsatellite markers. <i>Trees - Structure and Function</i> , 2015, 29, 1959-1971.	0.9	16
1282	Informativeness of minisatellite and microsatellite markers for genetic analysis in papaya. <i>Genetica</i> , 2015, 143, 613-631.	0.5	2
1283	Genetic diversity of diploid <i>Triticum</i> species in Iran assessed using inter-retroelement amplified polymorphisms (IRAP) markers. <i>Biologia (Poland)</i> , 2015, 70, 52-60.	0.8	15
1284	Genome scanning of Asiatic <i>Vigna</i> species for discerning population genetic structure based on microsatellite variation. <i>Molecular Breeding</i> , 2015, 35, 1.	1.0	29
1285	Development of 185 polymorphic simple sequence repeat (SSR) markers from walnut (<i>Juglans regia</i> L.). <i>Scientia Horticulturae</i> , 2015, 194, 160-167.	1.7	23
1286	Genetic diversity and population structure of an Italian landrace of runner bean (<i>Phaseolus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 5 8.5 11	0.5	11
1287	Fingerprinting 128 Chinese clonal tea cultivars using SSR markers provides new insights into their pedigree relationships. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	45
1288	Microsatellite markers developed by next-generation sequencing differentiate inbred lines of <i>Apis mellifera</i> . <i>Journal of Asia-Pacific Entomology</i> , 2015, 18, 801-805.	0.4	4
1289	Molecular phylogenetic analysis of Chinese indigenous blue-shelled chickens inferred from whole genomic region of the <i>SLCO1B3</i> gene. <i>Poultry Science</i> , 2015, 94, 1776-1786.	1.5	3
1290	Genetic diversity and population structure analysis of mandarin germplasm by nuclear, chloroplastic and mitochondrial markers. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	31
1291	Expression patterns, molecular markers and genetic diversity of insect-susceptible and resistant <i>Barbarea</i> genotypes by comparative transcriptome analysis. <i>BMC Genomics</i> , 2015, 16, 486.	1.2	16
1292	New Microsatellite Markers for <i>Campanula pyramidalis</i> (Campanulaceae) and Cross-Amplification in Closely Related Species. <i>Applications in Plant Sciences</i> , 2015, 3, 1400117.	0.8	5
1293	Genetic characterization of the wheat association mapping initiative (WAMI) panel for dissection of complex traits in spring wheat. <i>Theoretical and Applied Genetics</i> , 2015, 128, 453-464.	1.8	177
1294	Genetic characterization of chestnut (<i>Castanea sativa</i> Mill.) orchards and traditional nut varieties in El Bierzo, a glacial refuge and major cultivation site in northwestern Spain. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	12
1295	Identification of groundnut (<i>Arachis hypogaea</i>) SSR markers suitable for multiple resistance traits QTL mapping in African germplasm. <i>Electronic Journal of Biotechnology</i> , 2015, 18, 61-67.	1.2	15
1296	Genome-wide association study (GWAS) of carbon isotope ratio ($\delta^{13}C$) in diverse soybean [<i>Glycine max</i> (L.) Merr.] genotypes. <i>Theoretical and Applied Genetics</i> , 2015, 128, 73-91.	1.8	89

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1297	Genetic polymorphism of ten MiniSTR loci in the population of Punjab Pakistan for forensic application. <i>International Journal of Legal Medicine</i> , 2015, 129, 937-942.	1.2	4
1298	Molecular Characterization and Population Structure of the Macaw Palm, <i>Acrocomia aculeata</i> (Arecaceae), Ex Situ Germplasm Collection Using Microsatellites Markers. <i>Journal of Heredity</i> , 2015, 106, 102-112.	1.0	35
1299	Genome-wide association study for grain yield and related traits in an elite spring wheat population grown in temperate irrigated environments. <i>Theoretical and Applied Genetics</i> , 2015, 128, 353-363.	1.8	400
1300	Disjunct, highly divergent genetic lineages within two rare <i>Eremophila</i> (Scrophulariaceae: Myoporeae) species in a biodiversity hotspot: implications for taxonomy and conservation. <i>Botanical Journal of the Linnean Society</i> , 2015, 177, 96-111.	0.8	17
1301	Heterotic groups of tropical indica rice germplasm. <i>Theoretical and Applied Genetics</i> , 2015, 128, 421-430.	1.8	30
1302	Genetic data on 17 STR autosomal loci for a sample population of the State of Rio de Janeiro, Brazil. <i>Forensic Science International: Genetics</i> , 2015, 14, e4-e5.	1.6	3
1303	Identification of Anchored Simple Sequence Repeat Markers Associated with Calcium Content in Finger Millet (<i>Eleusine coracana</i>). <i>Proceedings of the National Academy of Sciences India Section B - Biological Sciences</i> , 2015, 85, 311-317.	0.4	33
1304	Genetic variation of an Italian long shelf-life tomato (<i>Solanum lycopersicon</i> L.) collection by using SSR and morphological fruit traits. <i>Genetic Resources and Crop Evolution</i> , 2015, 62, 721-732.	0.8	34
1305	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.	0.6	18
1306	Genetic diversity of the world's largest oil palm (<i>Elaeis guineensis</i> Jacq.) field genebank accessions using microsatellite markers. <i>Genetic Resources and Crop Evolution</i> , 2015, 62, 349-360.	0.8	47
1307	Dominance of a single clonal lineage in the <i>Phytophthora infestans</i> population from northern Shaanxi, China revealed by genetic and phenotypic diversity analysis. <i>Plant Pathology</i> , 2015, 64, 200-206.	1.2	28
1308	Allelic diversity between and within three wild annual <i>Cicer</i> species. <i>Genetic Resources and Crop Evolution</i> , 2015, 62, 177-188.	0.8	2
1309	Evaluation of rice genotypes for sugarcane borer resistance using phenotypic methods and molecular markers. <i>Crop Protection</i> , 2015, 67, 43-51.	1.0	5
1310	Genetic diversity and population structure of elite cotton (<i>Gossypium hirsutum</i> L.) germplasm revealed by SSR markers. <i>Plant Systematics and Evolution</i> , 2015, 301, 327-336.	0.3	25
1311	Genotypic and phenotypic relatedness of a farmer-discovered variant with high-yielding rice growing in the same field. <i>Plant Systematics and Evolution</i> , 2015, 301, 451-465.	0.3	0
1312	Detection of QTLs associated with salinity tolerance in durum wheat based on association analysis. <i>Euphytica</i> , 2015, 201, 29-41.	0.6	39
1313	De Novo Assembled Transcriptome Analysis and SSR Marker Development of a Mixture of Six Tissues from Liliium Oriental Hybrid "Sorbonne". <i>Plant Molecular Biology Reporter</i> , 2015, 33, 281-293.	1.0	54
1314	Development, Polymorphism and Cross-Species Transferability of Genomic SSR Markers in <i>Duabanga Moluccana</i> , an Indigenous Tree Species from Sarawak. <i>Online Journal of Biological Sciences</i> , 2016, 16, 56-70.	0.2	0

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1315	Utilization of STMS markers to verify admixture in clonal progenies of Acacia mapping populations and relabelling using assignment tests. <i>Journal of Forest Science</i> , 2015, 61, 200-209.	0.5	4
1316	Morphological and molecular genetic diversity of Syrian indigenous goat populations. <i>African Journal of Biotechnology</i> , 2016, 15, 745-758.	0.3	9
1317	Multiple marker-traits associations for maize agronomic traits. <i>Chilean Journal of Agricultural Research</i> , 2016, 76, 300-306.	0.4	4
1318	Genetic variability of sorghum landraces from lower Eastern Kenya based on simple sequence repeats (SSRs) markers. <i>African Journal of Biotechnology</i> , 2016, 15, 264-271.	0.3	11
1319	Genetic variability and homozygosity in a F4 castor bean population by microsatellite markers. <i>Bragantia</i> , 2016, 75, 307-313.	1.3	7
1320	Genetic diversity of rice (<i>Oryza sativa</i>) germplasm from six countries using simple sequence repeats markers. <i>African Journal of Biotechnology</i> , 2016, 15, 2038-2044.	0.3	4
1321	Molecular evaluation of Ethiopian sweet sorghum germplasm and their contribution to regional breeding programs. <i>Australian Journal of Crop Science</i> , 2016, 10, 520-527.	0.1	10
1322	Dissecting the Genetic Basis of Resistance to Soybean Cyst Nematode Combining Linkage and Association Mapping. <i>Plant Genome</i> , 2016, 9, plantgenome2015.04.0020.	1.6	27
1323	DNA markers reveal genetic structure and localized diversity of Ethiopian sorghum landraces. <i>African Journal of Biotechnology</i> , 2016, 15, 2301-2311.	0.3	9
1324	Genotyping the local banana landrace groups of East Africa. <i>Acta Horticulturae</i> , 2016, , 67-74.	0.1	10
1325	Genetic Diversity Studies on Selected Rice (<i>Oryza sativa</i> L.) Genotypes based on Gel Consistency and Alkali Digestion. <i>Rice Research Open Access</i> , 2016, 4, .	0.4	8
1326	Comparing Genotyping-by-Seq Sequencing and Single Nucleotide Polymorphism Chip Genotyping for Quantitative Trait Loci Mapping in Wheat. <i>Crop Science</i> , 2016, 56, 232-248.	0.8	35
1327	Inference of genetic diversity in popcorn S3 progenies. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	3
1328	Linkage disequilibrium, SNP frequency change due to selection, and association mapping in popcorn chromosome regions containing QTLs for quality traits. <i>Genetics and Molecular Biology</i> , 2016, 39, 97-110.	0.6	8
1329	Bulk segregant analysis (BSA) for improving cold stress resistance in maize using SSR markers. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	8
1330	Heterotic Patterns of IITA and CIMMYT Early-Maturing Yellow Maize Inbreds under Contrasting Environments. <i>Agronomy Journal</i> , 2016, 108, 1321-1336.	0.9	27
1331	Genetic structure from the oldest <i>Jatropha</i> germplasm bank of Brazil and contribution for the genetic improvement. <i>Anais Da Academia Brasileira De Ciencias</i> , 2016, 88, 2363-2374.	0.3	2
1332	Effect of fragmentation on the natural genetic diversity of <i>Theobroma speciosum</i> Willd. ex Spreng. populations. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	2

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1333	Development of a transposon-based marker system for mutation breeding in sorghum (<i>Sorghum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.3	4
1334	Population structure analysis and association mapping of blast resistance in indica rice (<i>Oryza sativa</i>) Tj ETQq1 1 0.784314 rgBT /Overlock	0.3	7
1335	Genetic Relationships between Elite Oil Palms from Nigeria and Selected Breeding and Germplasm Materials from Malaysia via Simple Sequence Repeat (SSR) Markers. <i>Journal of Agricultural Science</i> , 2016, 8, 159.	0.1	8
1336	Effective marker alleles associated with type 2 resistance to Fusarium head blight infection in fields. <i>Breeding Science</i> , 2016, 66, 350-357.	0.9	13
1337	Genetic Diversity, Population Structure, and Association Mapping of 10 Agronomic Traits in Sesame. <i>Crop Science</i> , 2016, 56, 331-343.	0.8	8
1338	Genetic diversity and association analysis among Egyptian barley (<i>Hordeum vulgare</i> L.) genotypes with different adaptations to saline conditions analyzed by SSR markers. <i>Australian Journal of Crop Science</i> , 2016, 10, 637-645.	0.1	6
1339	Population structure of jatropha and its implication for the breeding program. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	9
1340	Genetic diversity and population structure of common bean (<i>Phaseolus vulgaris</i> L) germplasm of Ethiopia as revealed by microsatellite markers. <i>African Journal of Biotechnology</i> , 2016, 15, 2824-2847.	0.3	20
1341	Genetic Diversity Analysis of South and East Asian Duck Populations Using Highly Polymorphic Microsatellite Markers. <i>Asian-Australasian Journal of Animal Sciences</i> , 2016, 29, 471-478.	2.4	13
1342	Assessment of genetic diversity in Brazilian barley using SSR markers. <i>Genetics and Molecular Biology</i> , 2016, 39, 86-96.	0.6	27
1343	Assessment of genetic diversity of Tunisian orange, <i>Citrus sinensis</i> (L.) Osbeck using microsatellite (SSR) markers. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	3
1344	Genetic Diversity and Structure of Tobacco in Greece on the Basis of Morphological and Microsatellite Markers. <i>Crop Science</i> , 2016, 56, 2652-2662.	0.8	5
1345	Genetic variation of rice (<i>Oryza sativa</i> L.) germplasm in Myanmar based on genomic compositions of DNA markers. <i>Breeding Science</i> , 2016, 66, 762-767.	0.9	10
1346	Mining Centuries Old In situ Conserved Turkish Wheat Landraces for Grain Yield and Stripe Rust Resistance Genes. <i>Frontiers in Genetics</i> , 2016, 7, 201.	1.1	51
1347	Analysis of Genetic Diversity and Population Structure of Sesame Accessions from Africa and Asia as Major Centers of Its Cultivation. <i>Genes</i> , 2016, 7, 14.	1.0	51
1348	Development of 12 Microsatellite Markers in <i>Dorcus titanus castanicolor</i> (Motschulsky, 1861) (Lucanidae, Coleoptera) from Korea Using Next-Generation Sequencing. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1621.	1.8	4
1349	Cross-Species, Amplifiable EST-SSR Markers for <i>Amentotaxus</i> Species Obtained by Next-Generation Sequencing. <i>Molecules</i> , 2016, 21, 67.	1.7	27
1350	Genetic diversity and structure in hill rice (<i>Oryza sativa</i> L.) landraces from the North-Eastern Himalayas of India. <i>BMC Genetics</i> , 2016, 17, 107.	2.7	58

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1351	Evaluation of Linkage Disequilibrium Pattern and Association Study on Seed Oil Content in Brassica napus Using ddRAD Sequencing. PLoS ONE, 2016, 11, e0146383.	1.1	63
1352	APOBEC3G Variants and Protection against HIV-1 Infection in Burkina Faso. PLoS ONE, 2016, 11, e0146386.	1.1	17
1353	Development of Gene-Based SSR Markers in Rice Bean (<i>Vigna umbellata</i> L.) Based on Transcriptome Data. PLoS ONE, 2016, 11, e0151040.	1.1	29
1354	Development of Microsatellite Markers and Analysis of Genetic Diversity and Population Structure of <i>Colletotrichum gloeosporioides</i> from Ethiopia. PLoS ONE, 2016, 11, e0151257.	1.1	41
1355	Characterization and Transferable Utility of Microsatellite Markers in the Wild and Cultivated <i>Arachis</i> Species. PLoS ONE, 2016, 11, e0156633.	1.1	21
1356	Phenotypic Characterization and Genetic Dissection of Growth Period Traits in Soybean (<i>Glycine max</i>) Using Association Mapping. PLoS ONE, 2016, 11, e0158602.	1.1	26
1357	Identification and Validation of Loci Governing Seed Coat Color by Combining Association Mapping and Bulk Segregation Analysis in Soybean. PLoS ONE, 2016, 11, e0159064.	1.1	46
1358	Genetic Diversity and Population Structure of Cowpea (<i>Vigna unguiculata</i> L. Walp). PLoS ONE, 2016, 11, e0160941.	1.1	120
1359	Genome-wide SSR-based association mapping for fiber quality in nation-wide upland cotton inbred cultivars in China. BMC Genomics, 2016, 17, 352.	1.2	124
1360	Population database on: D1S1656, D2S441, D2S1338, D3S1358, D8S1179, D10S1248, D22S1045, D12S391, D16S539, D18S51, D19S433, D21S11, FGA, TH01, vWA loci included in NGM system based on one thousand unrelated individuals from Lodz region of Central Poland. Archiwum Medycyny Sadowej i Kryminologii, 2016, 2, 83-94.	0.3	1
1361	Characterizing Variation of Branch Angle and Genome-Wide Association Mapping in Rapeseed (<i>Brassica napus</i>) Tj ETQq0 0 0 rgBT /Overlock 10	1.7	44
1362	Species Delimitation of the <i>Cycas segmentifida</i> Complex (Cycadaceae) Resolved by Phylogenetic and Distance Analyses of Molecular Data. Frontiers in Plant Science, 2016, 7, 134.	1.7	21
1363	Development and Identification of SSR Markers Associated with Starch Properties and β -Carotene Content in the Storage Root of Sweet Potato (<i>Ipomoea batatas</i> L.). Frontiers in Plant Science, 2016, 7, 223.	1.7	19
1364	Identification of a Candidate Gene for Panicle Length in Rice (<i>Oryza sativa</i> L.) Via Association and Linkage Analysis. Frontiers in Plant Science, 2016, 7, 596.	1.7	71
1365	Functional Studies of Heading Date-Related Gene TaPRR73, a Paralog of Ppd1 in Common Wheat. Frontiers in Plant Science, 2016, 7, 772.	1.7	23
1366	Genetic Diversity and Elite Allele Mining for Grain Traits in Rice (<i>Oryza sativa</i> L.) by Association Mapping. Frontiers in Plant Science, 2016, 7, 787.	1.7	26
1367	Population Structure and Genotype-Phenotype Associations in a Collection of Oat Landraces and Historic Cultivars. Frontiers in Plant Science, 2016, 7, 1077.	1.7	32
1368	Genetic Diversity of Cultivated Lentil (<i>Lens culinaris</i> Medik.) and Its Relation to the World's Agro-ecological Zones. Frontiers in Plant Science, 2016, 7, 1093.	1.7	110

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1369	Identification and Verification of QTL Associated with Frost Tolerance Using Linkage Mapping and GWAS in Winter Faba Bean. <i>Frontiers in Plant Science</i> , 2016, 7, 1098.	1.7	64
1370	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.	1.7	26
1371	Insights into the Genetic Relationships and Breeding Patterns of the African Tea Germplasm Based on nSSR Markers and cpDNA Sequences. <i>Frontiers in Plant Science</i> , 2016, 7, 1244.	1.7	39
1372	Genetic Diversity, Rather than Cultivar Type, Determines Relative Grain Cd Accumulation in Hybrid Rice. <i>Frontiers in Plant Science</i> , 2016, 7, 1407.	1.7	53
1373	GmSALT3, Which Confers Improved Soybean Salt Tolerance in the Field, Increases Leaf Cl- Exclusion Prior to Na+ Exclusion But Does Not Improve Early Vigor under Salinity. <i>Frontiers in Plant Science</i> , 2016, 7, 1485.	1.7	71
1374	An Efficient Strategy Combining SSR Markers- and Advanced QTL-seq-driven QTL Mapping Unravels Candidate Genes Regulating Grain Weight in Rice. <i>Frontiers in Plant Science</i> , 2016, 7, 1535.	1.7	21
1375	Genome-Enabled Prediction Models for Yield Related Traits in Chickpea. <i>Frontiers in Plant Science</i> , 2016, 7, 1666.	1.7	127
1376	Genetic diversity assessment of farmers and improved potato (<i>Solanum tuberosum</i>) cultivars from Eritrea using simple sequence repeat (SSR) markers. <i>African Journal of Biotechnology</i> , 2016, 15, 1883-1891.	0.3	9
1377	Genetic diversity reduction in improved durum wheat cultivars of Morocco as revealed by microsatellite markers. <i>Scientia Agricola</i> , 2016, 73, 134-141.	0.6	36
1378	Assessment of the genetic diversity of Kenyan coconut germplasm using simple sequence repeat (SSR) markers. <i>African Journal of Biotechnology</i> , 2016, 15, 2215-2223.	0.3	9
1379	Genetic Diversity and Population Structure of Tetraploid Accessions of the <i>Medicago sativa</i> "falcata" Complex. <i>Crop Science</i> , 2016, 56, 1146-1156.	0.8	17
1381	Association mapping identifies markers related to major early-maturing traits in upland cotton (<i>Gossypium hirsutum</i> L.). <i>Plant Breeding</i> , 2016, 135, 483-491.	1.0	28
1382	Exploring genetic diversity of rice cultivars for the presence of brown planthopper (<sc>BPH</sc>) resistance genes and development of <sc>SNP</sc> marker for <i>Bph18</i> . <i>Plant Breeding</i> , 2016, 135, 301-308.	1.0	8
1383	Cross-genera amplification of informative microsatellite markers from common bean and scarlet runner bean for assessment of genetic diversity in mungbean (<i>Vigna radiata</i>). <i>Plant Breeding</i> , 2016, 135, 499-505.	1.0	16
1384	Analysis of genetic diversity and population structure of peanut cultivars and breeding lines from China, India and the US using simple sequence repeat markers. <i>Journal of Integrative Plant Biology</i> , 2016, 58, 452-465.	4.1	18
1385	Differentiation in populations of the apple scab fungus <i>Venturia inaequalis</i> on cultivars in a mixed orchard remain over time. <i>Plant Pathology</i> , 2016, 65, 1133-1141.	1.2	12
1386	Genetic structure and diversity of natural and domesticated populations of <i>Citrus medica</i> L. in the Eastern Himalayan region of Northeast India. <i>Ecology and Evolution</i> , 2016, 6, 3898-3911.	0.8	21
1387	Root trait diversity, molecular marker diversity, and trait-marker associations in a core collection of <i>Lupinus angustifolius</i> . <i>Journal of Experimental Botany</i> , 2016, 67, 3683-3697.	2.4	20

#	ARTICLE	IF	CITATIONS
1388	A genetic delineation of Patchouli (<i>Pogostemon cablin</i>) revealed by specific locus amplified fragment sequencing. <i>Journal of Systematics and Evolution</i> , 2016, 54, 491-501.	1.6	16
1389	Association mapping of winter hardiness and yield traits in faba bean (<i>Vicia faba</i> L.). <i>Crop and Pasture Science</i> , 2016, 67, 55.	0.7	30
1390	Diversity of threatened local mango landraces on smallholder farms in Eastern Kenya. <i>Forests Trees and Livelihoods</i> , 2016, 25, 239-254.	0.5	7
1391	Virulence Characterization and Identification of Maize Lines Resistant to <i>Puccinia sorghi</i> Schwein. Present in the Argentine Corn Belt Region. <i>Plant Disease</i> , 2016, 100, 770-776.	0.7	10
1392	Breeding signature of combining ability improvement revealed by a genomic variation map from recurrent selection population in <i>Brassica napus</i> . <i>Scientific Reports</i> , 2016, 6, 29553.	1.6	21
1393	Characterizing the population structure and genetic diversity of maize breeding germplasm in Southwest China using genome-wide SNP markers. <i>BMC Genomics</i> , 2016, 17, 697.	1.2	106
1394	Genome scans for divergent selection in natural populations of the widespread hardwood species <i>Eucalyptus grandis</i> (Myrtaceae) using microsatellites. <i>Scientific Reports</i> , 2016, 6, 34941.	1.6	16
1395	An efficient identification strategy of clonal tea cultivars using long-core motif SSR markers. <i>SpringerPlus</i> , 2016, 5, 1152.	1.2	9
1396	Association mapping and favourable allele exploration for plant architecture traits in upland cotton (<i>Gossypium hirsutum</i> L.) accessions. <i>Journal of Agricultural Science</i> , 2016, 154, 567-583.	0.6	46
1397	Characterization of Three <i>Indica</i> Rice Multiparent Advanced Generation Intercross (MAGIC) Populations for Quantitative Trait Loci Identification. <i>Plant Genome</i> , 2016, 9, plantgenome2015.10.0109.	1.6	42
1398	Population structure and association analysis of yield and grain quality traits in hybrid rice primal parental lines. <i>Euphytica</i> , 2016, 212, 261-273.	0.6	12
1399	Impacts of biogeographic history and marginal population genetics on species range limits: a case study of <i>Liriodendron chinense</i> . <i>Scientific Reports</i> , 2016, 6, 25632.	1.6	44
1400	Characterization of <i>Brassica napus</i> L. genotypes utilizing sequence-related amplified polymorphism and genotyping by sequencing in association with cluster analysis. <i>Molecular Breeding</i> , 2016, 36, 155.	1.0	4
1401	Analysis of molecular variance and population structure in southern Indian finger millet genotypes using three different molecular markers. <i>Journal of Crop Science and Biotechnology</i> , 2016, 19, 275-283.	0.7	18
1402	Inter- and intra-specific diversity in <i>Agaricus endoxanthus</i> and allied species reveals a new taxon, <i>A. punjabensis</i> . <i>Phytotaxa</i> , 2016, 252, 1.	0.1	13
1403	Genetic Architecture of Resistance to Stripe Rust in a Global Winter Wheat Germplasm Collection. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2237-2253.	0.8	154
1404	Genome survey of pistachio (<i>Pistacia vera</i> L.) by next generation sequencing: Development of novel SSR markers and genetic diversity in <i>Pistacia</i> species. <i>BMC Genomics</i> , 2016, 17, 998.	1.2	78
1405	The Genetic Structure, Virulence, and Fungicide Sensitivity of <i>Fusarium fujikuroi</i> in Taiwan. <i>Phytopathology</i> , 2016, 106, 624-635.	1.1	19

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1406	Susceptibility of Maize to Stalk Rot Caused by <i>Fusarium graminearum</i> Deoxynivalenol and Zearalenone Mutants. <i>Phytopathology</i> , 2016, 106, 920-927.	1.1	28
1407	Molecular genetic tools to support genetic improvement of winged bean (<i>Psophocarpus</i>) Tj ETQq1 1 0.784314 0.1 /Overlock 10	0.1	4
1408	Genome-wide generation and use of informative intron-spanning and intron-length polymorphism markers for high-throughput genetic analysis in rice. <i>Scientific Reports</i> , 2016, 6, 23765.	1.6	19
1409	Genetic diversity and population structure analysis to construct a core collection from a large <i>Capsicum</i> germplasm. <i>BMC Genetics</i> , 2016, 17, 142.	2.7	96
1410	Maximizing the potential of multi-parental crop populations. <i>Applied & Translational Genomics</i> , 2016, 11, 9-17.	2.1	49
1411	Assessing genetic diversity of wheat genotypes from different origins by SNP markers. <i>Cereal Research Communications</i> , 2016, 44, 361-369.	0.8	6
1412	Haplotyping of Rice Genotypes Using Simple Sequence Repeat Markers Associated with Salt Tolerance. <i>Rice Science</i> , 2016, 23, 317-325.	1.7	30
1413	Development of microsatellite markers for genes related to defense responses in <i>Musa acuminata</i> . <i>Acta Horticulturae</i> , 2016, , 91-94.	0.1	0
1414	Genetic diversity of <i>Sorghum halepense</i> (L.) Pers. in Iran as revealed by IRAP markers. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2016, 14, 132-141.	0.4	4
1415	New development and validation of 50 SSR markers in breadfruit (<i>Artocarpus altilis</i> , Moraceae) by next-generation sequencing. <i>Applications in Plant Sciences</i> , 2016, 4, .	0.8	12
1416	Genetic diversity of <i>Vitis vinifera</i> L. in Azerbaijan. <i>Russian Journal of Genetics</i> , 2016, 52, 391-397.	0.2	4
1417	<i>FABP4</i> is a leading candidate gene associated with residual feed intake in growing Holstein calves. <i>Physiological Genomics</i> , 2016, 48, 367-376.	1.0	10
1418	A set of microsatellite markers for population genetics of leopard cat (<i>Prionailurus bengalensis</i>) and cross-species amplification in other felids. <i>Biochemical Systematics and Ecology</i> , 2016, 66, 196-200.	0.6	7
1419	Progress in Botany 77. <i>Progress in Botany Fortschritte Der Botanik</i> , 2016, , .	0.1	2
1420	Detecting the QTL-allele system of seed isoflavone content in Chinese soybean landrace population for optimal cross design and gene system exploration. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1557-1576.	1.8	70
1421	Population data of 15 autosomal STR loci in Chinese Han population from Liaoning Province, Northeast China. <i>Forensic Science International: Genetics</i> , 2016, 23, e20-e21.	1.6	23
1422	Comparative assessment of genetic diversity in cytoplasmic and nuclear genome of upland cotton. <i>Genetica</i> , 2016, 144, 289-306.	0.5	3
1423	Forensic timber identification: a case study of a CITES listed species, <i>Gonystylus bancanus</i> (Thymelaeaceae). <i>Forensic Science International: Genetics</i> , 2016, 23, 197-209.	1.6	33

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1424	Genetic diversity and population structure of endangered endemic <i>Paeonia jishanensis</i> in China and conservation implications. <i>Biochemical Systematics and Ecology</i> , 2016, 66, 319-325.	0.6	18
1425	Population genetic analysis of <i>Theileria parva</i> isolated in cattle and buffaloes in Tanzania using minisatellite and microsatellite markers. <i>Veterinary Parasitology</i> , 2016, 224, 20-26.	0.7	14
1426	Analysis of genetic diversity of African yam bean using SSR markers derived from cowpea. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2016, 14, 50-56.	0.4	18
1427	Association analysis for disease resistance to <i>Fusarium oxysporum</i> in cape gooseberry (<i>Physalis</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 41	1.2	41
1428	Assessment of genetic diversity amongst Ugandan sesame (<i>Sesamum indicum</i> L.) landraces based on agromorphological traits and genetic markers. <i>Journal of Crop Science and Biotechnology</i> , 2016, 19, 117-124.	0.7	17
1429	Association mapping and genetic dissection of nitrogen use efficiency-related traits in rice (<i>Oryza</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 41	1.4	41
1430	Haplotype hitchhiking promotes trait coselection in <i>Brassica napus</i> . <i>Plant Biotechnology Journal</i> , 2016, 14, 1578-1588.	4.1	31
1431	Identification of loci contributing to maize drought tolerance in a genome-wide association study. <i>Euphytica</i> , 2016, 210, 165-179.	0.6	15
1432	Genetic characterization of Moroccan and the exotic bread wheat cultivars using functional and random DNA markers linked to the agronomic traits for genomics-assisted improvement. <i>3 Biotech</i> , 2016, 6, 97.	1.1	3
1433	Exploring novel genetic sources of salinity tolerance in rice through molecular and physiological characterization. <i>Annals of Botany</i> , 2016, 117, 1083-1097.	1.4	102
1434	Assessment of genetic diversity in Ethiopian cowpea [<i>Vigna unguiculata</i> (L.) Walp.] germplasm using simple sequence repeat markers. <i>Plant Molecular Biology Reporter</i> , 2016, 34, 978-992.	1.0	13
1435	Microsatellite markers for the Ussuri white-toothed shrew (<i>Soricidae: Crocidura lasiura</i>) developed by Ion Torrent sequencing and their application to the shrew populations in disturbed forests. <i>Genes and Genomics</i> , 2016, 38, 351-357.	0.5	3
1436	Genome-wide association study of the husk number and weight in maize (<i>Zea mays</i> L.). <i>Euphytica</i> , 2016, 210, 195-205.	0.6	20
1437	Association analysis, genetic diversity and haplotyping of rice plants under salt stress using SSR markers linked to SalTol and morpho-physiological characteristics. <i>Plant Systematics and Evolution</i> , 2016, 302, 871-890.	0.3	30
1438	Novel microsatellite markers in <i>Pistacia vera</i> L. and their transferability across the genus <i>Pistacia</i> . <i>Scientia Horticulturae</i> , 2016, 198, 91-97.	1.7	20
1439	Genetic diversity, population structure and association analysis in cut chrysanthemum (<i>Chrysanthemum morifolium</i> Ramat.). <i>Molecular Genetics and Genomics</i> , 2016, 291, 1117-1125.	1.0	36
1440	Genetic diversity and population structure of Chinese <i>Lentinula edodes</i> revealed by InDel and SSR markers. <i>Mycological Progress</i> , 2016, 15, 1.	0.5	25
1441	Genome-wide SSR marker development in oil palm by Illumina HiSeq for parental selection. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2016, 14, 157-160.	0.4	2

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1442	Transferability of Simple Sequence Repeat (SSR) Markers Developed in Red Clover (<i>Trifolium pratense</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T 40, 59-62.	0.7	6
1443	Development of genomic simple sequence repeats (g-SSR) markers in <i>Tinospora cordifolia</i> and their application in diversity analyses. <i>Plant Gene</i> , 2016, 5, 118-125.	1.4	23
1444	Simultaneous genotyping of 4 SNPs in promoter III of the ovine ACACA. <i>Small Ruminant Research</i> , 2016, 138, 25-30.	0.6	2
1445	Geographical distribution of genetic diversity in <i>Secale landrace</i> and wild accessions. <i>BMC Plant Biology</i> , 2016, 16, 23.	1.6	38
1446	Co-linearity and divergence of the A subgenome of <i>Brassica juncea</i> compared with other <i>Brassica</i> species carrying different A subgenomes. <i>BMC Genomics</i> , 2016, 17, 18.	1.2	32
1447	Development of new PCR multiplex system by the simultaneous detection of 10 miniSTRs, SE33, Penta E, Penta D, and four Y-STRs. <i>International Journal of Legal Medicine</i> , 2016, 130, 1409-1419.	1.2	4
1448	Genetic diversity of naturalized cacao (<i>Theobroma cacao</i> L.) in Puerto Rico. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	30
1449	Population data of 15 autosomal STR loci in Chinese Han population from Jiangsu Province, Eastern China. <i>Forensic Science International: Genetics</i> , 2016, 24, 112-113.	1.6	17
1450	Experimental and genomic evidence for the indica-type cytoplasmic effect in <i>Oryza sativa</i> L. ssp. <i>japonica</i> . <i>Journal of Integrative Agriculture</i> , 2016, 15, 2183-2191.	1.7	4
1451	Genetic divergence, path analysis and molecular diversity analysis in cluster bean (<i>Cyamopsis</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 2.5	2.5	31
1452	Mapping highly informative SSR markers in the genome of <i>Magnaporthe oryzae</i> from wheat. <i>Tropical Plant Pathology</i> , 2016, 41, 331-335.	0.8	0
1453	Design and validation of an STR hexaplex assay for DNA profiling of grapevine cultivars. <i>Electrophoresis</i> , 2016, 37, 3059-3067.	1.3	3
1454	Genetics of carotenoids for provitamin A biofortification in tropical-adapted maize. <i>Crop Journal</i> , 2016, 4, 313-322.	2.3	30
1455	Population genetic data for 20 autosomal STR loci in an Iraqi Arab population: Application to the identification of human remains. <i>Forensic Science International: Genetics</i> , 2016, 25, e10-e11.	1.6	10
1456	Characterization of Microsatellites Identified by Next-Generation Sequencing in the Neotropical Tree <i>Handroanthus billbergii</i> (Bignoniaceae). <i>Applications in Plant Sciences</i> , 2016, 4, 1500135.	0.8	6
1457	Relative profile analysis of molecular markers for identification and genetic discrimination of loaches (Pisces, Nemacheilidae). <i>Comptes Rendus - Biologies</i> , 2016, 339, 364-370.	0.1	1
1458	Identification and validation of a major cadmium accumulation locus and closely associated SNP markers in North Dakota durum wheat cultivars. <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	25
1459	Genotyping by Sequencing (GBS) in Apricots and Genetic Diversity Assessment with GBS-Derived Single-Nucleotide Polymorphisms (SNPs). <i>Biochemical Genetics</i> , 2016, 54, 854-885.	0.8	15

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1460	Molecular characterization of endosperm and amino acids modifications among quality protein maize inbreds. <i>Plant Breeding</i> , 2016, 135, 47-54.	1.0	31
1461	Dissecting maize diversity in lowland South America: genetic structure and geographic distribution models. <i>BMC Plant Biology</i> , 2016, 16, 186.	1.6	14
1462	Targeted Metabolic and Genomic Profiling Reveals Parents for L-Dopa Breeding in <i>Mucuna pruriens</i> (L.) DC.. <i>Tropical Plant Biology</i> , 2016, 9, 239-251.	1.0	5
1463	Genome-wide development and deployment of informative intron-spanning and intron-length polymorphism markers for genomics-assisted breeding applications in chickpea. <i>Plant Science</i> , 2016, 252, 374-387.	1.7	12
1464	Association mapping of seed and disease resistance traits in <i>Theobroma cacao</i> L.. <i>Planta</i> , 2016, 244, 1265-1276.	1.6	30
1465	Genetic diversity and extinction risk in a small, declining Polish common hamster (<i>Cricetus cricetus</i>) population. <i>Mammalian Biology</i> , 2016, 81, 612-622.	0.8	2
1466	Association analysis of fruit traits in mulberry species (<i>Morus</i> L.). <i>Journal of Horticultural Science and Biotechnology</i> , 2016, 91, 645-655.	0.9	7
1467	Regional and Temporal Population Structure of <i>Pseudoperonospora cubensis</i> in Michigan and Ontario. <i>Phytopathology</i> , 2016, 106, 372-379.	1.1	28
1468	Virulence and Molecular Diversity of the <i>Puccinia striiformis</i> f. sp. <i>tritici</i> Population in Xinjiang in Relation to Other Regions of Western China. <i>Plant Disease</i> , 2016, 100, 99-107.	0.7	24
1469	Genome-wide SNP discovery and population structure analysis in pepper (<i>Capsicum annuum</i>) using genotyping by sequencing. <i>BMC Genomics</i> , 2016, 17, 943.	1.2	110
1470	Identification of stable QTLs for seed oil content by combined linkage and association mapping in <i>Brassica napus</i> . <i>Plant Science</i> , 2016, 252, 388-399.	1.7	63
1471	Phylogenetic Relationship of <i>Echinochloa</i> Species Based on Simple Sequence Repeat and Phenotypic Marker Analyses. <i>Weed Science</i> , 2016, 64, 441-454.	0.8	8
1472	Agro-Morphological, Physico-Chemical and Molecular Characterization of Rice Germplasm with Similar Names of Bangladesh. <i>Rice Science</i> , 2016, 23, 211-218.	1.7	19
1473	Genomic survey sequencing for development and validation of single-locus SSR markers in peanut (<i>Arachis hypogaea</i> L.). <i>BMC Genomics</i> , 2016, 17, 420.	1.2	33
1474	Diversity Among a Wide Asian Collection of Bitter Gourd Landraces and their Genetic Relationships with Commercial Hybrid Cultivars. <i>Journal of the American Society for Horticultural Science</i> , 2016, 141, 475-484.	0.5	22
1475	Population structure and marker-trait association of salt tolerance in barley (<i>Hordeum vulgare</i> L.). <i>Comptes Rendus - Biologies</i> , 2016, 339, 454-461.	0.1	28
1476	Identifying the genetic diversity, genetic structure and a core collection of <i>Ziziphus jujuba</i> Mill. var. <i>jujuba</i> accessions using microsatellite markers. <i>Scientific Reports</i> , 2016, 6, 31503.	1.6	54
1477	SSR markers reveal the population structure of Sri Lankan yellow dwarf coconuts (<i>Cocos nucifera</i>) Tj ETQq1 1 0.784314 rgBT ₆ /Overlook	0.6	6

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1478	Association analysis and population structure of flowering-related traits in super sweet corn inbred lines with simple sequence repeat markers. <i>Genes and Genomics</i> , 2016, 38, 891-901.	0.5	2
1479	Development of novel simple sequence repeat markers from ramie (<i>Boehmeria nivea</i> L. Gaudich) and analysis of genetic diversity in its genetic resources. <i>Horticulture Environment and Biotechnology</i> , 2016, 57, 519-528.	0.7	2
1480	Molecular markers for conservation genetic resources of four <i>Passiflora</i> species. <i>Scientia Horticulturae</i> , 2016, 212, 251-261.	1.7	5
1481	Novel 307 polymorphic SSR markers from BAC-end sequences in walnut (<i>Juglans regia</i> L.): Effects of motif types and repeat lengths on polymorphism and genetic diversity. <i>Scientia Horticulturae</i> , 2016, 213, 1-4.	1.7	20
1482	HBV/HIV co-infection and APOBEC3G polymorphisms in a population from Burkina Faso. <i>BMC Infectious Diseases</i> , 2016, 16, 336.	1.3	11
1483	Deletion of a Stay-Green Gene Associates with Adaptive Selection in <i>Brassica napus</i> . <i>Molecular Plant</i> , 2016, 9, 1559-1569.	3.9	58
1484	Detailed insight into genetic diversity of the Old Kladruber horse substructure in comparison to the Lipizzan breed. <i>Acta Agriculturae Scandinavica - Section A: Animal Science</i> , 2016, 66, 67-74.	0.2	5
1485	Population Structure and Association Analysis of Traits in Summer Soybeans. <i>Journal of Crop Improvement</i> , 2016, 30, 572-594.	0.9	2
1486	Genomic prediction contributing to a promising global strategy to turbocharge gene banks. <i>Nature Plants</i> , 2016, 2, 16150.	4.7	179
1487	Genetic diversity trend in Indian rice varieties: an analysis using SSR markers. <i>BMC Genetics</i> , 2016, 17, 127.	2.7	73
1488	Genome-wide association study for kernel weight-related traits using SNPs in a Chinese winter wheat population. <i>Euphytica</i> , 2016, 212, 173-185.	0.6	73
1489	Development of a SNP array and its application to genetic mapping and diversity assessment in pepper (<i>Capsicum</i> spp.). <i>Scientific Reports</i> , 2016, 6, 33293.	1.6	55
1490	Genetic Diversity of Seven Representative Germplasm Populations in Chinese Maize Breeding Programs. <i>Agronomy Journal</i> , 2016, 108, 1787-1793.	0.9	1
1491	Environmental and Historical Determinants of Patterns of Genetic Differentiation in Wild Soybean (<i>Glycine soja</i> Sieb. et Zucc). <i>Scientific Reports</i> , 2016, 6, 22795.	1.6	22
1492	Phenotypic evaluation and genetic dissection of resistance to <i>Phytophthora sojae</i> in the Chinese soybean mini core collection. <i>BMC Genetics</i> , 2016, 17, 85.	2.7	43
1493	Gene Action and Heterotic Groups of Early White Quality Protein Maize Inbreds under Multiple Stress Environments. <i>Crop Science</i> , 2016, 56, 183-199.	0.8	51
1494	Shift in precipitation regime promotes interspecific hybridization of introduced <i>Coffea</i> species. <i>Ecology and Evolution</i> , 2016, 6, 3240-3255.	0.8	15
1495	Development of a SCAR marker associated with salt tolerance in durum wheat (<i>Triticum turgidum</i> ssp.) Tj ETQq1 1 0,784314 rgBT /Over	0,5	

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1496	Using microsatellite DNA to determine whether American Hazelnut Clumps are multiclonal. <i>Agroforestry Systems</i> , 2016, 90, 927-931.	0.9	1
1497	Allelic diversity of newly characterized submergence-tolerant rice (<i>Oryza sativa</i> L.) germplasm from Bangladesh. <i>Genetic Resources and Crop Evolution</i> , 2016, 63, 859-867.	0.8	13
1498	Association mapping and favorable allele mining for node of first fruiting/sympodial branch and its height in Upland cotton (<i>Gossypium hirsutum</i> L.). <i>Euphytica</i> , 2016, 210, 57-68.	0.6	8
1499	Molecular characterization and genetic diversity in geographical indication (GI) rice (<i>Oryza sativa</i> L.) cultivars of Bangladesh. <i>Revista Brasileira De Botanica</i> , 2016, 39, 631-640.	0.5	3
1500	Molecular Evaluation of Genetic Diversity in Wild-Type Mastic Tree (<i>Pistacia lentiscus</i> L.). <i>Biochemical Genetics</i> , 2016, 54, 619-635.	0.8	10
1501	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
1502	De novo sequencing and characterization of seed transcriptome of the tree legume <i>Milletia pinnata</i> for gene discovery and SSR marker development. <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	17
1503	Development and Genetic Characterization of an Advanced Backcross-Nested Association Mapping (AB-NAM) Population of Wild A— Cultivated Barley. <i>Genetics</i> , 2016, 203, 1453-1467.	1.2	73
1504	The power of microsatellite markers and AFLPs in revealing the genetic diversity of Hashemi aromatic rice from Iran. <i>Journal of Integrative Agriculture</i> , 2016, 15, 1186-1197.	1.7	7
1505	Intraspecific classification of <i>Ficus deltoidea</i> Jack subsp. <i>deltoidea</i> (Moraceae) in Peninsular Malaysia based on morphological and molecular variations. <i>Biochemical Systematics and Ecology</i> , 2016, 67, 119-128.	0.6	3
1506	Ancient split of major genetic lineages of European Black Pine: evidence from chloroplast DNA. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	14
1507	Assessment of genetic diversity in <i>Mucuna</i> species of India using randomly amplified polymorphic DNA and inter simple sequence repeat markers. <i>Physiology and Molecular Biology of Plants</i> , 2016, 22, 207-217.	1.4	12
1508	Population Structure and Genetic Diversity in Sweet Cassava Cultivars from Paraná, Brazil. <i>Plant Molecular Biology Reporter</i> , 2016, 34, 1153-1166.	1.0	8
1509	Population genetic study for 24 STR loci and Y indel (GlobalFiler [®] , [®] PCR Amplification kit and) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	0.8	31
1510	SSR genetic diversity assessment of popular pigeonpea varieties in Malawi reveals unique fingerprints. <i>Electronic Journal of Biotechnology</i> , 2016, 21, 65-71.	1.2	21
1511	Uncovering novel loci for mesocotyl elongation and shoot length in indica rice through genome-wide association mapping. <i>Planta</i> , 2016, 243, 645-657.	1.6	91
1512	Assessment of genetic diversity in 48 landraces of <i>Momordica dioica</i> Roxb. ex Willd. from Odisha, India using RAPD and ISSR markers. <i>Nucleus (India)</i> , 2016, 59, 107-114.	0.9	4
1513	Genetic diversity and population structure of core watermelon (<i>Citrullus lanatus</i>) genotypes using DArTseq-based SNPs. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2016, 14, 226-233.	0.4	37

#	ARTICLE	IF	CITATIONS
1514	Advances in Genetic Diversity Analysis in Fruit Tree Crops. Progress in Botany Fortschritte Der Botanik, 2016, , 245-264.	0.1	4
1515	Population genetic structure of <i>Theileria parva</i> field isolates from indigenous cattle populations of Uganda. Ticks and Tick-borne Diseases, 2016, 7, 291-297.	1.1	6
1516	Functional mechanisms of drought tolerance in maize through phenotyping and genotyping under well watered and water stressed conditions. European Journal of Agronomy, 2016, 79, 43-57.	1.9	31
1517	Assessment of genetic diversity, population structure and relationships in Indian and non-Indian genotypes of finger millet (<i>Eleusine coracana</i> (L.) Gaertn) using genomic SSR markers. SpringerPlus, 2016, 5, 120.	1.2	44
1518	Assessment of genetic diversity in Nordic timothy (<i>Phleum pratense</i> L.). Hereditas, 2016, 153, 5.	0.5	6
1519	Tracking changes in chromosomal arrangements and their genetic content during adaptation. Journal of Evolutionary Biology, 2016, 29, 1151-1167.	0.8	16
1520	Genomewide introgressive hybridization patterns in wild Atlantic salmon influenced by inadvertent gene flow from hatchery releases. Molecular Ecology, 2016, 25, 1275-1293.	2.0	42
1521	Genetic diversity and population structure of Indian melon (<i>Cucumis melo</i> L.) landraces with special reference to disease and insect resistance loci. Plant Breeding, 2016, 135, 384-390.	1.0	10
1522	Microsatellite marker-based genetic diversity analyses of novel maize inbreds possessing rare allele of β -carotene hydroxylase (<i>crtRB1</i>) for their utilization in β -carotene enrichment. Journal of Plant Biochemistry and Biotechnology, 2016, 25, 12-20.	0.9	19
1523	Assessment of genetic diversity and relationships of Krachai Sayam, an endemic plant in Thailand using microsatellite markers. Plant Biosystems, 2016, 150, 963-970.	0.8	0
1524	Associations of polymorphisms in bovine DGAT1, FABP4, FASN, and PPARGC1A genes with intramuscular fat content and the fatty acid composition of muscle and subcutaneous fat in Fleckvieh bulls. Meat Science, 2016, 114, 18-23.	2.7	39
1525	Simple sequence repeat markers that identify <i>Claviceps</i> species and strains. Fungal Biology and Biotechnology, 2016, 3, 1.	2.5	34
1526	Genetic Diversity and Erosion in Plants. Sustainable Development and Biodiversity, 2016, , .	1.4	13
1527	Analytical and Decision Support Tools for Genomics-Assisted Breeding. Trends in Plant Science, 2016, 21, 354-363.	4.3	70
1528	Genetic diversity of Vietnamese lowland rice germplasms as revealed by SSR markers in relation to seedling vigour under submergence. Biotechnology and Biotechnological Equipment, 2016, 30, 17-25.	0.5	5
1529	How endogenous plant pararetroviruses shed light on <i>Musa</i> evolution. Annals of Botany, 2016, 117, 625-641.	1.4	18
1530	Genetic distribution of 15 autosomal STR markers in the Punjabi population of Pakistan. International Journal of Legal Medicine, 2016, 130, 1487-1488.	1.2	7
1531	Discovery of QTLs for water mining and water use efficiency traits in rice under water-limited condition through association mapping. Molecular Breeding, 2016, 36, 1.	1.0	21

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1532	The identification of presence/absence variants associated with the apparent differences of growth period structures between cultivated and wild soybeans. <i>Journal of Integrative Agriculture</i> , 2016, 15, 262-270.	1.7	2
1533	Life history traits and geographical divergence in wild rice (<i>Oryza rufipogon</i>) gene pool in Indochina Peninsula region. <i>Annals of Applied Biology</i> , 2016, 168, 52-65.	1.3	5
1534	Morpho-agronomic and AFLP characterization to explore guar (<i>Cyamopsis tetragonoloba</i> L.) genotypes for the Mediterranean environment. <i>Industrial Crops and Products</i> , 2016, 86, 23-30.	2.5	20
1535	Phylogenetic analysis, genetic diversity and relationships between the recently segregated species of <i>Corynandra</i> and <i>Cleoserrata</i> from the genus <i>Cleome</i> using DNA barcoding and molecular markers. <i>Comptes Rendus - Biologies</i> , 2016, 339, 123-132.	0.1	8
1536	Analysis of polymorphisms in the equine MSTN gene in Polish populations of horse breeds. <i>Livestock Science</i> , 2016, 187, 151-157.	0.6	7
1537	Endemic insular and coastal Tunisian date palm genetic diversity. <i>Genetica</i> , 2016, 144, 181-190.	0.5	14
1538	The Genetic Basis of Haploid Induction in Maize Identified with a Novel Genome-Wide Association Method. <i>Genetics</i> , 2016, 202, 1267-1276.	1.2	61
1539	Quantitative Trait Loci Mapping in Plants: Concepts and Approaches. <i>Sustainable Development and Biodiversity</i> , 2016, , 31-59.	1.4	22
1540	Genetic diversity and parentage analysis of aspen demes. <i>New Forests</i> , 2016, 47, 143-162.	0.7	1
1541	Nuclear microsatellites reveal the genetic architecture and breeding history of tea germplasm of East Africa. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	33
1542	A genome-wide association study reveals novel elite allelic variations in seed oil content of <i>Brassica napus</i> . <i>Theoretical and Applied Genetics</i> , 2016, 129, 1203-1215.	1.8	185
1543	Association mapping for drought tolerance in barley at the reproductive stage. <i>Comptes Rendus - Biologies</i> , 2016, 339, 51-59.	0.1	26
1544	Genetic distance revealed by genomic single nucleotide polymorphisms and their relationships with harvest index heterotic traits in rapeseed (<i>Brassica napus</i> L.). <i>Euphytica</i> , 2016, 209, 41-47.	0.6	16
1545	The triploid East African Highland Banana (EAHB) genepool is genetically uniform arising from a single ancestral clone that underwent population expansion by vegetative propagation. <i>Theoretical and Applied Genetics</i> , 2016, 129, 547-561.	1.8	45
1546	Y-chromosome phylogeographic analysis of the Greek-Cypriot population reveals elements consistent with Neolithic and Bronze Age settlements. <i>Investigative Genetics</i> , 2016, 7, 1.	3.3	20
1547	SSR assessment of the genetic diversity of emmer wheat with emphasis on Iranian landraces (<i>Triticum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	0.8	8
1548	Identification of candidate genes for dissecting complex branch number trait in chickpea. <i>Plant Science</i> , 2016, 245, 61-70.	1.7	21
1549	Molecular characterization of accessions of a rare genetic resource: sugary cassava (<i>Manihot</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	0.8	8

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1550	Analysis of population structure and genetic diversity of Egyptian and exotic rice (<i>Oryza sativa</i> L.) genotypes. <i>Comptes Rendus - Biologies</i> , 2016, 339, 1-9.	0.1	64
1551	Usefulness of the cloned and fine-mapped genes/QTL for grain yield and related traits in indica rice breeding for irrigated ecosystems. <i>Field Crops Research</i> , 2016, 187, 58-73.	2.3	15
1552	Fusarium head blight resistance loci in a stratified population of wheat landraces and varieties. <i>Euphytica</i> , 2016, 207, 551-561.	0.6	20
1553	Genetic Diversity and Conservation of Olive Genetic Resources. <i>Sustainable Development and Biodiversity</i> , 2016, , 337-356.	1.4	11
1554	SNP diversity within and among <i>Brassica rapa</i> accessions reveals no geographic differentiation. <i>Genome</i> , 2016, 59, 11-21.	0.9	15
1555	Baluchi and Pakhtun population data of 9 X-chromosomal short tandem repeat loci. <i>Journal of Clinical Forensic and Legal Medicine</i> , 2016, 37, 45-49.	0.5	1
1556	Large-scale developing of simple sequence repeat markers and probing its correlation with ramie (<i>Boehmeria nivea</i> L.) fiber quality. <i>Molecular Genetics and Genomics</i> , 2016, 291, 753-761.	1.0	6
1557	Parallel consideration of SSRs and differentially expressed genes under abiotic stress for targeted development of functional markers in almond and related <i>Prunus</i> species. <i>Scientia Horticulturae</i> , 2016, 198, 462-472.	1.7	14
1558	Genetic diversity among synthetic hexaploid wheat accessions (<i>Triticum aestivum</i>) with resistance to several fungal diseases. <i>Genetic Resources and Crop Evolution</i> , 2016, 63, 1285-1296.	0.8	43
1559	Genetic Diversity, Genotype Discrimination, and Population Structure of Mexican <i>Opuntia</i> sp., Determined by SSR Markers. <i>Plant Molecular Biology Reporter</i> , 2016, 34, 146-159.	1.0	27
1560	A comparison of polymorphism information content and mean of transformed kinships as criteria for selecting informative subsets of barley (<i>Hordeum vulgare</i> L. s. l.) from the USDA Barley Core Collection. <i>Genetic Resources and Crop Evolution</i> , 2016, 63, 477-482.	0.8	13
1561	Molecular and Phenotypic Characterization of 149 Finger Millet Accessions Using Microsatellite and Agro-Morphological Markers. <i>Proceedings of the National Academy of Sciences India Section B - Biological Sciences</i> , 2017, 87, 1217-1228.	0.4	13
1562	Characterization of indica-japonica subspecies-specific InDel loci in wild relatives of rice (<i>Oryza</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 405-418.	0.8	7
1563	Isolation and Characterization of Novel Polymorphic Microsatellite Loci in <i>Hippophae rhamnoides</i> . <i>Proceedings of the National Academy of Sciences India Section B - Biological Sciences</i> , 2017, 87, 727-732.	0.4	5
1564	Genetic diversity and origin of North American green foxtail [<i>Setaria viridis</i> (L.) Beauv.] accessions. <i>Genetic Resources and Crop Evolution</i> , 2017, 64, 367-378.	0.8	29
1565	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.	0.4	14
1566	Genetic diversity patterns in ex situ collections of <i>Oryza officinalis</i> Wall. ex G. Watt revealed by morphological and microsatellite markers. <i>Genetic Resources and Crop Evolution</i> , 2017, 64, 733-744.	0.8	3
1567	Genetic variability and population structure in a collection of inbred lines derived from a core germplasm of castor. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2017, 26, 27-34.	0.9	17

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1568	Development and Evaluation of a High Density Genotyping <i>â€</i> Axiom_Arachis ^{â€} ™ Array with 58â€%K SNPs for Accelerating Genetics and Breeding in Groundnut. <i>Scientific Reports</i> , 2017, 7, 40577.	1.6	144
1569	Morphological and molecular diversity patterns in castor germplasm accessions. <i>Industrial Crops and Products</i> , 2017, 97, 316-323.	2.5	31
1570	Genetic Diversity of Chinese and Global Pea (<i>Pisum sativum</i> L.) Collections. <i>Crop Science</i> , 2017, 57, 1574-1584.	0.8	12
1571	Genetic divergence in two tropical maize composites after four cycles of reciprocal recurrent selection. <i>Plant Breeding</i> , 2017, 136, 41-49.	1.0	12
1572	Genome-wide assessment of population structure, linkage disequilibrium and resistant QTLs in Chinese wild grapevine. <i>Scientia Horticulturae</i> , 2017, 215, 59-64.	1.7	12
1573	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.	1.4	25
1574	Pasting properties, grain-filling characteristics and allelic variation linked to the grain quality in diverse rice. <i>Euphytica</i> , 2017, 213, 1.	0.6	6
1575	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.	1.6	12
1576	Development and validation of EST derived SSR markers with relevance to downy mildew (<i>Sclerospora</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T Biochemistry and Biotechnology, 2017, 26, 356-365.	0.9	6
1577	The iSelect 9â€%K SNP analysis revealed polyploidization induced revolutionary changes and intense human selection causing strong haplotype blocks in wheat. <i>Scientific Reports</i> , 2017, 7, 41247.	1.6	37
1578	The genetic characterization of an isolated remnant population of an endangered rodent (<i>Cricetus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 759-775.	0.8	12
1579	Genomewide association study for seeding emergence and tiller number using SNP markers in an elite winter wheat population. <i>Journal of Genetics</i> , 2017, 96, 177-186.	0.4	27
1580	Molecular characterization of AIPL1 gene region in the Iranian population: application of novel informative haplotypes and detection of mutational founder effect. <i>Genes and Genomics</i> , 2017, 39, 433-443.	0.5	4
1581	Association mapping of aphid resistance in USDA cowpea (<i>Vigna unguiculata</i> L. Walp.) core collection using SNPs. <i>Euphytica</i> , 2017, 213, 1.	0.6	26
1582	Forensic and population genetic analyses of the GlobalFiler STR loci in the Mongolian population. <i>Genes and Genomics</i> , 2017, 39, 423-431.	0.5	22
1583	Resolving evolutionary relationships in closely related nonmodel organisms: a case study using chromosomally distinct members of a black fly species complex. <i>Systematic Entomology</i> , 2017, 42, 489-508.	1.7	10
1584	Microsatellite marker based genetic diversity analysis among cotton (<i>Gossypium hirsutum</i>) accessions differing for their response to drought stress. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2017, 26, 366-370.	0.9	10
1585	Genetic variations of 15 autosomal and 17 Y-STR markers in Sindhi population of Pakistan. <i>International Journal of Legal Medicine</i> , 2017, 131, 1239-1240.	1.2	9

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1586	Phenotypic and genotypic screening for rust resistance in common bean germplasm in Uganda. <i>Euphytica</i> , 2017, 213, 1.	0.6	3
1587	S_allele identification and genetic diversity analysis of apricot cultivars. <i>Journal of Horticultural Science and Biotechnology</i> , 2017, 92, 251-260.	0.9	6
1588	Cross-taxon application of sugarcane EST-SSR to genetic diversity analysis of bermudagrass (<i>Cynodon</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.8	9
1589	Genetic analysis of 19 X chromosome STR loci for forensic purposes in four Chinese ethnic groups. <i>Scientific Reports</i> , 2017, 7, 42782.	1.6	25
1590	Genetic polymorphisms of 12 X STR loci in Shaanxi Han population from China. <i>Legal Medicine</i> , 2017, 26, 76-78.	0.6	5
1591	Estimation of genetic diversity and relationship in sugar beet pollinators based on SSR markers. <i>Electronic Journal of Biotechnology</i> , 2017, 27, 1-7.	1.2	14
1592	Nuclear genetic diversity and population structure of a vulnerable and endemic orchid (<i>Cymbidium</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.7	11
1593	Allele mining in the Argentine public maize inbred line collection of two paralogous genes encoding NAC domains. <i>Molecular Breeding</i> , 2017, 37, 1.	1.0	4
1594	Reduced representation genome sequencing reveals patterns of genetic diversity and selection in apple. <i>Journal of Integrative Plant Biology</i> , 2017, 59, 190-204.	4.1	30
1595	Development and mapping of microsatellite markers from transcriptome sequences of European hazelnut (<i>Corylus avellana</i> L.) and use for germplasm characterization. <i>Molecular Breeding</i> , 2017, 37, 1.	1.0	33
1596	Genetic diversity of safflower (<i>Carthamus tinctorius</i> L.) germplasm as revealed by SSR markers. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2017, 15, 1-11.	0.4	25
1597	Genome-wide association study discovered genetic variation and candidate genes of fibre quality traits in <i>Gossypium hirsutum</i> L.. <i>Plant Biotechnology Journal</i> , 2017, 15, 982-996.	4.1	199
1598	The relative importance of conidia and ascospores as primary inoculum of <i>Venturia inaequalis</i> in a southeast England orchard. <i>Plant Pathology</i> , 2017, 66, 1445-1451.	1.2	18
1599	Molecular and cytological characterization of the global <i>Musa</i> germplasm collection provides insights into the treasure of banana diversity. <i>Biodiversity and Conservation</i> , 2017, 26, 801-824.	1.2	108
1600	Genetic diversity in some faba bean (<i>Vicia faba</i> L.) genotypes assessed by simple sequence repeats. <i>Biotechnology and Biotechnological Equipment</i> , 2017, 31, 29-35.	0.5	10
1601	Genetic structure of populations and natural hybridization between <i>Dactylorhiza salina</i> and <i>D. incarnata</i> (Orchidaceae). <i>Russian Journal of Genetics</i> , 2017, 53, 325-337.	0.2	2
1602	Genotyping of <i>Theileria lestoquardi</i> from sheep and goats in Sudan to support control of Malignant Ovine Theileriosis. <i>Veterinary Parasitology</i> , 2017, 239, 7-14.	0.7	9
1603	Validation of Seed Weight-Associated SSR Markers and Their Usefulness in Distinguishing Chickpea Genotypes According to Seed Size. <i>Agricultural Research</i> , 2017, 6, 130-138.	0.9	5

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1604	De novo assembly of transcriptome from <i>Rhododendron latoucheae</i> Franch. using Illumina sequencing and development of new EST-SSR markers for genetic diversity analysis in <i>Rhododendron</i> . <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	46
1605	Assessment of genetic relationships between cultivated arracacha (<i>Arracacia xanthorrhiza</i> Bancr.) and its wild close relatives in the area of domestication using microsatellite markers. <i>Conservation Genetics</i> , 2017, 18, 1267-1275.	0.8	1
1606	Genetic Diversity and Core Collection for Potato (<i>Solanum tuberosum</i> L.) Cultivars from Cameroon as Revealed by SSR Markers. <i>American Journal of Potato Research</i> , 2017, 94, 449-463.	0.5	13
1607	Genetic structure of <i>Cannabis sativa</i> var. <i>indica</i> cultivars based on genomic SSR (gSSR) markers: Implications for breeding and germplasm management. <i>Industrial Crops and Products</i> , 2017, 104, 171-178.	2.5	55
1608	Population analysis and forensic evaluation of 21 autosomal loci included in GlobalFiler [®] , [®] PCR Kit in Poland. <i>Forensic Science International: Genetics</i> , 2017, 29, e38-e39.	1.6	23
1609	Genetic association analysis of candidate loci under selection with size in the South African abalone. <i>Aquaculture International</i> , 2017, 25, 1197-1214.	1.1	2
1610	Development of High Quality EST-SSR Markers Without Stutter Bands in Peach and Their Application in Cultivar Discrimination and Hybrid Authentication. <i>Hortscience: A Publication of the American Society for Horticultural Science</i> , 2017, 52, 24-30.	0.5	3
1611	Development of a set of SSR markers for genetic polymorphism detection and interspecific hybrid jute breeding. <i>Crop Journal</i> , 2017, 5, 416-429.	2.3	35
1613	Towards new sources of resistance to the currant-lettuce aphid (<i>Nasonovia ribisnigri</i>). <i>Molecular Breeding</i> , 2017, 37, 4.	1.0	17
1614	Genetic diversity and population structure of pummelo (<i>Citrus maxima</i>) germplasm in China. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	16
1615	Genetic characterization of Czech local rabbit breeds using microsatellite analysis. <i>Livestock Science</i> , 2017, 201, 41-49.	0.6	6
1616	First microsatellite markers for <i>Scaligeria lazica</i> Boiss. (Apiaceae) by next-generation sequencing: population structure and genetic diversity analysis. <i>Biotechnology and Biotechnological Equipment</i> , 2017, 31, 535-543.	0.5	3
1617	Genome-wide Association Analysis Tracks Bacterial Leaf Blight Resistance Loci In Rice Diverse Germplasm. <i>Rice</i> , 2017, 10, 8.	1.7	49
1618	Identification and characterization of simple sequence repeats (SSRs) for population studies of <i>Puccinia novopanici</i> . <i>Journal of Microbiological Methods</i> , 2017, 139, 113-122.	0.7	6
1619	Genetic diversity and association mapping of agronomic yield traits in eighty six synthetic hexaploid wheat. <i>Euphytica</i> , 2017, 213, 1.	0.6	15
1620	Developmental validation of the HomyGene19+14Y System. <i>International Journal of Legal Medicine</i> , 2017, 131, 605-620.	1.2	8
1621	Population data of 18 autosomal STR loci in the Chinese Han population from Heilongjiang Province, Northeast China. <i>Forensic Science International: Genetics</i> , 2017, 29, e33-e34.	1.6	10
1622	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.	1.0	24

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1623	Self-(in)compatibility in apricot germplasm is controlled by two major loci, S and M. <i>BMC Plant Biology</i> , 2017, 17, 82.	1.6	24
1624	Genetic diversity of Southeastern Nigerian date palms reveals a secondary structure within Western populations. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	12
1625	Breeding histories and selection criteria for oilseed rape in Europe and China identified by genome wide pedigree dissection. <i>Scientific Reports</i> , 2017, 7, 1916.	1.6	16
1626	PCR optimization and allele distribution of SNAC1 gene coding region in rice (<i>Oryza sativa</i> L.). <i>Agri Gene</i> , 2017, 4, 30-36.	1.9	0
1627	Genetic analysis of early-maturing maize (<i>Zea Mays</i> L.) inbred lines under stress and nonstress conditions. <i>Journal of Crop Improvement</i> , 2017, 31, 560-588.	0.9	12
1628	Genome-wide association study of outcrossing in cytoplasmic male sterile lines of rice. <i>Scientific Reports</i> , 2017, 7, 3223.	1.6	13
1629	Single-Nucleotide Polymorphism of CYP3A5 Impacts the Exposure to Tacrolimus in Pediatric Renal Transplant Recipients: A Pharmacogenetic Substudy of the TWIST Trial. <i>Therapeutic Drug Monitoring</i> , 2017, 39, 21-28.	1.0	17
1630	Analysis on Solanesol Content and Genetic Diversity of Chinese Flue-cured Tobacco (<i>Nicotiana glauca</i> L.) Cultivars. <i>Journal of Agricultural Science</i> , 2017, 150, 1-11.	0.8	7
1631	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.	1.8	64
1632	SSR marker analysis points to population admixture and continuum of genetic variation among Indian landraces of brinjal (<i>Solanum melongena</i> L.). <i>Scientia Horticulturae</i> , 2017, 224, 68-73.	1.7	4
1633	Identification of (in)compatible <i>S</i> -genotypes and molecular characterisation of Italian sweet cherry cultivars. <i>Acta Horticulturae</i> , 2017, , 41-46.	0.1	2
1634	Chinese Sesame Cultivars, DNA Fingerprinting, and Two-dimensional Barcodes Using Single Nucleotide Polymorphisms, Insertions or Deletions, and Simple Sequence Repeat Markers. <i>Crop Science</i> , 2017, 57, 1941-1947.	0.8	4
1635	EST-SSR marker development and transcriptome sequencing analysis of different tissues of Korean pine (<i>Pinus koraiensis</i> Sieb. et Zucc.). <i>Biotechnology and Biotechnological Equipment</i> , 0, , 1-11.	0.5	10
1636	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.	1.0	19
1637	Genetic diversity of <i>Miscanthus sinensis</i> in US naturalized populations. <i>GCB Bioenergy</i> , 2017, 9, 965-972.	2.5	13
1638	Assessing the numbers of SNPs needed to establish molecular IDs and characterize the genetic diversity of soybean cultivars derived from Tokachi nagaha. <i>Crop Journal</i> , 2017, 5, 326-336.	2.3	12
1639	Population data of 15 autosomal STR loci in Chinese Han population from Yangjiang, Southern China. <i>Forensic Science International: Genetics</i> , 2017, 28, e14-e15.	1.6	3
1640	Genetic polymorphisms of 20 autosomal STR loci in 5141 individuals from the Han population of Xiamen, Southeast China. <i>Forensic Science International: Genetics</i> , 2017, 29, e31-e32.	1.6	25

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1641	Microsatellite-based genetic diversity analyses of sugary1-, shrunken2- and double mutant- sweet corn inbreds for their utilization in breeding programme. <i>Physiology and Molecular Biology of Plants</i> , 2017, 23, 411-420.	1.4	26
1642	Structural pattern and genetic diversity in blueberry (<i>Vaccinium</i>) clones and cultivars using EST-PCR and microsatellite markers. <i>Genetic Resources and Crop Evolution</i> , 2017, 64, 2071-2082.	0.8	11
1643	Molecular Diversity in some Ghanaian Cowpea [<i>Vigna unguiculata</i> L. (Walp)] Accessions. <i>Tropical Plant Biology</i> , 2017, 10, 57-67.	1.0	5
1644	New polymorphic microsatellite markers derived from hemocyte cDNA library of Manila clam <i>Ruditapes philippinarum</i> challenged by the protozoan parasite <i>Perkinsus olseni</i> . <i>Ocean Science Journal</i> , 2017, 52, 139-146.	0.6	0
1645	Marker detection and elite allele mining for yield traits in Upland cotton (<i>Gossypium hirsutum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 TF	0.6	6
1646	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.	1.8	1
1647	Genome-wide association mapping and Identification of candidate genes for fatty acid composition in <i>Brassica napus</i> L. using SNP markers. <i>BMC Genomics</i> , 2017, 18, 232.	1.2	105
1648	Population structure and genetic basis of the agronomic traits of upland cotton in China revealed by a genome-wide association study using high-density SNPs. <i>Plant Biotechnology Journal</i> , 2017, 15, 1374-1386.	4.1	196
1649	Population data of 19 autosomal STR loci in the Chinese Han population from Jiujiang, Southern China. <i>Forensic Science International: Genetics</i> , 2017, 28, e47-e48.	1.6	15
1650	Analysis of QTL for seed oil content in <i>Brassica napus</i> by association mapping and QTL mapping. <i>Euphytica</i> , 2017, 213, 1.	0.6	24
1651	Development and characterization of 23 microsatellite markers for the endangered beetle <i>Carabus lafossei</i> (Coleoptera, Carabidae). <i>Conservation Genetics Resources</i> , 2017, 9, 249-251.	0.4	0
1652	Assessing genetic variation for heat stress tolerance in Indian bread wheat genotypes using morpho-physiological traits and molecular markers. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2017, 15, 539-547.	0.4	18
1653	Population data of 15 autosomal STR loci in Chinese Han population from Jilin Province, Northeast China. <i>Forensic Science International: Genetics</i> , 2017, 27, 187-188.	1.6	13
1654	Development of a SNP-based panel for human identification for Indian populations. <i>Forensic Science International: Genetics</i> , 2017, 27, 58-66.	1.6	12
1655	Developmental validation of a custom panel including 273 SNPs for forensic application using Ion Torrent PGM. <i>Forensic Science International: Genetics</i> , 2017, 27, 50-57.	1.6	44
1656	Genetic diversity and linkage disequilibrium in the Argentine public maize inbred line collection. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2017, 15, 515-526.	0.4	7
1657	Taxonomic and geographic variation of the <i>Pinus mugo</i> complex on chloroplast microsatellite markers. <i>Systematics and Biodiversity</i> , 2017, 15, 464-479.	0.5	12
1658	Genetic Characterization of Chinese fir from Six Provinces in Southern China and Construction of a Core Collection. <i>Scientific Reports</i> , 2017, 7, 13814.	1.6	52

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1660	Genetic polymorphisms of 15 autosomal STR loci in 3962 individuals from the Han population of Jiangxi, Southeast China. <i>Forensic Science International: Genetics</i> , 2017, 31, e57-e58.	1.6	5
1661	Molecular genetic diversity of the Turkish national hazelnut collection and selection of a core set. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	17
1662	Comparative analysis of core collection sampling methods for mandarin germplasm based on molecular and phenotypic data. <i>Annals of Applied Biology</i> , 2017, 171, 327-339.	1.3	10
1663	Determination of genetic polymorphism in Guney Karaman local Turkish sheep breed by using STR markers. <i>AIP Conference Proceedings</i> , 2017, , .	0.3	0
1664	Genetic diversity and population structure of Indian soybean [<i>Glycine max</i> (L.) Merr.] revealed by simple sequence repeat markers. <i>Journal of Crop Science and Biotechnology</i> , 2017, 20, 221-231.	0.7	9
1665	Genome-Wide Association Mapping Reveals That Specific and Pleiotropic Regulatory Mechanisms Fine-Tune Central Metabolism and Growth in Arabidopsis. <i>Plant Cell</i> , 2017, 29, 2349-2373.	3.1	32
1666	Characterization of <i>Perilla frutescens</i> (Linn.) Britt based on morphological, biochemical and STMS markers. <i>Industrial Crops and Products</i> , 2017, 109, 773-785.	2.5	3
1667	Cross-genera Transferability of Microsatellite Loci for Asian Palmyra Palm (<i>Borassus flabellifer</i> L.). <i>Hortscience: A Publication of the American Society for Horticultural Science</i> , 2017, 52, 1164-1167.	0.5	3
1668	A genome-wide survey with different rapeseed ecotypes uncovers footprints of domestication and breeding. <i>Journal of Experimental Botany</i> , 2017, 68, 4791-4801.	2.4	52
1669	Associations between the δ^5 -terpineol synthase gene and δ^5 -terpineol content in different grapevine varieties. <i>Biotechnology and Biotechnological Equipment</i> , 2017, 31, 1100-1105.	0.5	5
1670	Molecular characterization of Vietnamese cocoa genotypes (<i>Theobroma cacao</i> L.) using microsatellite markers. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	6
1671	Genetic structure of putative heterotic populations of alfalfa. <i>Plant Breeding</i> , 2017, 136, 671-678.	1.0	4
1672	Massively parallel sequencing of 231 autosomal SNPs with a custom panel: a SNP typing assay developed for human identification with Ion Torrent PGM. <i>Forensic Sciences Research</i> , 2017, 2, 26-33.	0.9	8
1673	Genetic diversity and association mapping of forage quality in diverse bermudagrass accessions. <i>Euphytica</i> , 2017, 213, 1.	0.6	9
1674	Linkage disequilibrium based association mapping of micronutrients in common bean (<i>Phaseolus</i>) Tj ETQq1 1 0.784314 rgBT/Overlode	1.1	18
1675	Genetic diversity and population structure of <i>Cucumis sativus</i> L. by using SSR markers. <i>3 Biotech</i> , 2017, 7, 307.	1.1	18
1676	Pathogenic and genetic variability of <i>Fusarium verticillioides</i> from maize in northern Mexico. <i>Canadian Journal of Plant Pathology</i> , 2017, 39, 486-496.	0.8	6

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1678	Multiple locus genome-wide association studies for important economic traits of oil palm. Tree Genetics and Genomes, 2017, 13, 1.	0.6	24
1679	Genetic diversity analysis of Amomum tsao-ko in Jinping County of Yunnan Province using SSR markers. AIP Conference Proceedings, 2017, , .	0.3	2
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1682	Construction of fingerprinting for tea plant (Camellia sinensis) accessions using new genomic SSR markers. Molecular Breeding, 2017, 37, 1.	1.0	50
1683	Genetic analysis of winter hardiness and effect of sowing date on yield traits in winter faba bean. Scientia Horticulturae, 2017, 224, 296-301.	1.7	15
1684	Genetic and fruit trait differences between Chinese elite lines/varieties and American varieties of processing tomato. Scientia Horticulturae, 2017, 224, 251-257.	1.7	3
1685	Genetic diversity and structure of elite cotton germplasm (Gossypium hirsutum L.) using genome-wide SNP data. Genetica, 2017, 145, 409-416.	0.5	14
1686	Genome-wide association mapping of latex yield and girth in Amazonian accessions of Hevea brasiliensis grown in a suboptimal climate zone. Genomics, 2017, 109, 475-484.	1.3	30
1687	Unexpected pattern of pearl millet genetic diversity among ethno-linguistic groups in the Lake Chad Basin. Heredity, 2017, 118, 491-502.	1.2	25
1688	Candidate loci involved in domestication and improvement detected by a published 90K wheat SNP array. Scientific Reports, 2017, 7, 44530.	1.6	50
1689	Date Palm Genetic Diversity Analysis Using Microsatellite Polymorphism. Methods in Molecular Biology, 2017, 1638, 113-124.	0.4	6
1690	Developmental validation of a 6-dye typing system with 27 loci and application in Han population of China. Scientific Reports, 2017, 7, 4706.	1.6	35
1691	Marker-trait association analysis of frost tolerance of 672 worldwide pea (Pisum sativum L.) collections. Scientific Reports, 2017, 7, 5919.	1.6	23
1692	Genetic diversity and population structure of <i>Striga hermonthica</i> populations from Kenya and Nigeria. Weed Research, 2017, 57, 293-302.	0.8	23
1693	Genetic Diversity and Population Structure in the Landrace Accessions of <i>Gossypium hirsutum</i> . Crop Science, 2017, 57, 2457-2470.	0.8	12
1694	DNA-based diversity of tea plants grown in Italy. Genetic Resources and Crop Evolution, 2017, 64, 1905-1915.	0.8	7

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1696	Forensic application of EST-derived STR markers in opium poppy. <i>Biologia (Poland)</i> , 2017, 72, 587-594.	0.8	11
1697	Genome-wide association mapping reveals a rich genetic architecture of stripe rust resistance loci in emmer wheat (<i>Triticum turgidum</i> ssp. <i>dicoccum</i>). <i>Theoretical and Applied Genetics</i> , 2017, 130, 2249-2270.	1.8	80
1698	Characterization of molecular diversity and genome-wide mapping of loci associated with resistance to stripe rust and stem rust in Ethiopian bread wheat accessions. <i>BMC Plant Biology</i> , 2017, 17, 134.	1.6	99
1699	Genetic Diversity and Association Study of Aromatics in Grapevine. <i>Journal of the American Society for Horticultural Science</i> , 2017, 142, 225-231.	0.5	17
1700	S-genotype identification, genetic diversity and structure analysis of Italian sweet cherry germplasm. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	15
1701	Identification of transposable element markers associated with yield and quality traits from an association panel of independent mutants in peanut (<i>Arachis hypogaea</i> L.). <i>Euphytica</i> , 2017, 213, 1.	0.6	17
1702	Development of Novel Small InDel Markers in Jute (<i>Corchorus</i> spp.). <i>Tropical Plant Biology</i> , 2017, 10, 169-176.	1.0	10
1703	Genetic Diversity and Population Structure of <i>Gerbera delavayi</i> (Asteraceae) in Southwest China: Implications for Conservation. <i>Annales Botanici Fennici</i> , 2017, 54, 409-422.	0.0	3
1704	Genetic analysis of tropical quality protein maize (<i>Zea mays</i> L.) germplasm. <i>Euphytica</i> , 2017, 213, 261.	0.6	17
1705	Comparison of transcriptome-derived simple sequence repeat (SSR) and single nucleotide polymorphism (SNP) markers for genetic fingerprinting, diversity evaluation, and establishment of relationships in eggplants. <i>Euphytica</i> , 2017, 213, 1.	0.6	44
1706	Genetic diversity and relatedness among ornamental purslane (<i>Portulaca</i> L.) accessions unraveled by SRAP markers. <i>3 Biotech</i> , 2017, 7, 241.	1.1	5
1707	Genetic analyses reveal independent domestication origins of the emerging oil crop <i>Paeonia ostii</i> , a tree peony with a long-term cultivation history. <i>Scientific Reports</i> , 2017, 7, 5340.	1.6	19
1708	Development of RNA-Seq SSR Markers and Application to Genetic Relationship Analysis among Sea Buckthorn Germplasm. <i>Journal of the American Society for Horticultural Science</i> , 2017, 142, 200-208.	0.5	9
1709	Exploring Key Blast and Bacterial Blight Resistance Genes in Genetically Diverse Rice Accessions through Molecular and Phenotypic Evaluation. <i>Crop Science</i> , 2017, 57, 1881-1892.	0.8	2
1710	Microsatellite analysis of population structure in <i>Eucalyptus globulus</i> . <i>Genome</i> , 2017, 60, 770-777.	0.9	12
1711	Comparative assessment of genetic diversity in <i>Sesamum indicum</i> L. using RAPD and SSR markers. <i>3 Biotech</i> , 2017, 7, 10.	1.1	18
1712	Efficiency of SNP and SSR-based analysis of genetic diversity, population structure, and relationships among cowpea (<i>Vigna unguiculata</i> (L.) Walp.) germplasm from East Africa and IITA inbred lines. <i>Journal of Crop Science and Biotechnology</i> , 2017, 20, 107-128.	0.7	10

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1714	Genetic diversity and a population structure analysis of accessions in the Chinese cowpea [<i>Vigna unguiculata</i> (L.) Walp.] germplasm collection. <i>Crop Journal</i> , 2017, 5, 363-372.	2.3	52
1715	Brazilian melon landraces resistant to <i>Podosphaera xanthii</i> are unique germplasm resources. <i>Annals of Applied Biology</i> , 2017, 171, 214-228.	1.3	5
1716	Validation of a set of informative simple sequence repeats markers for variety identification in Pakchoi (<i>Brassica rapa</i> L. ssp. <i>chinensis</i> var. <i>communis</i>). <i>Plant Breeding</i> , 2017, 136, 410-419.	1.0	5
1717	Selection of soybean elite cultivars based on phenotypic and genomic characters related to lodging tolerance. <i>Plant Breeding</i> , 2017, 136, 526-538.	1.0	8
1718	Tracking the geographical origin of timber by DNA fingerprinting: a study of the endangered species <i>Cinnamomum kanehirae</i> in Taiwan. <i>Holzforschung</i> , 2017, 71, 853-862.	0.9	11
1719	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.	0.5	11
1720	Multiplex-ready PCR assay of SSR marker diversity among quality protein maize inbred parental lines. <i>South African Journal of Plant and Soil</i> , 2017, 34, 149-154.	0.4	1
1721	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.	1.0	21
1722	Genetic diversity and population structure of castor (<i>Ricinus communis</i> L.) germplasm within the US collection assessed with EST-SSR markers. <i>Genome</i> , 2017, 60, 193-200.	0.9	17
1723	Investigator® HDplex (Qiagen) reference population database for forensic use in Argentina. <i>Forensic Science International: Genetics</i> , 2017, 26, 91-95.	1.6	8
1724	Variation in TBX3 Gene Region in Dun Coat Color Polish Konik Horses. <i>Journal of Equine Veterinary Science</i> , 2017, 49, 60-62.	0.4	11
1725	Population Structure Analysis and Selection of Core Set among Common Bean Genotypes from Jammu and Kashmir, India. <i>Applied Biochemistry and Biotechnology</i> , 2017, 182, 16-28.	1.4	13
1726	Establishment of a Core Collection of Traditional Cuban <i>Theobroma cacao</i> Plants for Conservation and Utilization Purposes. <i>Plant Molecular Biology Reporter</i> , 2017, 35, 47-60.	1.0	9
1727	Genetic diversity of melon landraces (<i>Cucumis melo</i> L.) in the Xinjiang Uygur Autonomous Region on the basis of simple sequence repeat markers. <i>Genetic Resources and Crop Evolution</i> , 2017, 64, 1023-1035.	0.8	7
1728	Genetic diversity and relationship of Guinea yam (<i>Dioscorea cayenensis</i> Lam. "D. rotundata Poir.) Tj ETQq1 1 0.784314 rgBT /Overlock Evolution, 2017, 64, 1205-1219.	0.8	16
1729	An assessment of spatio-temporal genetic variation in the South African abalone (<i>Haliotis midae</i>), using SNPs: implications for conservation management. <i>Conservation Genetics</i> , 2017, 18, 17-31.	0.8	14
1730	Genetic stock identification of Atlantic salmon and its evaluation in a large population complex. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2017, 74, 327-338.	0.7	39

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1731	Evaluating Agronomic Performance and Investigating Molecular Structure of Drought and Heat Tolerant Wild Alfalfa (<i>Medicago sativa</i> L.) Collection from the Southeastern Turkey. <i>Biochemical Genetics</i> , 2017, 55, 63-76.	0.8	5
1732	Genetic distinctiveness of safflower cultivars of India and Mexico as revealed by SSR markers. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2017, 15, 474-487.	0.4	7
1733	Characterization and selection of exploitable genetic diversity in soursop (<i>Annona muricata</i> Linn.) accessions based on phenotypic attributes and RAPD markers. <i>Agroforestry Systems</i> , 2017, 91, 781-793.	0.9	4
1734	Phenotypic characterization and genetic dissection of nine agronomic traits in Tokachi nagaha and its derived cultivars in soybean (<i>Glycine max</i> (L.) Merr.). <i>Plant Science</i> , 2017, 256, 72-86.	1.7	25
1735	â€Rutpinkâ€™™ (Scarlet FireÂ®) Kousa Dogwood. <i>Hortscience: A Publication of the American Society for Horticultural Science</i> , 2017, 52, 1438-1442.	0.5	1
1736	Genetic diversity of fig (<i>Ficus carica</i> L.) genotypes grown in Southern Italy revealed by the use of SSR markers. <i>Acta Horticulturae</i> , 2017, , 75-80.	0.1	8
1737	Molecular characterization of local mango (<i>Mangifera indica</i> L.) germplasm in Oman. <i>Acta Horticulturae</i> , 2017, , 105-112.	0.1	0
1738	Microsatellite markers revealed moderate genetic diversity and population differentiation of moso bamboo (<i>Phyllostachys edulis</i>)â€™a primarily asexual reproduction species in China. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	19
1739	Genetic structure and demographic history of <i>Lymantria dispar</i> (Linnaeus, 1758) (Lepidoptera: Tj ETQq0 0 0 rgBT /Overlock 10 T	0.8	13
1740	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.	1.8	117
1741	Comparative transcriptomics uncovers alternative splicing and molecular marker development in radish (<i>Raphanus sativus</i> L.). <i>BMC Genomics</i> , 2017, 18, 505.	1.2	22
1742	Blastomycosis in Children: An Analysis of Clinical, Epidemiologic, and Genetic Features. <i>Journal of the Pediatric Infectious Diseases Society</i> , 2017, 6, 49-56.	0.6	32
1743	Genetic Evidence for the Introduction of <i>Rhagoletis pomonella</i> (Diptera: Tephritidae) into the Northwestern United States. <i>Journal of Economic Entomology</i> , 2017, 110, 2599-2608.	0.8	9
1744	Screening, compiling and validation of informative microsatellite sets for marker-assisted breeding of key Ethiopian sorghum cultivars. <i>Australian Journal of Crop Science</i> , 2017, 11, 557-566.	0.1	1
1745	Molecular Characterization and Genetic Diversity of Aman Rice (<i>Oryza sativa</i> L.) Landraces in Bangladesh. <i>Bangladesh Rice Journal</i> , 2017, 20, 1-11.	0.8	2
1746	Development of Novel SSR Markers for Flax (<i>Linum usitatissimum</i> L.) Using Reduced-Representation Genome Sequencing. <i>Frontiers in Plant Science</i> , 2017, 7, 2018.	1.7	25
1747	Identification of Marker-Trait Associations for Lint Traits in Cotton. <i>Frontiers in Plant Science</i> , 2017, 8, 86.	1.7	37
1748	Genetic Structure and Selection of a Core Collection for Long Term Conservation of Avocado in Mexico. <i>Frontiers in Plant Science</i> , 2017, 8, 243.	1.7	37

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1750	New Hypervariable SSR Markers for Diversity Analysis, Hybrid Purity Testing and Trait Mapping in <i>Pigeonpea</i> [<i>Cajanus cajan</i> (L.) Millspaugh]. <i>Frontiers in Plant Science</i> , 2017, 8, 377.	1.7	59
1751	Genetic Diversity and Structure of <i>Lolium</i> Species Surveyed on Nuclear Simple Sequence Repeat and Cytoplasmic Markers. <i>Frontiers in Plant Science</i> , 2017, 8, 584.	1.7	14
1752	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.	1.7	23
1753	Association Mapping Reveals Novel Genetic Loci Contributing to Flooding Tolerance during Germination in Indica Rice. <i>Frontiers in Plant Science</i> , 2017, 8, 678.	1.7	53
1754	A Novel Wheat C-bZIP Gene, <i>TabZIP14-B</i> , Participates in Salt and Freezing Tolerance in Transgenic Plants. <i>Frontiers in Plant Science</i> , 2017, 8, 710.	1.7	46
1755	<i>Sorghum</i> 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.	1.7	20
1756	Genetic Gains in Yield and Yield Related Traits under Drought Stress and Favorable Environments in a Maize Population Improved Using Marker Assisted Recurrent Selection. <i>Frontiers in Plant Science</i> , 2017, 8, 808.	1.7	45
1757	Genome-Wide Analysis of Simple Sequence Repeats in Bitter Gourd (<i>Momordica charantia</i>). <i>Frontiers in Plant Science</i> , 2017, 8, 1103.	1.7	26
1758	Association and Genetic Identification of Loci for Four Fruit Traits in Tomato Using InDel Markers. <i>Frontiers in Plant Science</i> , 2017, 8, 1269.	1.7	23
1759	Establishing the Bases for Introducing the Unexplored Portuguese Common Bean Germplasm into the Breeding World. <i>Frontiers in Plant Science</i> , 2017, 8, 1296.	1.7	30
1760	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.	1.7	72
1761	Development of Highly Informative Genome-Wide Single Sequence Repeat Markers for Breeding Applications in Sesame and Construction of a Web Resource: <i>SisatBase</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 1470.	1.7	29
1762	Diverse Rice Landraces of North-East India Enables the Identification of Novel Genetic Resources for <i>Magnaporthe</i> Resistance. <i>Frontiers in Plant Science</i> , 2017, 8, 1500.	1.7	30
1763	Genetic Variation and Population Structure of <i>Oryza glaberrima</i> and Development of a Mini-Core Collection Using <i>DARtseq</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 1748.	1.7	71
1764	Genetic and Cytological Analyses of the Natural Variation of Seed Number per Pod in Rapeseed (<i>Brassica napus</i> L.). <i>Frontiers in Plant Science</i> , 2017, 8, 1890.	1.7	20
1765	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.	1.7	45
1766	Genome-Wide Discovery and Deployment of Insertions and Deletions Markers Provided Greater Insights on Species, Genomes, and Sections Relationships in the Genus <i>Arachis</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 2064.	1.7	24

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1767	Genetic Variation and Association Mapping of Seed-Related Traits in Cultivated Peanut (<i>Arachis</i>) Tj ETQqO 0 0 rgBT /Overlock 10 Tf 50 7-2105.	1.7	27
1768	Setting Up Decision-Making Tools toward a Quality-Oriented Participatory Maize Breeding Program. <i>Frontiers in Plant Science</i> , 2017, 8, 2203.	1.7	9
1769	Genetic diversity of arboreal cotton populations of the Brazilian semiarid: a remnant primary gene pool for cotton cultivars. <i>Genetics and Molecular Research</i> , 2017, 16, .	0.3	6
1770	Development and Molecular Characterization of Novel Polymorphic Genomic DNA SSR Markers in <i>Lentinula edodes</i> . <i>Mycobiology</i> , 2017, 45, 105-109.	0.6	8
1771	Research Article Genetic diversity and population structure analysis in <i>Perilla frutescens</i> from Northern areas of China based on simple sequence repeats.. <i>Genetics and Molecular Research</i> , 2017, 16, .	0.3	12
1772	Genome Survey Sequencing of <i>Luffa Cylindrica</i> L. and Microsatellite High Resolution Melting (SSR-HRM) Analysis for Genetic Relationship of <i>Luffa</i> Genotypes. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1942.	1.8	17
1773	Development of novel InDel markers and genetic diversity in <i>Chenopodium quinoa</i> through whole-genome re-sequencing. <i>BMC Genomics</i> , 2017, 18, 685.	1.2	47
1774	Use of Molecular Markers to Assist the Development of Inbred Lines under Open Field Conditions: the Case of Criollo Peppers (<i>Capsicum annum</i> L.) from Mexico. <i>Notulae Botanicae Horti Agrobotanici Cluj-Napoca</i> , 2017, 45, 365-368.	0.5	2
1775	Morphological and molecular variability within the fig cultivar "Dottato"™ in the Italian protected designation origin area "Fichi di Cosenza". <i>Acta Horticulturae</i> , 2017, , 29-34.	0.1	3
1776	Molecular Characterizations of Kenyan <i>Brachiaria</i> Grass Ecotypes with Microsatellite (SSR) Markers. <i>Agronomy</i> , 2017, 7, 8.	1.3	6
1777	Phenotyping, Genotyping, and Selections within Italian Local Landraces of Romanesco Globe Artichoke. <i>Diversity</i> , 2017, 9, 14.	0.7	7
1778	Genetic Diversity of Walnut (<i>Juglans Regia</i> L.) in the Eastern Italian Alps. <i>Forests</i> , 2017, 8, 81.	0.9	25
1779	Development of Gene-Based SSR Markers in Winged Bean (<i>Psophocarpus tetragonolobus</i> (L.) DC.) for Diversity Assessment. <i>Genes</i> , 2017, 8, 100.	1.0	28
1780	Development of 44 Novel Polymorphic SSR Markers for Determination of <i>Shiitake</i> Mushroom (<i>Lentinula edodes</i>) Cultivars. <i>Genes</i> , 2017, 8, 109.	1.0	21
1781	Assessing Genetic Diversity and Population Differentiation of Colored Calla Lily (<i>Zantedeschia</i> Hybrid) for an Efficient Breeding Program. <i>Genes</i> , 2017, 8, 168.	1.0	12
1782	Development of Genome-Wide SSR Markers from <i>Angelica gigas</i> Nakai Using Next Generation Sequencing. <i>Genes</i> , 2017, 8, 238.	1.0	18
1783	Association Mapping Reveals Genetic Loci Associated with Important Agronomic Traits in <i>Lentinula edodes</i> , <i>Shiitake</i> Mushroom. <i>Frontiers in Microbiology</i> , 2017, 8, 237.	1.5	13
1784	Genetic variation in resistance to blast (<i>Pyricularia oryzae</i> Cavara) in rice (<i>Oryza sativa</i> L.) germplasms of Bangladesh. <i>Breeding Science</i> , 2017, 67, 493-499.	0.9	9

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1785	Genetic diversity in Brazilian soybean germplasm. <i>Crop Breeding and Applied Biotechnology</i> , 2017, 17, 373-381.	0.1	9
1786	Genetic Diversity Assessment of Upland Cotton Variety Resources in China Based on Phenotype Traits and Molecular Markers. <i>Crop Science</i> , 2017, 57, 290-301.	0.8	4
1787	Genetic diversity and population structure of native maize populations in Latin America and the Caribbean. <i>PLoS ONE</i> , 2017, 12, e0173488.	1.1	50
1788	Diversity of Algerian oases date palm (<i>Phoenix dactylifera</i> L., <i>Arecaceae</i>): Heterozygote excess and cryptic structure suggest farmer management had a major impact on diversity. <i>PLoS ONE</i> , 2017, 12, e0175232.	1.1	26
1789	In silico development and characterization of tri-nucleotide simple sequence repeat markers in hazelnut (<i>Corylus avellana</i> L.). <i>PLoS ONE</i> , 2017, 12, e0178061.	1.1	38
1790	Trait variation and genetic diversity in a banana genomic selection training population. <i>PLoS ONE</i> , 2017, 12, e0178734.	1.1	36
1791	Population genetic analysis of a global collection of <i>Fragaria vesca</i> using microsatellite markers. <i>PLoS ONE</i> , 2017, 12, e0183384.	1.1	32
1792	Molecular genetic diversity and population structure of Ethiopian white lupin landraces: Implications for breeding and conservation. <i>PLoS ONE</i> , 2017, 12, e0188696.	1.1	20
1793	Characterization and cross-species transferability of EST-SSRs from de novo transcriptome sequencing of white calla lily (<i>Zantedeschia aethiopica</i>). <i>Acta Horticulturae</i> , 2017, , 175-186.	0.1	1
1794	Structure of sweet potato (<i>Ipomoea batatas</i>) diversity in West Africa covaries with a climatic gradient. <i>PLoS ONE</i> , 2017, 12, e0177697.	1.1	21
1795	Use of molecular markers in identification and characterization of resistance to rice blast in India. <i>PLoS ONE</i> , 2017, 12, e0176236.	1.1	26
1796	A microsatellite diversity analysis and the development of core-set germplasm in a large hulless barley (<i>Hordeum vulgare</i> L.) collection. <i>BMC Genetics</i> , 2017, 18, 102.	2.7	13
1797	Genome-wide association mapping of black point reaction in common wheat (<i>Triticum aestivum</i> L.). <i>BMC Plant Biology</i> , 2017, 17, 220.	1.6	141
1798	Phenotypic and genotypic monitoring of <i>Schistosoma mansoni</i> in Tanzanian schoolchildren five years into a preventative chemotherapy national control programme. <i>Parasites and Vectors</i> , 2017, 10, 593.	1.0	23
1799	Screening transferable microsatellite markers across genus <i>Phalaenopsis</i> (<i>Orchidaceae</i>). , 2017, 58, 48.		3
1800	Genetic evidence of multiple invasions and a small number of founders of Asian Palmyra palm (<i>Borassus flabellifer</i>) in Thailand. <i>BMC Genetics</i> , 2017, 18, 88.	2.7	10
1801	De novo assembly and characterization of transcriptome and microsatellite marker development for Taro (<i>Colocasia esculenta</i> (L.) Schott.). <i>International Journal of Genetics and Molecular Biology</i> , 2017, 9, 26-36.	1.5	3
1802	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.	0.1	6

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1803	Genetic diversity assessment of Guzoita abyssinica using EST derived simple sequence repeats (SSRs) markers. African Journal of Plant Science, 2017, 11, 79-85.	0.4	7
1804	DNA fingerprinting and genetic diversities in some Bangladeshi aus rice (<i>Oryza sativa</i> L.) genotypes. SAARC Journal of Agriculture, 2017, 15, 123-137.	0.2	5
1805	De novo transcriptome assembly and SSR marker development in apricot (<i>Prunus armeniaca</i>). Turk Tarim Ve Ormançılık Dergisi/Turkish Journal of Agriculture and Forestry, 2017, 41, 305-315.	0.8	6
1806	POPULATION GENETIC ANALYSIS OF BRAZILIAN PEACH BREEDING GERMPLASM. Revista Brasileira De Fruticultura, 2017, 39, .	0.2	11
1807	Characterization of Progenies from Intergeneric Hybridization Between <i>Oryza sativa</i> L. and <i>Porteresia coarctata</i> (Roxb.) Tateoka. Plant Tissue Culture and Biotechnology, 2017, 27, 63-76.	0.1	7
1808	Analysis of genetic diversity of rapeseed genetic resources in Japan and core collection construction. Breeding Science, 2017, 67, 239-247.	0.9	45
1809	Lack of Association between FTO Gene Variations and Metabolic Healthy Obese (MHO) Phenotype: Tehran Cardio-Metabolic Genetic Study (TCGS). Journal of Obesity & Weight Loss Therapy, 2017, 07, .	0.1	0
1810	Assessment of the genetic diversity and population structure in temperate japonica rice germplasm used in breeding in Chile, with SSR markers. Chilean Journal of Agricultural Research, 2017, 77, 15-26.	0.4	9
1811	Genetic diversity and population structure of traditional sweet cassava accessions from Southern of Minas Gerais State, Brazil, using microsatellite markers. African Journal of Biotechnology, 2017, 16, 346-358.	0.3	8
1812	Markers Associated with Culm Length and Elongated Internode Length in Japonica Rice. Crop Science, 2017, 57, 2329-2344.	0.8	4
1813	Assessment of genetic diversity among released and elite Ethiopian barley genotypes using simple sequence repeat (SSR) markers. African Journal of Plant Science, 2017, 11, 114-122.	0.4	1
1814	Microsatellite Identification in Perennial Ryegrass using Next-Generation Sequencing. Crop Science, 2017, 57, S-331.	0.8	4
1815	Assessment of genetic variations of Nile Tilapia (<i>Oreochromis niloticus</i> L.) in the Volta Lake of Ghana using microsatellite markers. African Journal of Biotechnology, 2017, 16, 312-321.	0.3	11
1816	Genetic diversity of Cameroonian bread wheat (<i>Triticum aestivum</i> L.) cultivars revealed by microsatellite markers. African Journal of Biotechnology, 2017, 16, 1832-1839.	0.3	11
1817	Comparison of the Genetic Structure between In Situ and Ex Situ Populations of Dongxiang Wild Rice (<i>Oryza rufipogon</i> Griff.). Crop Science, 2017, 57, 3075-3084.	0.8	8
1818	Molecular characterization of red clover genotypes utilizing microsatellite markers. Chilean Journal of Agricultural Research, 2017, 77, 41-47.	0.4	9
1819	Genetic variation of world soybean maturity date and geographic distribution of maturity groups. Breeding Science, 2017, 67, 221-232.	0.9	43
1820	Phenotypic Screening and Molecular Characterization of 10 Rice (<i>Oryza sativa</i>) Landraces for Cold Tolerance. Journal of Environmental Science and Natural Resources, 2017, 10, 85-91.	0.1	1

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1821	Diversity and genetic analysis through DArTseq in common bean (<i>Phaseolus vulgaris</i> L.) germplasm from Turkey. <i>Turk Tarim Ve Ormancilik Dergisi/Turkish Journal of Agriculture and Forestry</i> , 2017, 41, 389-404.	0.8	17
1822	Molecular characterization of edible pea through EST-SSR markers. <i>Turkish Journal of Botany</i> , 2017, 41, 338-346.	0.5	9
1823	Allele frequencies of 15 STR loci in Bosnian and Herzegovinian population. <i>Croatian Medical Journal</i> , 2017, 58, 250-256.	0.2	8
1824	Analysis of genetic structure in a large sample of pomegranate (<i>Punica granatum</i> L.) using fluorescent SSR markers. <i>Journal of Horticultural Science and Biotechnology</i> , 2018, 93, 659-665.	0.9	8
1825	Implication of ITS phylogeny for biogeographic analysis, and comparative study of morphological and molecular interspecies diversity in Indian <i>Impatiens</i> . <i>Meta Gene</i> , 2018, 16, 108-116.	0.3	4
1826	Genetic diversity and population structure of ramie (<i>Boehmeria nivea</i> L.). <i>Industrial Crops and Products</i> , 2018, 115, 340-347.	2.5	23
1827	First report of <i>Varroa</i> genotype in western Asia based on genotype identification of Iranian <i>Varroa</i> destructor populations (Mesostigmata: Varroidae) using RAPD marker. <i>Systematic and Applied Acarology</i> , 2018, 23, 199.	0.5	3
1828	Genetic Variation and Association Analysis of the SSR Markers Linked to the Major Drought-Yield QTLs of Rice. <i>Biochemical Genetics</i> , 2018, 56, 356-374.	0.8	19
1829	Patterns of genomic variation in Chinese maize inbred lines and implications for genetic improvement. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1207-1221.	1.8	15
1830	Size homoplasmy and mutational behavior of chloroplast simple sequence repeats (cpSSRs) inferred from intra- and interspecific variations in four chloroplast regions of diploid and polyploid <i>Triticum</i> and <i>Aegilops</i> species. <i>Genetic Resources and Crop Evolution</i> , 2018, 65, 727-743.	0.8	8
1831	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.	0.9	4
1832	Assessment of genetic diversity in ragi [<i>Eleusine coracana</i> (L.) Gaertn] using morphological, RAPD and SSR markers. <i>Zeitschrift Fur Naturforschung - Section C Journal of Biosciences</i> , 2018, 73, 165-176.	0.6	8
1833	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.	0.7	9
1834	Detection of favorable alleles for yield and yield components by association mapping in upland cotton. <i>Genes and Genomics</i> , 2018, 40, 725-734.	0.5	8
1835	Genetic relationship of diploid wheat (<i>Triticum</i> spp.) species assessed by SSR markers. <i>Genetic Resources and Crop Evolution</i> , 2018, 65, 1441-1453.	0.8	21
1836	Differentiation of <i>Saccharomyces cerevisiae</i> populations from vineyards of the Azores Archipelago: Geography vs Ecology. <i>Food Microbiology</i> , 2018, 74, 151-162.	2.1	20
1837	SSR Analysis of Genetic Relationship and Classification in <i>Chrysanthemum</i> Germplasm Collection. <i>Horticultural Plant Journal</i> , 2018, 4, 73-82.	2.3	22
1838	Species identification, genetic diversity and population structure of sweet cherry commercial cultivars assessed by SSRs and the gametophytic self-incompatibility locus. <i>Scientia Horticulturae</i> , 2018, 237, 28-35.	1.7	10

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1839	Mining of favorable alleles for lodging resistance traits in rice (<i>Oryza sativa</i>) through association mapping. <i>Planta</i> , 2018, 248, 155-169.	1.6	19
1840	Cross-genera transferability of rice and finger millet genomic SSRs to barnyard millet (<i>Echinochloa</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 1.1 12	1.1	12
1841	Forensic genetic informativeness of an SNP panel consisting of 19 multi-allelic SNPs. <i>Forensic Science International: Genetics</i> , 2018, 34, 49-56.	1.6	19
1842	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.	1.0	21
1843	Responses of rice (<i>Oryza sativa</i> L.) genotypes to different levels of submergence. <i>Comptes Rendus - Biologies</i> , 2018, 341, 85-96.	0.1	17
1844	Development of an InDel polymorphism database for jute via comparative transcriptome analysis. <i>Genome</i> , 2018, 61, 323-327.	0.9	14
1845	Pedigree, marker recruitment, and genetic diversity of modern sugarcane cultivars in China and the United States. <i>Euphytica</i> , 2018, 214, 1.	0.6	5
1846	Exploration of genetic selection in rice leaf length and width. <i>Botany</i> , 2018, 96, 249-256.	0.5	6
1847	Current Status and Future Prospects of Next-Generation Data Management and Analytical Decision Support Tools for Enhancing Genetic Gains in Crops. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2018, 164, 277-292.	0.6	4
1848	Genetic monitoring of horses in the Czech Republic: A large-scale study with a focus on the Czech autochthonous breeds. <i>Journal of Animal Breeding and Genetics</i> , 2018, 135, 73-83.	0.8	12
1849	Genome-wide association study of cold tolerance of Chinese indica rice varieties at the bud burst stage. <i>Plant Cell Reports</i> , 2018, 37, 529-539.	2.8	41
1850	Population Genetics of the Endangered and Wild Edible Plant <i>Ottelia acuminata</i> in Southwestern China Using Novel SSR Markers. <i>Biochemical Genetics</i> , 2018, 56, 235-254.	0.8	20
1851	Development and validation of simple sequence repeat markers from <i>Arachis hypogaea</i> transcript sequences. <i>Crop Journal</i> , 2018, 6, 172-180.	2.3	17
1852	Gene-based SNP identification and validation in soybean using next-generation transcriptome sequencing. <i>Molecular Genetics and Genomics</i> , 2018, 293, 623-633.	1.0	16
1853	Population structure and association analysis of heat stress relevant traits in chickpea (<i>Cicer</i>) Tj ETQq0 0 0 rgBT /Overlock 1.1 17 50 182	1.1	17
1854	Genetic diversity of apple and crabapple infecting isolates of <i>Venturia inaequalis</i> in Pennsylvania, the United States, determined by microsatellite markers. <i>Forest Pathology</i> , 2018, 48, e12405.	0.5	10
1855	Development of AhMITE1 markers through genome-wide analysis in peanut (<i>Arachis hypogaea</i> L.). <i>BMC Research Notes</i> , 2018, 11, 10.	0.6	45
1856	The relationship between MnSOD Val16Ala gene polymorphism and the level of serum total antioxidant capacity with the risk of chronic kidney disease in type 2 diabetic patients: a nested case-control study in the Tehran lipid glucose study. <i>Nutrition and Metabolism</i> , 2018, 15, 25.	1.3	12

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1857	Genome-wide identification of simple sequence repeats and development of polymorphic SSR markers for genetic studies in tea plant (<i>Camellia sinensis</i>). <i>Molecular Breeding</i> , 2018, 38, 1.	1.0	44
1858	Association mapping and favourable QTL alleles for fibre quality traits in Upland cotton (<i>Gossypium</i>) Tj ETQq1 1 0.784314 rgBT /Over	0.4	0
1859	Molecular and phenotypic diversity among chickpea (<i>Cicer arietinum</i>) genotypes as a function of drought tolerance. <i>Crop and Pasture Science</i> , 2018, 69, 142.	0.7	14
1860	Genetic polymorphisms, forensic efficiency and phylogenetic analysis of 15 autosomal STR loci in the Kazak population of Ili Kazak Autonomous Prefecture, northwestern China. <i>Annals of Human Biology</i> , 2018, 45, 160-165.	0.4	3
1861	Genetic Loci Controlling Carotenoid Biosynthesis in Diverse Tropical Maize Lines. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1049-1065.	0.8	26
1862	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.	0.4	0
1863	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.	0.4	23
1864	In vitro propagation of the relict laperinne™s olive (<i>Olea europaea</i> L. subsp. <i>Laperrinei</i>). <i>Plant Biosystems</i> , 2018, 152, 621-630.	0.8	11
1865	The impact of modern plant breeding on dominant Chinese wheat cultivars (<i>Triticum aestivum</i> L.) revealed by SSR and functional markers. <i>Genetic Resources and Crop Evolution</i> , 2018, 65, 55-65.	0.8	5
1866	Uncovering the dispersion history, adaptive evolution and selection of wheat in China. <i>Plant Biotechnology Journal</i> , 2018, 16, 280-291.	4.1	62
1867	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.	0.8	25
1868	Establishment of 11 linked X-STR loci within 1.1 Mb to assist with kinship testing. <i>International Journal of Legal Medicine</i> , 2018, 132, 967-973.	1.2	3
1869	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> . <i>Plant Biotechnology Journal</i> , 2018, 16, 507-519.	4.1	39
1870	Molecular phylogeny and genetic diversity of genus <i>Capparis</i> (Capparaceae) based on plastid DNA sequences and ISSR markers. <i>Plant Systematics and Evolution</i> , 2018, 304, 205-217.	0.3	17
1871	Identification of genome-wide single-nucleotide polymorphisms (SNPs) associated with tolerance to chromium toxicity in spring wheat (<i>Triticum aestivum</i> L.). <i>Plant and Soil</i> , 2018, 422, 371-384.	1.8	21
1872	Effectiveness of predictive markers for marker assisted selection of pro-vitamin A carotenoids in medium-late maturing maize (<i>Zea mays</i> L.) inbred lines. <i>Journal of Cereal Science</i> , 2018, 79, 27-34.	1.8	26
1873	Genome-Wide Association Mapping of Loci for Resistance to Stripe Rust in North American Elite Spring Wheat Germplasm. <i>Phytopathology</i> , 2018, 108, 234-245.	1.1	50
1874	Assessment of genetic diversity of rice based on SNP markers for selection of parents for sheath rot (<i>Sarocladium oryzae</i>) resistance breeding. <i>South African Journal of Plant and Soil</i> , 2018, 35, 51-59.	0.4	7

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1875	Genetic variation, Heritability estimates and GXE effects on yield traits of Mesoamerican common bean (<i>Phaseolus vulgaris</i> L) germplasm in Uganda. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2018, 16, 237-248.	0.4	9
1876	Establishment and evaluation of a peanut association panel and analysis of key nutritional traits. <i>Journal of Integrative Plant Biology</i> , 2018, 60, 195-215.	4.1	11
1878	X-chromosomal STR-based genetic structure of Sichuan Tibetan minority ethnicity group and its relationships to various groups. <i>International Journal of Legal Medicine</i> , 2018, 132, 409-413.	1.2	48
1879	Genetic diversity of improved varieties of intraspecific (<i>O. sativa</i> and <i>O. glaberrima</i>) and interspecific (<i>O. sativa</i> × <i>O. glaberrima</i>) rice. <i>Genetic Resources and Crop Evolution</i> , 2018, 65, 797-809.	0.8	3
1880	Genic simple sequence repeat markers for measuring genetic diversity in a native food crop: a case study of Australian <i>Kunzea pomifera</i> F.Muell. (muntries). <i>Genetic Resources and Crop Evolution</i> , 2018, 65, 917-937.	0.8	1
1881	Molecular identification and genetic analysis of cherry cultivars using capillary electrophoresis with fluorescence-labeled SSR markers. <i>3 Biotech</i> , 2018, 8, 16.	1.1	11
1882	Genetic differentiation and diversity upon genotype and phenotype in cowpea (<i>Vigna unguiculata</i> L.) Tj ETQq0 0 0 ggBT /Overlock 10 Tf 0.6 13	0.6	13
1883	Development of genomic simple sequence repeat (gSSR) markers in cumin and their application in diversity analyses and cross-transferability. <i>Industrial Crops and Products</i> , 2018, 111, 158-164.	2.5	31
1884	Molecular diversity and population structure of oriental thin-skinned melons, <i>Cucumis melo</i> subsp. <i>agrestis</i> , revealed by a set of core SSR markers. <i>Scientia Horticulturae</i> , 2018, 229, 59-64.	1.7	9
1885	Relationships among cultivated <i>Opuntia ficus-indica</i> genotypes and related species assessed by cytoplasmic markers. <i>Genetic Resources and Crop Evolution</i> , 2018, 65, 759-773.	0.8	10
1886	Assessing genetic diversity of wild southeastern North American <i>Vaccinium</i> species using microsatellite markers. <i>Genetic Resources and Crop Evolution</i> , 2018, 65, 939-950.	0.8	12
1887	Characterization of <i>Fusarium oxysporum</i> f. sp. <i>melongenae</i> isolates from Turkey with ISSR markers and DNA sequence analyses. <i>European Journal of Plant Pathology</i> , 2018, 150, 609-621.	0.8	10
1888	Polymorphism of the <i>STAT5A</i> , <i>MTNR1A</i> and <i>TNFα</i> genes and their effect on dairy production in <i>Bubalus bubalis</i> . <i>Italian Journal of Animal Science</i> , 2018, 17, 31-37.	0.8	6
1889	Evaluation of maize genotypes for fodder quality traits and SSR diversity. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2018, 27, 78-89.	0.9	15
1890	Phenotypic and genotypic screening of rice genotypes at reproductive stage for salt tolerance. <i>SAARC Journal of Agriculture</i> , 2018, 15, 69-80.	0.2	0
1891	Assessment of salt tolerance and variability within some rice germplasm using microsatellites. <i>Journal of Plant Breeding and Crop Science</i> , 2018, 10, 262-272.	0.8	0
1892	Genetic Diversity and Structure through Three Cycles of a <i>Eucalyptus urophylla</i> S.T.Blake Breeding Program. <i>Forests</i> , 2018, 9, 372.	0.9	10
1893	DNA Fingerprinting and Genetic Diversity in Aus Rice (<i>Oryza sativa</i> L.) Landraces of Bangladesh. <i>Bangladesh Rice Journal</i> , 2018, 21, 59-65.	0.8	0

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1894	Genetic diversity and relatedness of oil palm progenies determined by microsatellite and agronomic markers. <i>African Journal of Biotechnology</i> , 2018, 17, 614-625.	0.3	3
1895	Evaluation of genetic diversity of pearl millet (<i>Pennisetum glaucum</i> L.) landraces from West Africa using microsatellite markers. <i>African Journal of Biotechnology</i> , 2018, 17, 1339-1351.	0.3	1
1896	Single nucleotide polymorphism (SNP)-based genetic diversity in a set of Burkina Faso cowpea germplasm. <i>African Journal of Agricultural Research Vol Pp</i> , 2018, 13, 978-987.	0.2	7
1897	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.	1.2	33
1898	Genetic diversity and population structure of <i>Gossypium arboreum</i> L. collected in China. <i>Journal of Cotton Research</i> , 2018, 1, .	1.0	10
1899	Development of a Core Collection Based on EST-SSR Markers and Phenotypic Traits in Foxtail Millet [<i>Setaria italica</i> (L.) P. Beauv.]. <i>Journal of Crop Science and Biotechnology</i> , 2018, 21, 395-405.	0.7	3
1900	Research on video transmission Ad Hoc network routing technology oriented multimedia applications. <i>Journal of Intelligent and Fuzzy Systems</i> , 2018, 34, 879-886.	0.8	2
1901	GENETIC DIVERSITY IN AUS RICE LANDRACES OF BANGLADESH USING SSR MARKERS. <i>Bangladesh Journal of Plant Breeding and Genetics</i> , 2018, 30, 11-20.	0.0	1
1902	Optimizing sample size for molecular characterization of open-pollinated maize (<i>Zea mays</i> L.) varieties using simple sequence repeat markers. <i>Cereal Research Communications</i> , 2018, 46, 569-579.	0.8	1
1903	Genetic diversity in wild diploid wheat <i>T. urartu</i> revealed by SSR markers. <i>Cereal Research Communications</i> , 2018, 46, 580-590.	0.8	2
1904	Genetic diversity of blackberry (<i>Rubus</i> subgenus <i>Rubus</i> Watson) in selected counties in Kenya using simple sequence repeats (SSRs) markers. <i>African Journal of Biotechnology</i> , 2018, 17, 1247-1264.	0.3	2
1905	Agronomic and molecular characterization of wild germplasm <i>Saccharum spontaneum</i> for sugarcane and energycane breeding purposes. <i>Scientia Agricola</i> , 2018, 75, 329-338.	0.6	10
1906	Selection of legitimate dwarf coconut hybrid seedlings using DNA fingerprinting. <i>Crop Breeding and Applied Biotechnology</i> , 2018, 18, 409-416.	0.1	14
1907	A simple way to visualize detailed phylogenetic tree of huge genome-wide SNP data constructed by SNPhylo. <i>Journal of Integrative Agriculture</i> , 2018, 17, 1972-1978.	1.7	5
1908	Research Article The genetic diversity and population structure of <i>Genipa Americana</i> (Rubiaceae) in Northern Mato Grosso, Brazil. <i>Genetics and Molecular Research</i> , 2018, 17, .	0.3	4
1909	Highly informative SSR genotyping reveals large genetic diversity and limited differentiation in European larch (<i>Larix decidua</i>) populations from Romania. <i>Turk Tarim Ve Ormancilik Dergisi/Turkish Journal of Agriculture and Forestry</i> , 2018, 42, 165-175.	0.8	16
1910	Core collection of ramie comprising 1151 germplasms based on simple sequence repeats and phenotypic markers. <i>Revista Brasileira De Botanica</i> , 2018, 41, 859-866.	0.5	2
1911	Genome-Wide Mining and Characterization of SSR Markers for Gene Mapping and Gene Diversity in <i>Gossypium barbadense</i> L. and <i>Gossypium darwinii</i> G. Watt Accessions. <i>Agronomy</i> , 2018, 8, 181.	1.3	6

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1912	Development of Simple Sequence Repeat Markers in Hazelnut (<i>Corylus avellana</i> L.) by Next-Generation Sequencing and Discrimination of Turkish Hazelnut Cultivars. <i>Plant Molecular Biology Reporter</i> , 2018, 36, 800-811.	1.0	8
1913	Genetic Structure, Core Collection, and Regeneration Quality in White Dent Corn Landraces. <i>Crop Science</i> , 2018, 58, 1644-1658.	0.8	4
1914	Allelic variation of low molecular weight glutenin subunits composition and the revealed genetic diversity in durum wheat (“ <i>Triticum turgidum</i> “ L. ssp. “durum“ (Desf)). <i>Breeding Science</i> , 2018, 68, 524-535.	0.9	4
1915	A hermaphrodite genotype in dioecious papaya progeny: sex reversal or contamination?. <i>Euphytica</i> , 2018, 214, 1.	0.6	4
1916	A genome-wide associate study reveals favorable alleles conferring apical and basal spikelet fertility in wheat (<i>Triticum aestivum</i> L.). <i>Molecular Breeding</i> , 2018, 38, 1.	1.0	2
1917	Whole-genome sequencing of 175 Mongolians uncovers population-specific genetic architecture and gene flow throughout North and East Asia. <i>Nature Genetics</i> , 2018, 50, 1696-1704.	9.4	38
1918	Linkage disequilibrium in North China and Xingjiang apricot cultivars (<i>Prunus armeniaca</i> L.). <i>Acta Horticulturae</i> , 2018, , 269-284.	0.1	1
1919	Genetic characterization in local hazelnut (<i>Corylus avellana</i>) accessions of Hizan province in Turkey. <i>Acta Horticulturae</i> , 2018, , 101-108.	0.1	3

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1930	Genetic Diversity and Population Structure Analysis of Citrus Germplasm with Single Nucleotide Polymorphism Markers. <i>Journal of the American Society for Horticultural Science</i> , 2018, 143, 399-408.	0.5	7
1931	Genome-wide association study of kernel moisture content at harvest stage in maize. <i>Breeding Science</i> , 2018, 68, 622-628.	0.9	24
1932	Development and application of SSR markers derived from <i>Bauhinia Strychnifolia</i> a semi-endemic plant in Thailand. <i>Journal of Herbs, Spices and Medicinal Plants</i> , 2018, 24, 386-393.	0.5	4
1933	GWAS analysis in spring barley (<i>Hordeum vulgare</i> L.) for morphological traits exposed to drought. <i>PLoS ONE</i> , 2018, 13, e0204952.	1.1	55
1934	Genetic relationships and heterotic structure of quality protein maize (<i>Zea mays</i> L.) inbred lines adapted to eastern and southern Africa. <i>Euphytica</i> , 2018, 214, 1.	0.6	1
1935	Characterization and Identification of Indigenous Olive Germplasm from Cyprus Using Morphological and Simple Sequence Repeat Markers. <i>Hortscience: A Publication of the American Society for Horticultural Science</i> , 2018, 53, 1306-1313.	0.5	6
1936	Analysis of genetic diversity of <i>Centella asiatica</i> using SSR markers. <i>International Journal of Applied Sciences and Biotechnology</i> , 2018, 6, 103-109.	0.4	6
1937	Characterization of hawthorn (<i>Crataegus</i> spp.) genotypes by SSR markers. <i>Physiology and Molecular Biology of Plants</i> , 2018, 24, 1221-1230.	1.4	26
1938	Genetic Variation and Alleviation of Salinity Stress in Barley (<i>Hordeum vulgare</i> L.). <i>Molecules</i> , 2018, 23, 2488.	1.7	55
1939	Molecular and Cytogenetic Study of East African Highland Banana. <i>Frontiers in Plant Science</i> , 2018, 9, 1371.	1.7	50
1940	Development and Characterization of Novel Genic-SSR Markers in Apple-Juniper Rust Pathogen <i>Gymnosporangium yamadae</i> (Pucciniales: Pucciniaceae) Using Next-Generation Sequencing. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1178.	1.8	10
1941	Genetic structure of populations of several endangered and endemic <i>Dianthus</i> species revealed by microsatellite markers. <i>Acta Botanica Croatica</i> , 2018, 77, 181-188.	0.3	3
1942	Genome-wide generation and genotyping of informative SNPs to scan molecular signatures for seed yield in chickpea. <i>Scientific Reports</i> , 2018, 8, 13240.	1.6	27
1943	Genetic diversity and population structure analyses of <i>Plectranthus edulis</i> (Vatke) Agnew collections from diverse agro-ecologies in Ethiopia using newly developed EST-SSRs marker system. <i>BMC Genetics</i> , 2018, 19, 92.	2.7	26
1944	Discovery, Characterization, and Linkage Mapping of Simple Sequence Repeat Markers In Hazelnut. <i>Journal of the American Society for Horticultural Science</i> , 2018, 143, 347-362.	0.5	11
1945	Genetic Diversity Patterns and Heterosis Prediction Based on SSRs and SNPs in Hybrid Parents of Pearl Millet. <i>Crop Science</i> , 2018, 58, 2379-2390.	0.8	15
1946	Molecular analysis of genetic diversity, population structure, and phylogeny of wild and cultivated tulips (<i>Tulipa</i> L.) by genic microsatellites. <i>Horticulture Environment and Biotechnology</i> , 2018, 59, 875-888.	0.7	14
1947	Genotypic Characterization of <i>Catha edulis</i> in Mt. Kenya Region, Kenya. <i>Journal of Phylogenetics & Evolutionary Biology</i> , 2018, 06, .	0.2	0

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1948	Genetic diversity in <i>Radix</i> species from the middle and south of Iraq based on simple sequence repeats. <i>African Journal of Biotechnology</i> , 2018, 17, 1119-1128.	0.3	1
1949	Genetic diversity and population structure of a mini-core subset from the world cowpea (<i>Vigna</i>) Tj ETQq1 1 0.784314 rgBT /Oyerlock 10	1.6	63
1950	Improved characterization of <i>Clematis</i> based on new chloroplast microsatellite markers and nuclear ITS sequences. <i>Horticulture Environment and Biotechnology</i> , 2018, 59, 889-897.	0.7	3
1951	Fifty shades of grey: black beech and mountain beech are genetically distinct but locally admixed. <i>New Zealand Journal of Botany</i> , 2018, 56, 343-359.	0.8	2
1952	The Prehistoric Indian Ayurvedic Rice <i>Shashtika</i> Is an Extant Early Domesticated With a Distinct Selection History. <i>Frontiers in Plant Science</i> , 2018, 9, 1203.	1.7	2
1953	Determination of Heterotic Groups and Heterosis Analysis of Yield Performance in indica Rice. <i>Rice Science</i> , 2018, 25, 261-269.	1.7	20
1954	Development of Species-Specific InDel Markers in Citrus. <i>Plant Molecular Biology Reporter</i> , 2018, 36, 653-662.	1.0	9
1955	Plant Genetics and Molecular Biology. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2018, , .	0.6	6
1956	Genetic analysis of resistance to stripe rust in durum wheat (<i>Triticum turgidum</i> L. var. durum). <i>PLoS ONE</i> , 2018, 13, e0203283.	1.1	17
1957	Analysis of Genetic Diversity and Population Structure of Buckwheat (<i>Fagopyrum esculentum</i>) Tj ETQq1 1 0.784314 rgBT /Oyerlock 10	2	2
1958	Evaluation of the Genetic Diversity and Differentiation of Black Locust (<i>Robinia pseudoacacia</i> L.) Based on Genomic and Expressed Sequence Tag-Simple Sequence Repeats. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2492.	1.8	11
1959	Survey of Candidate Genes for Maize Resistance to Infection by <i>Aspergillus flavus</i> and/or Aflatoxin Contamination. <i>Toxins</i> , 2018, 10, 61.	1.5	15
1960	Limited genetic evidence for host plant-related differentiation in the Western cherry fruit fly, <i>Rhagoletis indifferens</i> . <i>Entomologia Experimentalis Et Applicata</i> , 2018, 166, 739-751.	0.7	5
1961	Conserving maize in gene banks: Changes in genetic diversity revealed by morphological and SSR markers. <i>Chilean Journal of Agricultural Research</i> , 2018, 78, 30-38.	0.4	9
1962	Systematic Evaluation of Landrace Tea Populations in Northern Sichuan, China, Based on Morphology, DNA Markers, and Biochemistry Analyses. <i>Hortscience: A Publication of the American Society for Horticultural Science</i> , 2018, 53, 1095-1101.	0.5	4
1963	Ethnic Differences in Susceptibility to the Effects of Platinum- Based Chemotherapy. , 0, , .		2
1964	Association of miR-208b polymorphism with meat quality traits and texture parameters in pigs. <i>Czech Journal of Animal Science</i> , 2018, 63, 435-442.	0.5	0
1966	Molecular assessment of maize inbred lines (<i>Zea mays</i> L.) Using microsatellite markers. <i>Bangladesh Journal of Agricultural Research</i> , 2018, 43, 533-542.	0.0	2

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1967	Development and characterization of chloroplast microsatellite markers for <i>Pinus massoniana</i> and their application in <i>Pinus</i> (Pinaceae) species. <i>Journal of Genetics</i> , 2018, 97, 53-59.	0.4	10
1968	Using soybean pedigrees to identify genomic selection signatures associated with long-term breeding for cultivar improvement. <i>Canadian Journal of Plant Science</i> , 2018, 98, 1176-1187.	0.3	7
1969	Genetic and environmental parameters show associations with essential oil composition in West Australian sandalwood (<i>Santalum spicatum</i>). <i>Australian Journal of Botany</i> , 2018, 66, 48.	0.3	9
1970	Single nucleotide polymorphism (SNP) characterization of drought-responsive genes to estimate genetic variation of <i>Populus tremula</i> var. <i>dauriana</i> and eight other <i>Populus</i> species. <i>Canadian Journal of Forest Research</i> , 2018, 48, 689-696.	0.8	4
1971	Male individualization using 12 rapidly mutating Y-STRs in Araeini ethnic group and shared paternal lineage of Pakistani population. <i>International Journal of Legal Medicine</i> , 2018, 132, 1621-1624.	1.2	8
1972	Genetic Diversity Analysis Reveals Genetic Differentiation and Strong Population Structure in <i>Calotropis</i> Plants. <i>Scientific Reports</i> , 2018, 8, 7832.	1.6	28
1973	Diversity and population structure of red rice germplasm in Bangladesh. <i>PLoS ONE</i> , 2018, 13, e0196096.	1.1	43
1974	Genetic diversity and admixture in three native draught horse breeds assessed using microsatellite markers. <i>Czech Journal of Animal Science</i> , 2018, 63, 85-93.	0.5	3
1975	Elucidating the contribution of wild related species on autochthonous pear germplasm: A case study from Mount Etna. <i>PLoS ONE</i> , 2018, 13, e0198512.	1.1	15
1976	Limited dispersal and geographic barriers cause population differentiation and structuring in <i>Begonia maxwelliana</i> at both large and small scales. <i>Plant Ecology and Diversity</i> , 2018, 11, 69-83.	1.0	6
1977	Identification of rice landraces with promising yield and the associated genomic regions under low nitrogen. <i>Scientific Reports</i> , 2018, 8, 9200.	1.6	23
1978	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.	2.3	7
1979	First characterisation of minor and neglected <i>Vitis vinifera</i> L. cultivars from Mount Etna. <i>Zahradnictvi (Prague, Czech Republic: 1992)</i> , 2018, 45, 37-46.	0.3	6
1980	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.	1.0	7
1981	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.	1.7	46
1982	Genetic diversity of <i>Aspergillus flavus</i> and occurrence of aflatoxin contamination in stored maize across three agro-ecological zones in Kenya. <i>Agriculture and Food Security</i> , 2018, 7, .	1.6	8
1983	Towards Defining Heterotic Gene Pools in Pearl Millet [<i>Pennisetum glaucum</i> (L.) R. Br.]. <i>Frontiers in Plant Science</i> , 2017, 8, 1934.	1.7	42
1984	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.	1.7	25

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1985	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.	1.7	42
1986	Morphological and Molecular Data Reveal Three Distinct Populations of Indian Wild Rice <i>Oryza rufipogon</i> Griff. Species Complex. <i>Frontiers in Plant Science</i> , 2018, 9, 123.	1.7	25
1987	Association Study Reveals Novel Genes Related to Yield and Quality of Fruit in Cape Gooseberry (<i>Physalis peruviana</i> L.). <i>Frontiers in Plant Science</i> , 2018, 9, 362.	1.7	12
1988	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.	1.7	45
1989	An Integration of Genome-Wide Association Study and Gene Co-expression Network Analysis Identifies Candidate Genes of Stem Lodging-Related Traits in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 796.	1.7	36
1990	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.	0.6	7
1991	Characterization of new microsatellite markers based on the transcriptome sequencing of <i>Clematis finetiana</i> . <i>Hereditas</i> , 2018, 155, 23.	0.5	13
1992	Genome-wide Association Study of Agronomic Traits in a Spring-planted North American Elite Hard Red Spring Wheat Panel. <i>Crop Science</i> , 2018, 58, 1838-1852.	0.8	29
1993	Relative Response of Indigenous Rice Genotypes to Low Versus Normal Planting Density for Determination of Differential Phenotypic Plasticity in Traits Related to Grain Yield. <i>Plant Tissue Culture and Biotechnology</i> , 2018, 28, 109-124.	0.1	0
1994	Barley heads east: Genetic analyses reveal routes of spread through diverse Eurasian landscapes. <i>PLoS ONE</i> , 2018, 13, e0196652.	1.1	54
1995	Genome-Wide Association Study of Haploid Male Fertility in Maize (<i>Zea Mays</i> L.). <i>Frontiers in Plant Science</i> , 2018, 9, 974.	1.7	27
1996	Genetic Diversity and Population Structure of F3:6 Nebraska Winter Wheat Genotypes Using Genotyping-By-Sequencing. <i>Frontiers in Genetics</i> , 2018, 9, 76.	1.1	183
1997	Exploration and Exploitation of Novel SSR Markers for Candidate Transcription Factor Genes in <i>Lilium</i> Species. <i>Genes</i> , 2018, 9, 97.	1.0	25
1998	Assessment of genetic diversity in Egyptian barley (<i>Hordeum vulgare</i> L.) genotypes using SSR and SNP markers. <i>Genetic Resources and Crop Evolution</i> , 2018, 65, 1937-1951.	0.8	17
1999	Molecular phylogeography of East Asian <i>Boea clarkeana</i> (Gesneriaceae) in relation to habitat restriction. <i>PLoS ONE</i> , 2018, 13, e0199780.	1.1	4
2000	Variability Assessment of Aromatic Rice Germplasm by Pheno-Genomic traits and Population Structure Analysis. <i>Scientific Reports</i> , 2018, 8, 9911.	1.6	20
2001	Variable Levels of Tolerance to Water Stress (Drought) and Associated Biochemical Markers in Tunisian Barley Landraces. <i>Molecules</i> , 2018, 23, 613.	1.7	25
2002	Multi-Environment Evaluation and Genetic Characterisation of Common Bean Breeding Lines for Organic Farming Systems. <i>Sustainability</i> , 2018, 10, 777.	1.6	14

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2003	Analysis of the Genetic Diversity and Population Structure of Austrian and Belgian Wheat Germplasm within a Regional Context Based on DArT Markers. <i>Genes</i> , 2018, 9, 47.	1.0	26
2004	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.	1.0	3
2005	Genetic diversity of sweet corn inbreds using agro-morphological traits and microsatellite markers. <i>3 Biotech</i> , 2018, 8, 332.	1.1	12
2006	Development of EST-SSR markers in <i>Larix principis-rupprechtii</i> Mayr and evaluation of their polymorphism and cross-species amplification. <i>Trees - Structure and Function</i> , 2018, 32, 1559-1571.	0.9	28
2007	Genome-wide characterization of simple sequence repeats in <i>Pyrus bretschneideri</i> and their application in an analysis of genetic diversity in pear. <i>BMC Genomics</i> , 2018, 19, 473.	1.2	22
2008	Genetic Variability in Farmed Brood Stocks of the Siberian Sturgeon in Poland. , 2018, , 337-346.		0
2009	Association of yield-related traits in founder genotypes and derivatives of common wheat (<i>Triticum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.6	28
2010	Sequence investigation of 34 forensic autosomal STRs with massively parallel sequencing. <i>Scientific Reports</i> , 2018, 8, 6810.	1.6	6
2011	Analysis of genetic diversity and population structure of a worldwide collection of <i>Corchorus olitorius</i> L. germplasm using microsatellite markers. <i>Biotechnology and Biotechnological Equipment</i> , 2018, 32, 961-967.	0.5	12
2012	Geographical comparison of genetic diversity in Asian landrace wheat (<i>Triticum aestivum</i> L.) germplasm based on high-molecular-weight glutenin subunits. <i>Genetic Resources and Crop Evolution</i> , 2018, 65, 1591-1602.	0.8	13
2013	Detection of rust resistance in selected Zimbabwean and ICARDA bread wheat (<i>Triticum aestivum</i>) germplasm using conventional and molecular techniques. <i>South African Journal of Plant and Soil</i> , 2018, 35, 101-110.	0.4	4
2014	Development and characterization of polymorphic microsatellite markers for <i>Spathoglottis plicata</i> (Orchidaceae). <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2018, 16, 572-575.	0.4	0
2015	Development and validation of microsatellite markers for Karnal bunt (<i>Tilletia indica</i>) and loose smut (<i>Ustilago segetum tritici</i>) of wheat from related fungal species. <i>Journal of Phytopathology</i> , 2018, 166, 729-738.	0.5	11
2016	Genetic analysis of 15 autosomal STRs in Yousafzai population of Pakistan. <i>International Journal of Legal Medicine</i> , 2018, 132, 1635-1636.	1.2	2
2017	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
2018	Genetic Diversity of Puerto Rican Farmer-held Papaya (<i>Carica papaya</i>) Using SSR Markers. <i>Hortscience: A Publication of the American Society for Horticultural Science</i> , 2018, 53, 1109-1114.	0.5	2
2019	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.	1.8	45
2020	Evaluation of the genetic diversity and population structure of <i>Gasterophilus pecorum</i> in Xinjiang Province, China, using fluorescent microsatellites (SSR) markers. <i>Veterinary Parasitology</i> , 2018, 261, 53-58.	0.7	1

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2021	De Novo Transcriptome Assembly and Population Genetic Analyses for an Endangered Chinese Endemic <i>Acer miaotaiense</i> (Aceraceae). <i>Genes</i> , 2018, 9, 378.	1.0	44
2022	Assessment of Genetic Diversity, Population Structure, and Evolutionary Relationship of Uncharacterized Genes in a Novel Germplasm Collection of Diploid and Allotetraploid <i>Gossypium</i> Accessions Using EST and Genomic SSR Markers. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2401.	1.8	20
2023	Genetic diversity and population structure among accessions of <i>Perilla frutescens</i> (L.) Britton in East Asia using new developed microsatellite markers. <i>Genes and Genomics</i> , 2018, 40, 1319-1329.	0.5	44
2024	Molecular Characterization of Mung Bean Germplasm from the USDA Core Collection Using Newly Developed KASP-based SNP Markers. <i>Crop Science</i> , 2018, 58, 1659-1670.	0.8	25
2025	Genetic diversity and association mapping of Ethiopian and exotic finger millet accessions. <i>Crop and Pasture Science</i> , 2018, 69, 879.	0.7	19
2026	In silico polymorphic novel SSR marker development and the first SSR-based genetic linkage map in pistachio. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	23
2027	Understanding the genetic relationships and breeding patterns of Sri Lankan tea cultivars with genomic and EST-SSR markers. <i>Scientia Horticulturae</i> , 2018, 240, 72-80.	1.7	10
2028	Structural chromosome rearrangements and polymorphisms identified in Chinese wheat cultivars by high-resolution multiplex oligonucleotide FISH. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1967-1986.	1.8	83
2029	Population structure analysis and determination of neurotoxin content in a set of grass pea (<i>Lathyrus sativus</i> L.) accessions of Bangladesh origin. <i>Crop Journal</i> , 2018, 6, 435-442.	2.3	15
2030	Effect of multiple allelic combinations of genes on regulating grain size in rice. <i>PLoS ONE</i> , 2018, 13, e0190684.	1.1	29
2031	Polymorphism in ovine <i>ANXA9</i> gene and the physiochemical properties and the fraction of protein in milk. <i>Journal of the Science of Food and Agriculture</i> , 2018, 98, 5396-5400.	1.7	3
2032	Analysis of genetic diversity and population structure in upland cotton (<i>Gossypium hirsutum</i> L.) germplasm using simple sequence repeats. <i>Journal of Genetics</i> , 2018, 97, 513-522.	0.4	15
2033	Assessment of genetic diversity and population genetic structure of <i>Carthamus</i> species and Iranian cultivar collection using developed SSR markers. <i>Journal of Genetics</i> , 2018, 97, 67-78.	0.4	7
2034	Detection of QTL (quantitative trait loci) associated with wood density by evaluating genetic structure and linkage disequilibrium of teak. <i>Journal of Forestry Research</i> , 2019, 30, 2247-2258.	1.7	6
2035	Genetic polymorphism of 15 autosomal short tandem repeats in Baloch population of Pakistan. <i>International Journal of Legal Medicine</i> , 2019, 133, 775-776.	1.2	2
2036	Molecular diversity and genetic variability of kernel tocopherols among maize inbreds possessing favourable haplotypes of β^3 -tocopherol methyl transferase (<i>ZmVTE4</i>). <i>Journal of Plant Biochemistry and Biotechnology</i> , 2019, 28, 253-262.	0.9	16
2037	A comparative assessment of diversity of greater yam (<i>Dioscorea alata</i>) in China. <i>Scientia Horticulturae</i> , 2019, 243, 116-124.	1.7	12
2038	Genome-wide marker-trait association analysis in a core set of <i>Dolichos</i> bean germplasm. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2019, 17, 1-11.	0.4	9

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2039	Advanced software programs for the analysis of genetic diversity in livestock genomics: a mini review. <i>Biological Rhythm Research</i> , 2019, , 1-11.	0.4	6
2040	CebÃ, Thailand and Taiwanese aboriginal populations according to Y-STR loci. <i>Gene: X</i> , 2019, 1, 100001.	2.3	3
2041	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.	1.7	22
2042	Transcriptome analysis and codominant markers development in caper, a drought tolerant orphan crop with medicinal value. <i>Scientific Reports</i> , 2019, 9, 10411.	1.6	23
2043	Multiple Maize Reference Genomes Impact the Identification of Variants by Genome-Wide Association Study in a Diverse Inbred Panel. <i>Plant Genome</i> , 2019, 12, 180069.	1.6	37
2044	Genome-wide SNP-based diversity analysis and association mapping in linseed (<i>Linum usitatissimum</i> L.). <i>Euphytica</i> , 2019, 215, 1.	0.6	16
2045	Analysis of genetic diversity and population structure using SSR markers and validation of a Cleavage Amplified Polymorphic Sequences (CAPS) marker involving the sodium transporter <i>OsHKT1;5</i> in saline tolerant rice (<i>Oryza sativa</i> L.) landraces. <i>Gene</i> , 2019, 713, 143976.	1.0	11
2046	Construction of a core collection of eggplant (&i&t;Solanum melongena&i&t; L.) based on genome-wide SNP and SSR genotypes. <i>Breeding Science</i> , 2019, 69, 498-502.	0.9	36
2047	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.	0.4	17
2048	SRAP analysis of the genetic diversity of wild castor (<i>Ricinus communis</i> L.) in South China. <i>PLoS ONE</i> , 2019, 14, e0219667.	1.1	11
2049	WA-CMS-based iso-cytoplasmic restorers derived from commercial rice hybrids reveal distinct population structure and genetic divergence towards restorer diversification. <i>3 Biotech</i> , 2019, 9, 299.	1.1	6
2050	Population genetics and evolutionary history of <i>Miscanthus</i> species in China. <i>Journal of Systematics and Evolution</i> , 2019, 57, 530-542.	1.6	12
2051	Genetic characterization and population structure of maize populations using SSR markers. <i>Annals of Agricultural Sciences</i> , 2019, 64, 47-54.	1.1	25
2052	Morpho-agronomic characterization and genetic variability assessment of a guar germplasm collection by a novel SSR panel. <i>Industrial Crops and Products</i> , 2019, 138, 111568.	2.5	10
2053	Candidate screening of blast resistance donors for rice breeding. <i>Journal of Genetics</i> , 2019, 98, 1.	0.4	10
2054	Dissecting the Genetic Architecture of Seed Protein and Oil Content in Soybean from the Yangtze and Huaihe River Valleys Using Multi-Locus Genome-Wide Association Studies. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3041.	1.8	22
2055	Research Article Genetic diversity of Brazil-nut populations naturally occurring in the municipality of Alta Floresta, MT, Brazil. <i>Genetics and Molecular Research</i> , 2019, 18, .	0.3	1
2056	Genetic diversity of <i>Fusarium oxysporum</i> f. sp. <i>ciceris</i> isolates affecting chickpea in Syria. <i>Crop Protection</i> , 2019, 124, 104863.	1.0	7

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2057	Genetic Diversity and Allelic Frequency of Selected Thai and Exotic Rice Germplasm Using SSR Markers. <i>Rice Science</i> , 2019, 26, 393-403.	1.7	30
2058	Genome-Wide Association Analysis and Allelic Mining of Grain Shape-Related Traits in Rice. <i>Rice Science</i> , 2019, 26, 384-392.	1.7	11
2059	Genetic diversity and differentiation of the African wild rice (<i>Oryza longistaminata</i> chev. et roehr) in Ethiopia. <i>Scientific African</i> , 2019, 6, e00138.	0.7	4
2060	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.	0.7	5
2061	Genetic diversity of leafy amaranth (<i>Amaranthus tricolor</i> L.) resources in Vietnam. <i>Breeding Science</i> , 2019, 69, 640-650.	0.9	23
2062	Geographic and Ecological Dimensions of Host Plant-Associated Genetic Differentiation and Speciation in the <i>Rhagoletis cingulata</i> (Diptera: Tephritidae) Sibling Species Group. <i>Insects</i> , 2019, 10, 275.	1.0	12
2063	Phenotypic and Genotypic Diversity Among Symbiotic and Non-symbiotic Bacteria Present in Chickpea Nodules in Morocco. <i>Frontiers in Microbiology</i> , 2019, 10, 1885.	1.5	17
2064	Molecular Characterization of 170 New gDNA-SSR Markers for Genetic Diversity in Button Mushroom (<i>Agaricus bisporus</i>). <i>Mycobiology</i> , 2019, 47, 527-532.	0.6	7
2065	Rice of Northeast India harbor rich genetic diversity as measured by SSR markers and Zn/Fe content. <i>BMC Genetics</i> , 2019, 20, 79.	2.7	21
2066	Association of Twelve Candidate Gene Polymorphisms with the Intramuscular Fat Content and Average Backfat Thickness of Chinese Suhuai Pigs. <i>Animals</i> , 2019, 9, 858.	1.0	22
2067	Effects of parental genetic distance on offspring growth performance in <i>Pinus massoniana</i> : significance of parental-selection in a clonal seed orchard. <i>Euphytica</i> , 2019, 215, 1.	0.6	3
2068	Narrow gene pool can threaten the survival of <i>Calamus nagbetta</i> R. R. Fernald & Dey: a highly, endemic dioecious rattan species in the Western Ghats of India. <i>Journal of Genetics</i> , 2019, 98, 1.	0.4	1
2069	Assessment of genetic diversity of Brazilian and Mediterranean cactus cultivars by SSR markers and morphological traits. <i>Acta Horticulturae</i> , 2019, , 171-182.	0.1	0
2070	A Novel Software and Method for the Efficient Development of Polymorphic SSR Loci Based on Transcriptome Data. <i>Genes</i> , 2019, 10, 917.	1.0	4
2071	InDel Marker Based Estimation of Multi-Gene Allele Contribution and Genetic Variations for Grain Size and Weight in Rice (<i>Oryza sativa</i> L.). <i>International Journal of Molecular Sciences</i> , 2019, 20, 4824.	1.8	12
2072	Host Genotype and Precipitation Influence of Fungal Endophyte Symbiosis and Mycotoxin Abundance in a Locoweed. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5285.	1.8	7
2073	Genetic diversity and population structure of the sweet leaf herb, <i>Stevia rebaudiana</i> B., cultivated and landraces germplasm assessed by EST-SSRs genotyping and steviol glycosides phenotyping. <i>BMC Plant Biology</i> , 2019, 19, 436.	1.6	14
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2077	Cross-species transferability of EST-SSR markers derived from the transcriptome of kenaf (<i>Hibiscus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 1543-1556.	0.8	10
2078	Genetic loci and candidate genes of symbiotic nitrogen fixation-related characteristics revealed by a genome-wide association study in soybean. <i>Molecular Breeding</i> , 2019, 39, 1.	1.0	10
2079	Evaluation of polyembryony for genetic resources and efficacy of simple sequence repeat markers for the identification of nucellar and zygotic embryo-derived individuals in citrus. <i>Applied Biological Chemistry</i> , 2019, 62, .	0.7	14
2080	Molecular markers: an important tool to analyze the genetic diversity of local Tunisian olive varieties. <i>Euro-Mediterranean Journal for Environmental Integration</i> , 2019, 4, 1.	0.6	4
2081	Whole Genome Diversity, Population Structure, and Linkage Disequilibrium Analysis of Chickpea (<i>Cicer</i>) Tj ETQq0 0,0rgBT /Overlock 10 25	1.0	25
2082	Genetic diversity and population structure of <i>Perilla frutescens</i> collected from Korea and China based on simple sequence repeats (SSRs). <i>Genes and Genomics</i> , 2019, 41, 1329-1340.	0.5	11
2083	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.	0.6	3
2084	Genetic diversity and population structure analysis of <i>Capsicum</i> germplasm accessions. <i>Journal of Integrative Agriculture</i> , 2019, 18, 1312-1320.	1.7	21
2085	Development of SSR markers via de novo transcriptome assembly in <i>Akebia trifoliata</i> (Thunb.) Koidz. <i>Genome</i> , 2019, 62, 817-831.	0.9	24
2086	Genetic polymorphisms of 20 autosomal STR loci in the Han population of Putian City, Southeastern China. <i>Annals of Human Biology</i> , 2019, 46, 509-513.	0.4	1
2087	SSR Marker-Assisted Management of Parental Germplasm in Sugarcane (<i>Saccharum</i> spp. hybrids) Breeding Programs. <i>Agronomy</i> , 2019, 9, 449.	1.3	20
2088	Assessment of Genetic Diversity in Differently Colored Raspberry Cultivars Using SSR Markers Located in Flavonoid Biosynthesis Genes. <i>Agronomy</i> , 2019, 9, 518.	1.3	11
2089	Association analysis uncovers the genetic basis of general combining ability of 11 yield-related traits in parents of hybrid rice. <i>AoB PLANTS</i> , 2019, 11, ply077.	1.2	6
2090	Blast resistance in Indian rice landraces: Genetic dissection by gene specific markers. <i>PLoS ONE</i> , 2019, 14, e0211061.	1.1	33
2091	Evolution of SSR diversity from wild types to U.S. advanced cultivars in the Andean and Mesoamerican domestications of common bean (<i>Phaseolus vulgaris</i>). <i>PLoS ONE</i> , 2019, 14, e0211342.	1.1	39
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2094	Identification and Analysis of a Candidate <i>WRKY</i> Transcription Factor Gene Affecting Adventitious Root Formation Using Association Mapping in <i>Catalpa</i> Scop.. <i>DNA and Cell Biology</i> , 2019, 38, 297-306.	0.9	15
2095	Dispersal route of the Asian house rat (<i>Rattus tanezumi</i>) on mainland China: insights from microsatellite and mitochondrial DNA. <i>BMC Genetics</i> , 2019, 20, 11.	2.7	16
2096	Genetic characterization of maize germplasm derived from Suwan population and temperate resources. <i>Hereditas</i> , 2019, 156, 2.	0.5	14
2097	Genetic diversity and population structure analysis of wild <i>Malus</i> genotypes including the crabapples (<i>M. baccata</i> (L.) Borkh. & <i>M. sikkimensis</i> (Wenzig) Koehne ex C. Schneider) collected from the Indian Himalayan region using microsatellite markers. <i>Genetic Resources and Crop Evolution</i> , 2019, 66, 1311-1326.	0.8	11
2098	AFLP-based genetic diversity analysis distinguishes apomictically and sexually reproducing <i>Cenchrus</i> species. <i>Revista Brasileira De Botanica</i> , 2019, 42, 361-371.	0.5	6
2099	Classification and Identification of indica P/TGMS Lines in China. <i>Rice Science</i> , 2019, 26, 195-198.	1.7	3
2100	Comparing assignment-based approaches to breed identification within a large set of horses. <i>Journal of Applied Genetics</i> , 2019, 60, 187-198.	1.0	8
2101	Genome-Wide Linkage Disequilibrium and the Extent of Effective Population Sizes in Six Chinese Goat Populations Using a 50K Single Nucleotide Polymorphism Panel. <i>Animals</i> , 2019, 9, 350.	1.0	14
2102	Late Pleistocene speciation of three closely related tree peonies endemic to the Qinling-Daba Mountains, a major glacial refugium in Central China. <i>Ecology and Evolution</i> , 2019, 9, 7528-7548.	0.8	19
2103	Molecular-genetic diversity of the endangered Dalmatian barbelgudgeon, <i>Aulopyge huegelii</i> from the BuÅko Blato reservoir. <i>Genetica</i> , 2019, 147, 269-280.	0.5	3
2104	Assessment of genome-wide DArT-seq markers for tea <i>Camellia sinensis</i> (L.) O. Kuntze germplasm analysis. <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	0.6	3
2105	Genome-wide cis-regulatory signatures for modulation of agronomic traits as exemplified by drought yield index (DYI) in chickpea. <i>Functional and Integrative Genomics</i> , 2019, 19, 973-992.	1.4	1
2106	Genome-wide variation patterns between landraces and cultivars uncover divergent selection during modern wheat breeding. <i>Theoretical and Applied Genetics</i> , 2019, 132, 2509-2523.	1.8	56
2107	Detecting novel loci underlying rice blast resistance by integrating a genome-wide association study and RNA sequencing. <i>Molecular Breeding</i> , 2019, 39, 1.	1.0	10
2108	Morphological and Molecular Characterization of Novel Salt-tolerant Rice Germplasm from the Philippines and Bangladesh. <i>Rice Science</i> , 2019, 26, 178-188.	1.7	5
2109	EST-SSR marker development based on RNA-sequencing of <i>E. sibiricus</i> and its application for phylogenetic relationships analysis of seventeen <i>Elymus</i> species. <i>BMC Plant Biology</i> , 2019, 19, 235.	1.6	34
2110	Evaluation of linkage disequilibrium, population structure, and genetic diversity in the U.S. peanut mini core collection. <i>BMC Genomics</i> , 2019, 20, 481.	1.2	39

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2112	An efficient strategy for developing genotype identification markers based on simple sequence repeats in grapevine. <i>Horticulture Environment and Biotechnology</i> , 2019, 60, 363-372.	0.7	2
2113	Exploring genetic diversity of tomato (<i>Solanum lycopersicum</i> L.) germplasm of genebank collection employing SSR and SCAR markers. <i>Genetic Resources and Crop Evolution</i> , 2019, 66, 1295-1309.	0.8	22
2114	Comparative Analyses of Genetic Variation in a Tomato (<i>Solanum lycopersicum</i> L.) Germplasm Collection with Single Nucleotide Polymorphism and Insertion-Deletion Markers. <i>Russian Journal of Genetics</i> , 2019, 55, 204-211.	0.2	1
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2116	Development of a core set of KASP markers for assaying genetic diversity in <i>Brassica rapa</i> subsp. <i>chinensis</i> Makino. <i>Plant Breeding</i> , 2019, 138, 309-324.	1.0	9
2117	Development of a core SNP arrays based on the KASP method for molecular breeding of rice. <i>Rice</i> , 2019, 12, 21.	1.7	60
2118	Evaluation of a microhaplotypes panel for forensic genetics using massive parallel sequencing technology. <i>Forensic Science International: Genetics</i> , 2019, 41, 120-127.	1.6	57
2119	Evaluation of Genetic Diversity Among Exotic Sorghum (<i>Sorghum bicolor</i> L. Moench) Genotypes Through Molecular Based Analysis (RAPD-PCR). <i>Gesunde Pflanzen</i> , 2019, 71, 187-196.	1.7	3
2120	Identification and development of a core set of informative genic SNP markers for assaying genetic diversity in Chinese cabbage. <i>Horticulture Environment and Biotechnology</i> , 2019, 60, 411-425.	0.7	7
2121	Utilization of Molecular Marker Based Genetic Diversity Patterns in Hybrid Parents to Develop Better Forage Quality Multi-Cut Hybrids in Pearl Millet. <i>Agriculture (Switzerland)</i> , 2019, 9, 97.	1.4	9
2122	Phenotypic variability, path analysis and molecular diversity analysis in chickpea (<i>Cicer arietinum</i> L.). <i>Vegetos</i> , 2019, 32, 167-180.	0.8	12
2123	Diversity Assessment of Some Sesame (<i>Sesamum indicum</i> L.) Genotypes Cultivated in Northern Ghana Using Morphological and Simple Sequence Repeat (SSR) Markers. <i>Advances in Agriculture</i> , 2019, 2019, 1-10.	0.3	6
2124	Favorable alleles mining for gelatinization temperature, gel consistency and amylose content in <i>Oryza sativa</i> by association mapping. <i>BMC Genetics</i> , 2019, 20, 34.	2.7	16
2125	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. <i>Frontiers in Plant Science</i> , 2019, 10, 596.	1.7	41
2126	Genetic architecture of grain yield in bread wheat based on genome-wide association studies. <i>BMC Plant Biology</i> , 2019, 19, 168.	1.6	172
2127	Genome-Wide Analyses Reveal Footprints of Divergent Selection and Drought Adaptive Traits in Synthetic-Derived Wheats. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1957-1973.	0.8	53
2128	Genetic diversity, population structure and key phenotypic traits driving variation within soyabean (<i>Glycine max</i>) Tj ETQq1 1 0.784314 rgBT / Over	1.0	12

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2130	Microsatellite Markers Reveal Genetic Diversity and Relationships within a Melon Collection Mainly Comprising Asian Cultivated and Wild Germplasms. <i>BioMed Research International</i> , 2019, 2019, 1-10.	0.9	2
2131	Genome-wide association study of resistance to stripe rust (<i>Puccinia striiformis</i> f. sp. <i>tritici</i>) in Sichuan wheat. <i>BMC Plant Biology</i> , 2019, 19, 147.	1.6	39
2132	Genetic diversity and genetic structure of natural populations in an extremely narrowly distributed perennial species <i>Glycine tabacina</i> (Labill.) Benth. on the southeast islands in China. <i>Genetic Resources and Crop Evolution</i> , 2019, 66, 989-1008.	0.8	3
2133	Genetic diversity and population structure in multiple Chinese goat populations using a <sc>SNP</sc> panel. <i>Animal Genetics</i> , 2019, 50, 242-249.	0.6	19
2134	Differentiation and evolution among geographic and seasonal eco-populations of soybean germplasm in Southern China. <i>Crop and Pasture Science</i> , 2019, 70, 121.	0.7	2
2135	Genetic diversity of Iranian and some European grapes as revealed by nuclear and chloroplast microsatellite and SNP molecular markers. <i>Journal of Horticultural Science and Biotechnology</i> , 2019, 94, 599-610.	0.9	16
2136	Genetic diversity among tropical provitamin a maize inbred lines and implications for a biofortification program. <i>Cereal Research Communications</i> , 2019, 47, 134-144.	0.8	9
2137	Genetic diversity of 10 indigenous chicken ecotypes from Southern Highlands of Tanzania based on Major Histocompatibility Complex-linked microsatellite LEI0258 marker typing. <i>Poultry Science</i> , 2019, 98, 2734-2746.	1.5	23
2138	Morphological, biochemical and molecular characterization for genetic variability analysis of <i>Capsicum annuum</i> . <i>Vegetos</i> , 2019, 32, 131-141.	0.8	8
2139	Assessment of diversity and population structure of mango (<i>Mangifera indica</i> L.) germplasm based on microsatellite (SSR) markers. <i>Australian Journal of Crop Science</i> , 2019, 13, 315-320.	0.1	7
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2141	Genetic diversity of 324 cultivated tomato germplasm resources using agronomic traits and InDel markers. <i>Euphytica</i> , 2019, 215, 1.	0.6	17
2142	Genetic variation and population genetic structure of <i>Laodelphax striatellus</i> via genome-wide single nucleotide polymorphisms from specific locus amplified fragment sequencing. <i>Journal of Applied Entomology</i> , 2019, 143, 315-327.	0.8	8
2143	Development and validation of an SNP genotyping array and construction of a high-density linkage map in castor. <i>Scientific Reports</i> , 2019, 9, 3003.	1.6	17
2144	Characterization of quince (<i>Cydonia oblonga</i> Mill.) accessions by simple sequence repeat markers. <i>Turk Tarim Ve Ormancilik Dergisi/Turkish Journal of Agriculture and Forestry</i> , 2019, 43, 69-79.	0.8	22
2145	Morphological and genetic differentiation of wolf trees in Scots pine stands based on chloroplast microsatellite markers. <i>European Journal of Forest Research</i> , 2019, 138, 527-537.	1.1	2
2146	Haplotype analysis of Ethiopian bread wheat (<i>Triticum aestivum</i>) cultivars and elite lines for yellow rust resistance genes using linked molecular markers. <i>African Journal of Biotechnology</i> , 2019, 18, 37-57.	0.3	1

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2148	Dissection of the genetic variation and candidate genes of lint percentage by a genome-wide association study in upland cotton. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1991-2002.	1.8	36
2149	Utility of TRAP markers to determine indel mutation frequencies induced by gamma-ray irradiation of faba bean (<i>Vicia faba</i> L.) seeds. <i>International Journal of Radiation Biology</i> , 2019, 95, 1160-1171.	1.0	4
2150	Population genetics of 15 autosomal STR loci in the Han population of Ili Kazakh Autonomous Prefecture, Northwestern China. <i>Annals of Human Genetics</i> , 2019, 83, 318-324.	0.3	3
2151	Uncovering Genomic Regions Associated With 36 Agro-Morphological Traits in Indian Spring Wheat Using GWAS. <i>Frontiers in Plant Science</i> , 2019, 10, 527.	1.7	70
2152	Development of model web-server for crop variety identification using throughput SNP genotyping data. <i>Scientific Reports</i> , 2019, 9, 5122.	1.6	16
2153	Genetic diversity and population structure of <i>Miscanthus lutarioriparius</i> , an endemic plant of China. <i>PLoS ONE</i> , 2019, 14, e0211471.	1.1	24
2154	ABC Transporter-Mediated Transport of Glutathione Conjugates Enhances Seed Yield and Quality in Chickpea. <i>Plant Physiology</i> , 2019, 180, 253-275.	2.3	21
2155	Transcriptional signatures modulating shoot apical meristem morphometric and plant architectural traits enhance yield and productivity in chickpea. <i>Plant Journal</i> , 2019, 98, 864-883.	2.8	6
2156	Comparative transcriptomics analysis uncovers alternative splicing events and molecular markers in cabbage (<i>Brassica oleracea</i> L.). <i>Planta</i> , 2019, 249, 1599-1615.	1.6	11
2157	Assessment of genetic diversity and population structure of <i>Magnaporthe oryzae</i> causing rice blast disease using SSR markers. <i>Physiological and Molecular Plant Pathology</i> , 2019, 106, 157-165.	1.3	16
2158	Development and validation of whole genome-wide and genic microsatellite markers in oil palm (<i>Elaeis</i>) Tj ETQq1 1 0,784314 rgBT /Over	1.6	19
2159	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). <i>Molecular Breeding</i> , 2019, 39, 1.	1.0	11
2160	Application of High-Throughput Sequencing to Evaluate the Genetic Diversity Among Wild Apple Species Indigenous to Shandong, China, and Introduced Cultivars. <i>Plant Molecular Biology Reporter</i> , 2019, 37, 63-73.	1.0	2
2161	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.	0.4	8
2162	Study of the Molecular Biodiversity of the Saharan Bread Wheat in Algeria. <i>Cereal Research Communications</i> , 2019, 47, 724-739.	0.8	1
2163	In silico polymorphism analysis for the development of simple sequence repeat markers in pistachio. <i>Acta Horticulturae</i> , 2019, , 533-536.	0.1	0
2164	Application of simple sequence repeat (SSR) markers to the genetic diversity of a chrysanthemum germplasm collection. <i>Acta Horticulturae</i> , 2019, , 61-72.	0.1	0

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2166	When West Meets East: The Origins and Spread of Weedy Rice Between Continental and Island Southeast Asia. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2941-2950.	0.8	8
2167	Combining Quantitative Data on Growth, Wood Density and Other Traits with SSR Markers to Evaluate Genetic Diversity and Structure in a Planted Population of <i>Eucalyptus camaldulensis</i> Dehn.. <i>Forests</i> , 2019, 10, 1090.	0.9	2
2168	Research Article ISSR and SSR markers for determining genetic relationships among three wild species of <i>Passiflora</i> . <i>Genetics and Molecular Research</i> , 2019, 18, .	0.3	3
2169	Domestication and Spread of Broomcorn Millet (<i>Panicum miliaceum</i> L.) Revealed by Phylogeography of Cultivated and Weedy Populations. <i>Agronomy</i> , 2019, 9, 835.	1.3	9
2170	Microsatellite-based analysis of genetic structure and gene flow of <i>Mythimna separata</i> (Walker) (Lepidoptera: Noctuidae) in China. <i>Ecology and Evolution</i> , 2019, 9, 13426-13437.	0.8	11
2171	Genetic Diversity, Population Structure, and Marker-Trait Association for Drought Tolerance in US Rice Germplasm. <i>Plants</i> , 2019, 8, 530.	1.6	13
2172	ddRAD sequencing-based identification of inter-genepool SNPs and association analysis in <i>Brassica juncea</i> . <i>BMC Plant Biology</i> , 2019, 19, 594.	1.6	25
2173	Line \tilde{A} -tester analysis for seed yield, protein and oil content and SSR based diversity in sesame (<i>Sesamum indicum</i> L.). <i>Ecological Genetics and Genomics</i> , 2019, 13, 100048.	0.3	0
2174	Genetic Diversity, Structure, and Core Collection of Korean Apple Germplasm Using Simple Sequence Repeat Markers. <i>Horticulture Journal</i> , 2019, 88, 329-337.	0.3	12
2175	Genetic Diversity and Classification of the Cytoplasm of Chinese Elite Foxtail Millet [<i>Setaria italica</i> (L.) P. Beauv.] Parental Lines Revealed by Chloroplast Deoxyribonucleic Acid Variation. <i>Frontiers in Genetics</i> , 2019, 10, 1198.	1.1	2
2176	Multi-Level Characterization of Eggplant Accessions from Greek Islands and the Mainland Contributes to the Enhancement and Conservation of this Germplasm and Reveals a Large Diversity and Signatures of Differentiation between both Origins. <i>Agronomy</i> , 2019, 9, 887.	1.3	9
2177	Evaluation of the genetic diversity of fibre quality traits in upland cotton (<i>Gossypium hirsutum</i> L.) inferred from phenotypic variations. <i>Journal of Cotton Research</i> , 2019, 2, .	1.0	1
2178	Genetic polymorphisms, forensic efficiency and phylogenetic analysis of 17 autosomal STR loci in the Han population of Wuxi, Eastern China. <i>Annals of Human Biology</i> , 2019, 46, 601-605.	0.4	3
2179	A Cointegration Analysis of Economic Growth and CO ₂ Emissions: A Case Study of Malaysia.. <i>Environmental Management and Sustainable Development</i> , 2019, 9, 1.	0.1	4
2180	Characterization of genome-wide genetic variations between two varieties of tea plant (<i>Camellia</i>) Tj ETQq1 1 0.784314 rgBT /Overloc 1.2 38	1.2	38
2182	Genetic polymorphisms, forensic efficiency, and phylogenetic analysis of 15 autosomal STR loci in the Uygur population of Ili Kazakh Autonomous Prefecture, Northwestern China. <i>Annals of Human Genetics</i> , 2019, 83, 46-53.	0.3	0
2183	A pilot study of genetic structure of <i>Porphyra umbilicalis</i> KÄ¼tzing in the Gulf of Maine using SNP markers from RNA-Seq. <i>Journal of Applied Phycology</i> , 2019, 31, 1493-1503.	1.5	1

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2185	Genetic characterization of <i>Pistacia atlantica</i> subsp. <i>kurdica</i> from northern Zagros forests in Iran. <i>Trees - Structure and Function</i> , 2019, 33, 481-490.	0.9	8
2186	Integration of molecular and geographical data analysis of Iranian <i>Prunus scoparia</i> populations in order to assess genetic diversity and conservation planning. <i>Scientia Horticulturae</i> , 2019, 247, 49-57.	1.7	6
2187	Population Differentiation Within <i>Anisogramma anomala</i> in North America. <i>Phytopathology</i> , 2019, 109, 1074-1082.	1.1	14
2188	Genetic Diversity and Population Structure in Upland Rice (<i>Oryza sativa</i> L.) of Mizoram, North East India as Revealed by Morphological, Biochemical and Molecular Markers. <i>Biochemical Genetics</i> , 2019, 57, 421-442.	0.8	7
2189	High-throughput genotyping in onion reveals structure of genetic diversity and informative SNPs useful for molecular breeding. <i>Molecular Breeding</i> , 2019, 39, 1.	1.0	20
2190	Resolving population structure and genetic differentiation associated with RAD-SNP loci under selection in tossa jute (<i>Corchorus olitorius</i> L.). <i>Molecular Genetics and Genomics</i> , 2019, 294, 479-492.	1.0	20
2191	Mapping loci controlling fatty acid profiles, oil and protein content by genome-wide association study in <i>Brassica napus</i> . <i>Crop Journal</i> , 2019, 7, 217-226.	2.3	19
2192	Genetic Diversity, Population Structure and Correlation Study in <i>Moringa oleifera</i> Lam. Using ISSR and SRAP Markers. <i>Proceedings of the National Academy of Sciences India Section B - Biological Sciences</i> , 2019, 89, 1361-1371.	0.4	5
2193	Development of New SSR (Simple Sequence Repeat) Markers for Lentils (<i>Lens culinaris</i> Medik.) from Genomic Library Enriched with AG and AC Microsatellites. <i>Biochemical Genetics</i> , 2019, 57, 338-353.	0.8	10
2194	Genetische Diversitätsanalyse von <i>Brassica</i> -Arten unter Verwendung von PCR-basierten SSR-Markern. <i>Gesunde Pflanzen</i> , 2019, 71, 1-7.	1.7	25
2195	Genetic diversity and population structure analysis in <i>Perilla</i> crop and their weedy types from northern and southern areas of China based on simple sequence repeat (SSRs). <i>Genes and Genomics</i> , 2019, 41, 267-281.	0.5	23
2196	Development and application of EST-SSRs markers for analysis of genetic diversity in erect milkvetch (<i>Astragalus adsurgens</i> Pall.). <i>Molecular Biology Reports</i> , 2019, 46, 1323-1326.	1.0	9
2197	Genetic relationship, population structure analysis and allelic characterization of flowering and maturity genes E1, E2, E3 and E4 among 90 Indian soybean landraces. <i>Physiology and Molecular Biology of Plants</i> , 2019, 25, 387-398.	1.4	10
2198	Genetic diversity, linkage disequilibrium, and population structure in a panel of Brazilian rice accessions. <i>Journal of Applied Genetics</i> , 2019, 60, 27-31.	1.0	4
2199	Development of chloroplast microsatellite markers for identification of <i>Glycyrrhiza</i> species. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2019, 17, 95-98.	0.4	5
2200	Genome-wide regulatory gene-derived SSRs reveal genetic differentiation and population structure in fiber flax genotypes. <i>Journal of Applied Genetics</i> , 2019, 60, 13-25.	1.0	15
2201	Reliability Authentication of <i>Glycyrrhiza glabra</i> L. Populations from South Iran Using SSR and SNP-Based Markers. <i>Proceedings of the National Academy of Sciences India Section B - Biological Sciences</i> , 2019, 89, 1283-1294.	0.4	0

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2202	Molecular analysis of mutant granule-bound starch synthase-I (waxy1) gene in diverse waxy maize inbreds. <i>3 Biotech</i> , 2019, 9, 3.	1.1	21
2203	Exploring the genomic resources of carrot for cross-genera transferability and phylogenetic assessment among orphan spices and vegetables of Apiaceae family. <i>Horticulture Environment and Biotechnology</i> , 2019, 60, 81-93.	0.7	8
2204	Spatial distribution and genetic diversity of wild date palm (<i>Phoenix sylvestris</i>) growing in coastal Bangladesh. <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	0.6	12
2205	Reconstituting the genome of a young allopolyploid crop, <i>Brassica napus</i> , with its related species. <i>Plant Biotechnology Journal</i> , 2019, 17, 1106-1118.	4.1	18
2206	Genetic diversity of <i>Aegilops</i> L. species from Azerbaijan and Georgia using SSR markers. <i>Genetic Resources and Crop Evolution</i> , 2019, 66, 453-463.	0.8	13
2207	Characterization of genetic diversity and structures in natural <i>Glycine tomentella</i> populations on the southeast islands of China. <i>Genetic Resources and Crop Evolution</i> , 2019, 66, 47-59.	0.8	2
2208	Transmission of early ripening trait related loci in grapevines from backbone cultivar Pearl of Csaba to its descendants. <i>Scientia Horticulturae</i> , 2019, 244, 151-156.	1.7	5
2209	Molecular and morphological characterisation of the oldest <i>Cucumis melo</i> L. seeds found in the Western Mediterranean Basin. <i>Archaeological and Anthropological Sciences</i> , 2019, 11, 789-810.	0.7	17
2210	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.	1.3	44
2211	Lack of association between FTO gene variations and metabolic healthy obese (MHO) phenotype: Tehran Cardio-metabolic Genetic Study (TCGS). <i>Eating and Weight Disorders</i> , 2020, 25, 25-35.	1.2	11
2212	Molecular profiling in relation to drought tolerance in advance breeding lines of rice using microsatellite markers. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2020, 29, 36-46.	0.9	0
2213	Genetic diversity among cultivated and wild <i>Panax ginseng</i> populations revealed by high-resolution microsatellite markers. <i>Journal of Ginseng Research</i> , 2020, 44, 637-643.	3.0	20
2214	Kashmiris phylogenetic depictions through uniparental and biparental genetic markers. <i>International Journal of Legal Medicine</i> , 2020, 134, 1311-1312.	1.2	1
2215	Using <i>Heading date 1</i> preponderant alleles from <i>indica</i> cultivars to breed high yield, high quality <i>japonica</i> rice varieties for cultivation in south China. <i>Plant Biotechnology Journal</i> , 2020, 18, 119-128.	4.1	30
2216	Phylogenetic analysis and haplotype diversity in Christian residents of Lahore, Pakistan, using 17 Y-chromosomal STR loci. <i>International Journal of Legal Medicine</i> , 2020, 134, 521-522.	1.2	1
2217	Molecular genetic diversity analysis for heat tolerance of indigenous and exotic wheat genotypes. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2020, 29, 15-23.	0.9	10
2218	Molecular and Biochemical Characterisation of Indian Germplasm of <i>Pisum sativum</i> L.. Proceedings of the National Academy of Sciences India Section B - Biological Sciences, 2020, 90, 103-111.	0.4	4
2219	Population genetic data of 30 insertion-deletion markers in Punjabi population of Pakistan. <i>International Journal of Legal Medicine</i> , 2020, 134, 511-512.	1.2	5

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2220	The emergence of a new weed in maize plantations: characterization and genetic structure using microsatellite markers. <i>Genetic Resources and Crop Evolution</i> , 2020, 67, 225-239.	0.8	6
2221	Evaluation of SSR-based genetic diversity, protein and mineral content in black gram genotypes. <i>Journal of King Saud University - Science</i> , 2020, 32, 1029-1033.	1.6	10
2222	Characterization of genetic diversity and population structure in wheat using array based SNP markers. <i>Molecular Biology Reports</i> , 2020, 47, 293-306.	1.0	60
2223	Assessment of Genetic Diversity of Soybean (<i>Glycine max</i>) Genotypes Using Qualitative Traits and Microsatellite Markers. <i>Agricultural Research</i> , 2020, 9, 23-34.	0.9	12
2224	Evaluation of genetic diversity of parental lines for development of heterotic groups in hybrid rice (<i>Oryza sativa</i> L.). <i>Journal of Plant Biochemistry and Biotechnology</i> , 2020, 29, 236-252.	0.9	13
2225	Rapid and repeatable host plant shifts drive reproductive isolation following a recent human-mediated introduction of the apple maggot fly, <i>Rhagoletis pomonella</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2020, 74, 156-168.	1.1	15
2226	Characterization of a repertoire of tomato fruit genetic variants in the San marzano genetic background. <i>Scientia Horticulturae</i> , 2020, 261, 108927.	1.7	12
2227	Phylogenetic origin and dispersal pattern of Taiwan weedy rice. <i>Pest Management Science</i> , 2020, 76, 1639-1651.	1.7	9
2228	Significant Association of miR-605 rs2043556 with Susceptibility to Breast Cancer. <i>MicroRNA (Sharjah, United Arab Emirates)</i> , 2020, 9, 133-141.	0.6	4
2229	Genetic Diversity and Population Structure of Broomcorn Sorghum Investigated with Simple Sequence Repeat Markers. <i>Tropical Plant Biology</i> , 2020, 13, 62-72.	1.0	5
2230	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.	1.4	14
2231	Screening of molecular markers associated to cold tolerance- related traits in Citrus. <i>Scientia Horticulturae</i> , 2020, 263, 109145.	1.7	8
2232	Association analysis between constructed SNPLDBs and GCA effects of 9 quality-related traits in parents of hybrid rice (<i>Oryza sativa</i> L.). <i>BMC Genomics</i> , 2020, 21, 31.	1.2	6
2233	Molecular evidence for three genetic species of <i>Dipteryx</i> in the Peruvian Amazon. <i>Genetica</i> , 2020, 148, 1-11.	0.5	5
2234	Development of SNP markers and validation assays in commercial Korean melon cultivars, using Genotyping-by-sequencing and Fluidigm analyses. <i>Scientia Horticulturae</i> , 2020, 263, 109113.	1.7	15
2235	Heterosis and combining ability analysis in CMS hybrid rice. <i>Euphytica</i> , 2020, 216, 1.	0.6	24
2236	Development and characterization of novel microsatellite markers in <i>Puccinia striiformis</i> f.sp. <i>tritici</i> and their transferability in <i>Puccinia</i> species. <i>Journal of Phytopathology</i> , 2020, 168, 120-128.	0.5	3
2237	Genome-Wide Association Study of Resistance to Potato Common Scab. <i>Potato Research</i> , 2020, 63, 253-266.	1.2	28

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2238	Population Structure and Genetic Diversity in Sweet Cassava Accessions in Paran�ı and Santa Catarina, Brazil. <i>Plant Molecular Biology Reporter</i> , 2020, 38, 25-38.	1.0	5
2239	Association mapping for mungbean yellow mosaic India virus resistance in mungbean (<i>Vigna radiata</i> L.) Tj ETQq1 1 0,784314,rgBT /Ov	1.1	18
2240	Characterization of Sicilian rosemary (<i>Rosmarinus officinalis</i> L.) germplasm through a multidisciplinary approach. <i>Planta</i> , 2020, 251, 37.	1.6	14
2241	Development of genomic microsatellite markers in cluster bean using next-generation DNA sequencing and their utility in diversity analysis. <i>Current Plant Biology</i> , 2020, 21, 100134.	2.3	15
2242	Combining ability and heterosis for grain minerals, grain weight and yield in pearl millet and SSR markers based diversity of lines and testers. <i>Journal of King Saud University - Science</i> , 2020, 32, 1536-1543.	1.6	9
2243	Genetic diversity and population structure in Beninese pigeon pea [<i>Cajanus cajan</i> (L.) Huth] landraces collection revealed by SSR and genome wide SNP markers. <i>Genetic Resources and Crop Evolution</i> , 2020, 67, 191-208.	0.8	26
2244	Geographic differentiation and phylogeographic relationships among world soybean populations. <i>Crop Journal</i> , 2020, 8, 260-272.	2.3	16
2245	Analysis of genetic diversity of ancient Ginkgo populations using SSR markers. <i>Industrial Crops and Products</i> , 2020, 145, 111942.	2.5	37
2246	Transferability and Polymorphism of SSR Markers Located in Flavonoid Pathway Genes in <i>Fragaria</i> and <i>Rubus</i> Species. <i>Genes</i> , 2020, 11, 11.	1.0	21
2247	Identification of polymorphic SSR markers in elite genotypes of pearl millet and diversity analysis. <i>Ecological Genetics and Genomics</i> , 2020, 14, 100051.	0.3	6
2248	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.	1.0	4
2249	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.	1.0	5
2250	Grain Fe and Zn contents linked SSR markers based genetic diversity in rice. <i>PLoS ONE</i> , 2020, 15, e0239739.	1.1	13
2251	Genetic dissection of eating and cooking qualities in different subpopulations of cultivated rice (<i>Oryza sativa</i> L.) through association mapping. <i>BMC Genetics</i> , 2020, 21, 119.	2.7	7
2252	Simple sequence repeat markers revealed genetic divergence and population structure of okra [<i>Abelmoschus esculentus</i>] collections of diverse geographic origin. <i>Australian Journal of Crop Science</i> , 2020, , 1032-1041.	0.1	1
2253	Genetic Diversity and Population Structure of Asian and European Common Wheat Accessions Based on Genotyping-By-Sequencing. <i>Frontiers in Genetics</i> , 2020, 11, 580782.	1.1	31
2254	The landscape of microsatellites in the enset (<i>Ensete ventricosum</i>) genome and web-based marker resource development. <i>Scientific Reports</i> , 2020, 10, 15312.	1.6	11
2255	Mining and validation of novel genotyping-by-sequencing (GBS)-based simple sequence repeats (SSRs) and their application for the estimation of the genetic diversity and population structure of coconuts (<i>Cocos nucifera</i> L.) in Thailand. <i>Horticulture Research</i> , 2020, 7, 156.	2.9	14

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2256	Development of EST-SSR markers and association mapping with floral traits in <i>Syringa oblata</i> . <i>BMC Plant Biology</i> , 2020, 20, 436.	1.6	16
2257	Genetic diversity in anchote (<i>Coccinia abyssinica</i> (Lam.) Cogn) using microsatellite markers. <i>Current Plant Biology</i> , 2020, 24, 100167.	2.3	7
2258	High Resolution Melting and Insertion Site-Based Polymorphism Markers for Wheat Variability Analysis and Candidate Genes Selection at Drought and Heat MQTL Loci. <i>Agronomy</i> , 2020, 10, 1294.	1.3	25
2259	Genotyping-by-Sequencing to Unlock Genetic Diversity and Population Structure in White Yam (<i>Dioscorea rotundata</i> Poir.). <i>Agronomy</i> , 2020, 10, 1437.	1.3	16
2260	Genetic Diversity, Population Structure and Inter-Trait Relationships of Combined Heat and Drought Tolerant Early-Maturing Maize Inbred Lines from West and Central Africa. <i>Agronomy</i> , 2020, 10, 1324.	1.3	8
2261	Molecular identification of Date palm (<i>Phoenix dactylifera</i> L.) "Deglet noor" pollinator through analysis of genetic diversity of Algerian male and female ecotypes using SSRs markers. <i>Scientia Horticulturae</i> , 2020, 274, 109668.	1.7	4
2262	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
2263	American oil palm from Brazil: Genetic diversity, population structure, and core collection. <i>Crop Science</i> , 2020, 60, 3212-3227.	0.8	10
2264	Polymorphism levels of some SSR markers (Simple Sequence Repeat) for parental line identification on low temperature tolerance. <i>IOP Conference Series: Earth and Environmental Science</i> , 2020, 454, 012165.	0.2	1
2265	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.	0.8	2
2266	Population genetic portrait of Pakistani Lahore-Christians based on 32 STR loci. <i>Scientific Reports</i> , 2020, 10, 18960.	1.6	3
2267	Low genetic diversity indicating the threatened status of <i>Rhizophora apiculata</i> (Rhizophoraceae) in Malaysia: declined evolution meets habitat destruction. <i>Scientific Reports</i> , 2020, 10, 19112.	1.6	14
2268	Genetic variation of a widespread subdominant tree species (<i>Acer campestre</i> L.) in Bosnia and Herzegovina. <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	0.6	2
2269	Genome-Wide Association Analysis for Phosphorus Use Efficiency Traits in Mungbean (<i>Vigna radiata</i> L.) Tj ETQq1 1 0,784314,rgBT /Over	1.7	28
2270	Complete Mitochondrial Genome and a Set of 10 Novel Kompetitive Allele-Specific PCR Markers in Ginseng (<i>Panax ginseng</i> C. A. Mey.). <i>Agronomy</i> , 2020, 10, 1868.	1.3	10
2271	Genetic diversity and structure analysis of <i>Vigna unguiculata</i> L. (Walp.) landraces from southeastern Mexico using ISSR markers. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2020, 18, 201-210.	0.4	0
2272	Genetic Diversity of <i>Phyllanthus emblica</i> From Two Different Climate Type Areas. <i>Frontiers in Plant Science</i> , 2020, 11, 580812.	1.7	19
2273	Development of novel microsatellite markers using RAD sequencing technology for diversity assessment of rambutan (<i>Nephelium lappaceum</i> L.) germplasm. <i>Heliyon</i> , 2020, 6, e05077.	1.4	2

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2274	Shining a light on species delimitation in the tree genus <i>Engelhardia</i> Leschenault ex Blume (Juglandaceae). <i>Molecular Phylogenetics and Evolution</i> , 2020, 152, 106918.	1.2	16
2275	Analysis of molecular characterizations of beets, <i>Beta vulgaris</i> in response to cyst nematodes, <i>Heterodera schachtii</i> . <i>Physiological and Molecular Plant Pathology</i> , 2020, 112, 101518.	1.3	17
2276	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.	0.5	6
2277	Identification of soybean (<i>Glycine max</i> [L.] Merr.) mutants and improved varieties having diverse drought tolerance character using SSR marker. <i>IOP Conference Series: Earth and Environmental Science</i> , 2020, 482, 012014.	0.2	1
2278	Development of Laos Khao Kai Noi rice landrace (<i>Oryza sativa</i> L.) core collection as a model for rice genetic resources management in the Laos National Genebank. <i>IOP Conference Series: Earth and Environmental Science</i> , 2020, 482, 012039.	0.2	2
2279	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.	1.1	15
2280	The relationship of the immune response mediator genes' polymorphic variants with the methotrexate efficacy in juvenile idiopathic arthritis. <i>Turkish Journal of Medical Sciences</i> , 2020, 50, 1038-1047.	0.4	2
2281	rs1542705'67,992,843-1,050,239 represents a novel informative haplotype at the SMPD1 locus in the Iranian population. <i>Meta Gene</i> , 2020, 25, 100744.	0.3	0
2282	Development of SSR markers from transcriptome data for the pear rust pathogen <i>Gymnosporangium asiaticum</i> . <i>Journal of Phytopathology</i> , 2020, 168, 559-570.	0.5	1
2283	Indigenous Mota-named coarse rice germplasm is distinct from fine-grained rice collected from south-central coastal Bangladesh as compared with the morphological descriptors and molecular markers. <i>Revista Brasileira De Botanica</i> , 2020, 43, 933-945.	0.5	4
2284	Molecular characterization and insights into the origin of common bean (<i>Phaseolus vulgaris</i> L.) landraces of north western Himalayas. <i>Nucleus (India)</i> , 2020, 63, 271-279.	0.9	9
2285	Assessment of genetic diversity and population structure among a collection of Korean <i>Perilla</i> germplasms based on SSR markers. <i>Genes and Genomics</i> , 2020, 42, 1419-1430.	0.5	10
2286	Transcriptome wide SSR discovery cross-taxa transferability and development of marker database for studying genetic diversity population structure of <i>Lilium</i> species. <i>Scientific Reports</i> , 2020, 10, 18621.	1.6	17
2287	Assessing Diversity in the <i>Camelina</i> Genus Provides Insights into the Genome Structure of <i>Camelina sativa</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1297-1308.	0.8	33
2288	Genetic Diversity and Inter-Trait Relationships among Maize Inbreds Containing Genes from <i>Zea diploperennis</i> and Hybrid Performance under Contrasting Environments. <i>Agronomy</i> , 2020, 10, 1478.	1.3	3
2289	Assessment of genetic diversity and identification of core germplasm in single-flowered amaryllis (<i>Hippeastrum hybridum</i>) using SRAP markers. <i>Biotechnology and Biotechnological Equipment</i> , 2020, 34, 966-974.	0.5	4
2290	Genome-wide association analysis of stripe rust resistance in modern Chinese wheat. <i>BMC Plant Biology</i> , 2020, 20, 491.	1.6	17
2291	Ecological genomics of Chinese wheat improvement: implications in breeding for adaptation. <i>BMC Plant Biology</i> , 2020, 20, 494.	1.6	5

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2292	An extended KASP-SNP resource for molecular breeding in Chinese cabbage (<i>Brassica rapa</i> L. ssp.)	1.1	16
2293	Genetic diversity in leafy mustard (<i>Brassica juncea</i> var. <i>rugosa</i>) as revealed by agro-morphological traits and SSR markers. <i>Physiology and Molecular Biology of Plants</i> , 2020, 26, 2005-2018.	1.4	12
2294	Genome-wide association mapping revealed numerous novel genomic loci for grain nutritional and yield-related traits in rice (<i>Oryza sativa</i> L.) landraces. <i>3 Biotech</i> , 2020, 10, 487.	1.1	11
2295	Forensic and phylogenetic characterization of 15 autosomal STRs in Hazara population of Pakistan. <i>Legal Medicine</i> , 2020, 47, 101786.	0.6	0
2296	Oral <i>Candida albicans</i> colonization in healthy individuals: prevalence, genotypic diversity, stability along time and transmissibility. <i>Journal of Oral Microbiology</i> , 2020, 12, 1820292.	1.2	11
2297	Development of SSR markers and association studies of markers with phenology and yield-related traits in grass pea (<i>Lathyrus sativus</i>). <i>Crop and Pasture Science</i> , 2020, 71, 768.	0.7	6
2298	The genetic structure and mating system of a recovered Chinese pangolin population (<i>Manis</i>)	1.0	11
2299	ddRAD sequencing-based genotyping for population structure analysis in cultivated tomato provides new insights into the genomic diversity of Mediterranean "da serbo" type long shelf-life germplasm. <i>Horticulture Research</i> , 2020, 7, 134.	2.9	30
2300	Conservation recommendations for <i>Oryza rufipogon</i> Griff. in China based on genetic diversity analysis. <i>Scientific Reports</i> , 2020, 10, 14375.	1.6	12
2301	Molecular and Phenotypic Characterization for Cold Tolerance in Rice (<i>Oryza sativa</i> L.). <i>Bangladesh Rice Journal</i> , 2020, 23, 1-15.	0.8	2
2302	Efficiencies of Heterotic Grouping Methods for Classifying Early Maturing Maize Inbred Lines. <i>Agronomy</i> , 2020, 10, 1198.	1.3	15
2303	Marker association study of yield attributing traits in common bean (<i>Phaseolus vulgaris</i> L.). <i>Molecular Biology Reports</i> , 2020, 47, 6769-6783.	1.0	14
2304	Population structure and diversity assessment of barley (<i>Hordeum vulgare</i> L.) introduction from ICARDA. <i>Journal of Genetics</i> , 2020, 99, 1.	0.4	8
2305	Genetic diversity and fingerprinting of 33 standard flue-cured tobacco varieties for use in distinctness, uniformity, and stability testing. <i>BMC Plant Biology</i> , 2020, 20, 378.	1.6	9
2306	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.	1.6	13
2307	Epigenetic Variation Induced by Gamma Rays, DNA Methyltransferase Inhibitors, and Their Combination in Rice. <i>Plants</i> , 2020, 9, 1088.	1.6	2
2308	First de novo genome specific development, characterization and validation of simple sequence repeat (SSR) markers in Genus <i>Salvadora</i> . <i>Molecular Biology Reports</i> , 2020, 47, 6997-7008.	1.0	14
2309	Genetic Diversity and Population Structure of <i>Brachiaria</i> (syn. <i>Urochloa</i>) Ecotypes from Uganda. <i>Agronomy</i> , 2020, 10, 1193.	1.3	7

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2310	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.	0.5	9
2311	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.	1.4	14
2312	Genetic Diversity, Pedigree Relationships, and A Haplotype-Based DNA Fingerprinting System of Red Bayberry Cultivars. <i>Frontiers in Plant Science</i> , 2020, 11, 563452.	1.7	5
2313	Development of novel g-SSR markers in guava (<i>Psidium guajava</i> L.) cv. Allahabad Safeda and their application in genetic diversity, population structure and cross species transferability studies. <i>PLoS ONE</i> , 2020, 15, e0237538.	1.1	24
2314	Fusarium Species and Fusarium oxysporum Species Complex Genotypes Associated With Yam Wilt in South-Central China. <i>Frontiers in Microbiology</i> , 2020, 11, 1964.	1.5	27
2315	Genetic Diversity of <i>Orobanche crenata</i> Populations in Ethiopia Using Microsatellite Markers. <i>International Journal of Genomics</i> , 2020, 2020, 1-8.	0.8	6
2316	Detection of genomic regions associated with tiller number in Iranian bread wheat under different water regimes using genome-wide association study. <i>Scientific Reports</i> , 2020, 10, 14034.	1.6	40
2317	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.	2.9	10
2318	Development of Novel Genomic Simple Sequence Repeat (g-SSR) Markers and Their Validation for Genetic Diversity Analyses in Kalmegh [<i>Andrographis paniculata</i> (Burm. F.) Nees]. <i>Plants</i> , 2020, 9, 1734.	1.6	11
2319	Evidence for spatial clines and mixed geographic modes of speciation for North American cherry- <i>Rhagoletis</i> (Diptera: Tephritidae) flies. <i>Ecology and Evolution</i> , 2020, 10, 12727-12744.	0.8	6
2320	Diversity assessment of vanilla (<i>Vanilla</i> species) accessions in selected counties of Kenya using simple sequence repeats (SSRs) markers. <i>African Journal of Biotechnology</i> , 2020, 19, 736-746.	0.3	0
2321	Assessment of diversity of Indian aromatic rice germplasm collections for morphological, agronomical, quality traits and molecular characters to identify a core set for crop improvement. <i>CABI Agriculture and Bioscience</i> , 2020, 1, .	1.1	14
2322	The genetic relationships of Indian jujube (<i>Ziziphus mauritiana</i> Lam.) cultivars using SSR markers. <i>Heliyon</i> , 2020, 6, e05078.	1.4	8
2323	Understanding genetic diversity, population structure and development of a core collection of Indian accessions of watermelon (<i>Citrullus lanatus</i> (Thunb.) Matsum. and Nakai). <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2020, 18, 359-368.	0.4	4
2324	Suitability of target region amplified polymorphism (TRAP) markers to discern genetic variability in sweet sorghum. <i>Journal of Genetic Engineering and Biotechnology</i> , 2020, 18, 59.	1.5	1
2325	Population genetic structure of the giant panda staple food bamboo (<i>Fargesia spathacea</i>) Tj ETQq1 1 0.784314 rgBT /Overlock	1.6	8
2326	Genetic diversity and population structure of sugarcane (<i>Saccharum</i> spp.) accessions by means of microsatellites markers. <i>Acta Scientiarum - Agronomy</i> , 2020, 42, e45088.	0.6	3
2327	Genetic Variation May Have Promoted the Successful Colonization of the Invasive Gall Midge, <i>Obolodiplosis robiniae</i> , in China. <i>Frontiers in Genetics</i> , 2020, 11, 387.	1.1	8

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2328	Development of 18 microsatellite markers for <i>Atractylodes japonica</i> . <i>Applications in Plant Sciences</i> , 2020, 8, e11350.	0.8	1
2329	QTL mapping and GWAS for identification of loci conferring partial resistance to <i>Pythium sylvaticum</i> in soybean (<i>Glycine max</i> (L.) Merr). <i>Molecular Breeding</i> , 2020, 40, 1.	1.0	16
2330	Genetic Diversity Patterns and Discrimination of 172 Korean Soybean (<i>Glycine max</i> (L.) Merrill) Varieties Based on SSR Analysis. <i>Agriculture (Switzerland)</i> , 2020, 10, 77.	1.4	13
2331	Identification of a novel ERF gene, TaERF8, associated with plant height and yield in wheat. <i>BMC Plant Biology</i> , 2020, 20, 263.	1.6	18
2332	Mapping QTLs underpin nutrition components in aromatic rice germplasm. <i>PLoS ONE</i> , 2020, 15, e0234395.	1.1	13
2333	African and Asian origin pearl millet populations: Genetic diversity pattern and its association with yield heterosis. <i>Crop Science</i> , 2020, 60, 3035-3048.	0.8	11
2334	Genetic diversity analysis for narrow-leafed lupin (<i>Lupinus angustifolius</i> L.) by SSR markers. <i>Molecular Biology Reports</i> , 2020, 47, 5215-5224.	1.0	5
2335	Genome-Wide Association Mapping of Adult-Plant Resistance to Stripe Rust in Common Wheat (<i>Triticum aestivum</i>). <i>Plant Disease</i> , 2020, 104, 2174-2180.	0.7	6
2336	Estimation of genetic diversity and population structure in <i>Tinospora cordifolia</i> using SSR markers. <i>3 Biotech</i> , 2020, 10, 310.	1.1	8
2337	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
2338	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.	1.7	8
2339	Genetic polymorphisms of 20 autosomal STR loci in the Han population of Zhangzhou City, Southeastern China. <i>Legal Medicine</i> , 2020, 46, 101726.	0.6	3
2340	Genetic diversity of released Malaysian rice varieties based on single nucleotide polymorphism markers. <i>Czech Journal of Genetics and Plant Breeding</i> , 2020, 56, 62-70.	0.4	6
2341	Genome survey of Chinese fir (<i>Cunninghamia lanceolata</i>): Identification of genomic SSRs and demonstration of their utility in genetic diversity analysis. <i>Scientific Reports</i> , 2020, 10, 4698.	1.6	19
2342	Microsatellite Markers Analysis for the Genetic Characterization and Relationships among Some of Iranian Local Grapevine Accessions (<i>Vitis Vinifera</i> L.). <i>International Journal of Fruit Science</i> , 2020, 20, S387-S404.	1.2	4
2343	Polymorphism of VRTN Gene g.20311_20312ins291 Was Associated with the Number of Ribs, Carcass Diagonal Length and Cannon Bone Circumference in Suhuai Pigs. <i>Animals</i> , 2020, 10, 484.	1.0	10
2344	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.	1.6	4
2345	Genetic relatedness among Ethiopian <i>Oryza longistaminata</i> populations and other AA genome <i>Oryza</i> species. <i>Plant Growth Regulation</i> , 2020, 91, 175-183.	1.8	4

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2346	Evaluation of Whole-Genome Sequence, Genetic Diversity, and Agronomic Traits of Basmati Rice (<i>Oryza</i>) Tj ETQq0 0.0 rgBT /Oyerlock 10	1.1	14
2347	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.	0.8	11
2348	Morphological characterization and analysis of genetic diversity and population structure in Citrus <i>Ä— jambhiri</i> Lush. using SSR markers. <i>Genetic Resources and Crop Evolution</i> , 2020, 67, 1259-1275.	0.8	21
2349	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.	0.4	12
2350	Virulence of Leaf Rust Physiological Races in Iran From 2010 to 2017. <i>Plant Disease</i> , 2020, 104, 363-372.	0.7	14
2351	Identification of Stripe Rust Resistance Loci in U.S. Spring Wheat Cultivars and Breeding Lines Using Genome-Wide Association Mapping and <i>Yr<i></i> Gene Markers. <i>Plant Disease</i> , 2020, 104, 2181-2192.	0.7	34
2352	Identification of Genic SSRs Provide a Perspective for Studying Environmental Adaptation in the Endemic Shrub <i>Tetraena mongolica</i> . <i>Genes</i> , 2020, 11, 322.	1.0	14
2353	Molecular Analysis of the Official Algerian Olive Collection Highlighted a Hotspot of Biodiversity in the Central Mediterranean Basin. <i>Genes</i> , 2020, 11, 303.	1.0	14
2354	Understanding the genetic relationships between Indonesian bambara groundnut landraces and investigating their origins. <i>Genome</i> , 2020, 63, 319-327.	0.9	10
2355	Diversity in sea buckthorn (<i>Hippophae rhamnoides</i> L.) accessions with different origins based on morphological characteristics, oil traits, and microsatellite markers. <i>PLoS ONE</i> , 2020, 15, e0230356.	1.1	17
2356	Development and Characterization of Simple Sequence Repeat Markers for, and Genetic Diversity Analysis of <i>Liquidambar formosana</i> . <i>Forests</i> , 2020, 11, 203.	0.9	18
2357	Phylogeographic diversity and population structure of <i>Carica papaya</i> L. revealed through nuclear microsatellites. <i>Revista Brasileira De Botanica</i> , 2020, 43, 147-154.	0.5	7
2358	Genome-wide association analysis of stem water-soluble carbohydrate content in bread wheat. <i>Theoretical and Applied Genetics</i> , 2020, 133, 2897-2914.	1.8	20
2359	Transcriptome profiling, simple sequence repeat markers development and genetic diversity analysis of potential industrial crops <i>Capsicum chinense</i> and <i>C. frutescens</i> of Northeast India. <i>Industrial Crops and Products</i> , 2020, 154, 112687.	2.5	13
2360	Genome-wide discovery of microsatellite markers and, population genetic diversity inferences revealed high anthropogenic pressure on endemic populations of <i>Trillium govanianum</i> . <i>Industrial Crops and Products</i> , 2020, 154, 112698.	2.5	12
2361	Diversity Under Threat: Connecting Genetic Diversity and Threat Mapping to Set Conservation Priorities for <i>Juglans regia</i> L. Populations in Central Asia. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	22
2362	Phenotypic Variability and Genetic Diversity in a <i>Pinus koraiensis</i> Clonal Trial in Northeastern China. <i>Genes</i> , 2020, 11, 673.	1.0	12
2363	Genetic diversity among wild pomegranate (<i>Punica granatum</i>) in Azad Jammu and Kashmir region of Pakistan. <i>Electronic Journal of Biotechnology</i> , 2020, 46, 50-54.	1.2	10

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2364	Development and application of indica-japonica SNP assays using the Fluidigm platform for rice genetic analysis and molecular breeding. <i>Molecular Breeding</i> , 2020, 40, 1.	1.0	22
2365	RNA-Seq analysis and development of SSR and KASP markers in lentil (<i>Lens culinaris</i> Medikus subsp.) Tj ETQq1 1 0.784314 rgBT /Over	2.3	15
2366	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.	0.5	4
2367	Molecular genetic analysis of spring wheat core collection using genetic diversity, population structure, and linkage disequilibrium. <i>BMC Genomics</i> , 2020, 21, 434.	1.2	44
2368	Unveiling the genetic basis of Sclerotinia head rot resistance in sunflower. <i>BMC Plant Biology</i> , 2020, 20, 322.	1.6	6
2369	Construction of DNA fingerprint for chili pepper varieties using SNAP markers. <i>IOP Conference Series: Earth and Environmental Science</i> , 2020, 482, 012038.	0.2	1
2370	Cross-amplification of microsatellite markers across agarwood-producing species of the Aquilarieae tribe (Thymelaeaceae). <i>3 Biotech</i> , 2020, 10, 103.	1.1	5
2371	SSR based association mapping analysis for fatty acid content in coconut flesh and exploration of the elite alleles in <i>Cocos nucifera</i> L. <i>Current Plant Biology</i> , 2020, 21, 100141.	2.3	11
2372	Morpho-molecular screening of wheat genotypes for heat tolerance. <i>African Journal of Biotechnology</i> , 2020, 19, 71-83.	0.3	7
2373	Genetic Diversity and Intraspecific Relationships of <i>Trifolium fragiferum</i> L. in Iran. <i>Iranian Journal of Science and Technology, Transaction A: Science</i> , 2020, 44, 345-354.	0.7	5
2374	Genetic diversity and population structure analysis of Ghanaian and exotic cassava accessions using simple sequence repeat (SSR) markers. <i>Heliyon</i> , 2020, 6, e03154.	1.4	22
2375	Population Structure and Aggressiveness of <i>Sclerotinia sclerotiorum</i> From Rapeseed (<i>Brassica napus</i>) in Chongqing City. <i>Plant Disease</i> , 2020, 104, 1201-1206.	0.7	11
2376	Genomic Prediction for Grain Yield and Yield-Related Traits in Chinese Winter Wheat. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1342.	1.8	27
2377	Genome wide identification, characterization and validation of novel miRNA-based SSR markers in pomegranate (<i>Punica granatum</i> L.). <i>Physiology and Molecular Biology of Plants</i> , 2020, 26, 683-696.	1.4	28
2378	Genome-wide development of simple sequence repeats database for flax (<i>Linum usitatissimum</i> L.) and its use for genetic diversity assessment. <i>Genetic Resources and Crop Evolution</i> , 2020, 67, 865-874.	0.8	9
2379	Assessment of Genetic Diversity Based on Phenotypic Traits and Microsatellite Markers in <i>Brassica napus</i> L. Landrace in the Kanto Region, Japan (Norabona). <i>Horticulture Journal</i> , 2020, 89, 12-21.	0.3	1
2380	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
2381	Genetic diversity and population structure analysis based on the high density SNP markers in Ethiopian durum wheat (<i>Triticum turgidum</i> ssp. durum). <i>BMC Genetics</i> , 2020, 21, 18.	2.7	52

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2382	Identification of a new set of drought-related miRNA-SSR markers and association analysis under drought stress in rice (<i>Oryza sativa</i> L.). <i>Plant Gene</i> , 2020, 21, 100220.	1.4	19
2383	Analysis of genetic divergence and population structure through microsatellite markers in normal and quality protein maize genotypes from NW Himalayan region of India. <i>Vegetos</i> , 2020, 33, 194-202.	0.8	2
2384	Genetic diversity and population structure of feral rapeseed (<i>Brassica napus</i> L.) in Japan. <i>PLoS ONE</i> , 2020, 15, e0227990.	1.1	25
2385	Analysis of evolutionary relationships provides new clues to the origins of weedy rice. <i>Ecology and Evolution</i> , 2020, 10, 891-900.	0.8	8
2386	Analysis of complete chloroplast genome sequence of Korean landrace <i>Cymbidium goeringii</i> . <i>3 Biotech</i> , 2020, 10, 29.	1.1	2
2387	Identification of standard type cultivars in <i>Chrysanthemum</i> (<i>Dendranthema grandiflorum</i>) using SSR markers. <i>Horticulture Environment and Biotechnology</i> , 2020, 61, 153-161.	0.7	9
2388	Genetic Diversity of Sugar Palm Populations from Cianjur and Banten revealed by Simple Sequence Repeat (SSR) Markers. <i>IOP Conference Series: Earth and Environmental Science</i> , 2020, 418, 012038.	0.2	2
2389	Maize genetic diversity in traditionally cultivated polycultures in an isolated rural community in Mexico: implications for management and sustainability. <i>Plant Ecology and Diversity</i> , 2020, 13, 15-28.	1.0	4
2390	SINE Retrotransposon variation drives Ecotypic disparity in natural populations of <i>Coilia nasus</i> . <i>Mobile DNA</i> , 2020, 11, 4.	1.3	8
2391	Linkage disequilibrium mapping for grain Fe and Zn enhancing QTLs useful for nutrient dense rice breeding. <i>BMC Plant Biology</i> , 2020, 20, 57.	1.6	74
2392	High Genetic Diversity and Low Differentiation in <i>Michelia shiluensis</i> , an Endangered Magnolia Species in South China. <i>Forests</i> , 2020, 11, 469.	0.9	15
2393	Genetic diversity and population structure of indigenous chicken in Rwanda using microsatellite markers. <i>PLoS ONE</i> , 2020, 15, e0225084.	1.1	13
2394	Reverse introduction of two- and six-rowed barley lines from the United States into Egypt. <i>Crop Science</i> , 2020, 60, 812-829.	0.8	1
2395	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.	0.8	10
2396	Genome-wide association study reveals the genetic basis of cold tolerance in wheat. <i>Molecular Breeding</i> , 2020, 40, 1.	1.0	41
2397	Predicting heterosis in grain sorghum hybrids using sequence-based genetic similarity estimates. <i>Journal of Crop Improvement</i> , 2020, 34, 600-617.	0.9	12
2398	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.	2.4	14
2399	Identifying heterotic groups and testers for hybrid development in early maturing yellow maize (<i>Zea mays</i> L.) inbred lines. <i>Journal of Crop Improvement</i> , 2020, 34, 618-630.	1.0	90

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2400	Exploring the genetic base of the soybean germplasm from Africa, America and Asia as well as mining of beneficial allele for flowering and seed weight. <i>3 Biotech</i> , 2020, 10, 195.	1.1	4
2401	CG/CA genotypes represent novel markers in the NPHS2 gene region associated with nephrotic syndrome. <i>Journal of Genetics</i> , 2020, 99, 1.	0.4	1
2402	Insights into genetic diversity and population structure of Indian carrot (<i>Daucus carota</i> L.) accessions. <i>Journal of Applied Genetics</i> , 2020, 61, 303-312.	1.0	26
2403	Analysis of forensic genetic parameters of 22 autosomal STR markers (PowerPlex® Fusion System) in a population sample from Bosnia and Herzegovina. <i>Annals of Human Biology</i> , 2020, 47, 273-283.	0.4	5
2404	Analysis of Genetic Diversity and Population Structure of Wild Strains and Cultivars Using Genomic SSR Markers in <i>Lentinula edodes</i> . <i>Mycobiology</i> , 2020, 48, 115-121.	0.6	6
2405	Screening for drought tolerance in wheat genotypes by morphological and SSR markers. <i>Journal of Crop Science and Biotechnology</i> , 2021, 24, 27-39.	0.7	27
2406	Unravelling the genetic variability and population structure of buckwheat (<i>Fagopyrum</i> spp.): a collection of north western Himalayas. <i>Nucleus (India)</i> , 2021, 64, 93-101.	0.9	8
2407	Genetic characterisation and population structure analysis of indigenous and exotic eggplant (<i>Solanum</i> spp) accessions using microsatellite markers. <i>Journal of Horticultural Science and Biotechnology</i> , 2021, 96, 73-86.	0.9	4
2408	Distribution and genetic diversity of <i>Echinochloa oryzicola</i> resistant to ALS and ACCase inhibitors in Korea. <i>International Journal of Pest Management</i> , 2021, 67, 222-231.	0.9	1
2409	Hybrid performance as related to genomic diversity and population structure in public sorghum inbred lines. <i>Crop Science</i> , 2021, 61, 357-371.	0.8	4
2410	Analysis of genetic diversity in rosemary (<i>Salvia rosmarinus</i> Schleid.) using SSR molecular marker for its management and sustainable use in Ethiopian genebank. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 279-293.	0.8	9
2411	Genetic diversity of rice germplasm (<i>Oryza sativa</i> L.) of java island, Indonesia. <i>Journal of Crop Science and Biotechnology</i> , 2021, 24, 93-101.	0.7	2
2412	Population structure and genetic diversity as revealed by SSR markers in Ethiopian mustard (<i>Brassica</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf <i>Crop Evolution</i> , 2021, 68, 321-333.	0.8	5
2413	Genetic, metabolic and antioxidant differences among three different Calabrian populations of <i>Cynara cardunculus</i> subsp. <i>cardunculus</i> . <i>Plant Biosystems</i> , 2021, 155, 598-608.	0.8	2
2414	Identification of an olive (<i>Olea europaea</i> L.) core collection with a new set of SSR markers. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 117-133.	0.8	9
2415	Genetic diversity of selected pigmented traditional rice (<i>Oryza sativa</i> L.) varieties from Mindanao, Philippines using agromorphological traits and simple sequence repeats markers. <i>Journal of Crop Science and Biotechnology</i> , 2021, 24, 259-277.	0.7	8
2416	A diagnostic marker kit for Fusarium wilt and sterility mosaic diseases resistance in pigeonpea. <i>Theoretical and Applied Genetics</i> , 2021, 134, 367-379.	1.8	10
2417	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.	0.8	9

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2418	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.	1.8	12
2419	Genetic diversity and genetic structure of <i>Acer monspessulanum</i> L. across Zagros forests of Iran using molecular markers. <i>Gene</i> , 2021, 769, 145245.	1.0	9
2420	Genetic diversity of Guatemalan climbing bean collections. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 639-656.	0.8	10
2421	Genetic diversity among commercial arabica coffee (<i>Coffea arabica</i> L.) varieties in Ethiopia using simple sequence repeat markers. <i>Journal of Crop Improvement</i> , 2021, 35, 147-168.	0.9	20
2422	Development and characterization of 101 SNP markers in jumbo flying squid, <i>Dosidicus gigas</i> . <i>Conservation Genetics Resources</i> , 2021, 13, 13-20.	0.4	5
2423	Population genetic structure and classification of cultivated and wild pea (<i>Pisum</i> sp.) based on morphological traits and SSR markers. <i>Journal of Systematics and Evolution</i> , 2021, , .	1.6	3
2424	Genetic and Agro-morphological diversity in global barley (<i>Hordeum vulgare</i> L.) collection at ICARDA. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 1315-1330.	0.8	13
2425	Evaluation of dark jute SSR markers and morphological traits in genetic diversity assessment of jute mallow (<i>Corchorus olitorius</i> L.) cultivars. <i>South African Journal of Botany</i> , 2021, 137, 290-297.	1.2	6
2426	Genetic diversity and identification of interspecific hybrids of <i>Anacardium</i> species using microsatellites. <i>Revista Brasileira De Botanica</i> , 2021, 44, 139-148.	0.5	4
2427	Forensic features and genetic structure of 20 autosomal STR loci in the Han population of Ningde City, Southeastern China. <i>Annals of Human Biology</i> , 2021, 48, 56-61.	0.4	1
2428	SNP marker assay and candidate gene identification for sex expression via genotyping-by-sequencing-based genome-wide associations (GWAS) analyses in Oriental melon (<i>Cucumis melo</i> L.var.makuwa). <i>Scientia Horticulturae</i> , 2021, 276, 109711.	1.7	16
2429	Mining Favorable Alleles for Rice Coleoptile Elongation Length Sensitivity to Exogenous Gibberellin Under Submergence Condition. <i>Journal of Plant Growth Regulation</i> , 2021, 40, 1422-1439.	2.8	3
2430	Genetic diversity of <i>Prunus sibirica</i> L. superior accessions based on the SSR markers developed using restriction-site associated DNA sequencing. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 615-628.	0.8	7
2431	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. <i>BMC Genomics</i> , 2021, 22, 34.	1.2	18
2432	Comparative analysis of genetic diversity of rice (<i>Oryza sativa</i> L.) varieties cultivated in different periods in China. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 1439-1451.	0.8	6
2433	SNP genotyping for fast and consistent clustering of maize inbred lines into heterotic groups. <i>Crop Breeding and Applied Biotechnology</i> , 2021, 21, .	0.1	1
2434	Genetic Purity of Cacao Criollo from Honduras Is Revealed by SSR Molecular Markers. <i>Agronomy</i> , 2021, 11, 225.	1.3	6
2435	Genetic Enhancement in Mungbean (<i>Vigna radiata</i>) as Revealed by Genome-Wide Mapped Microsatellite Markers. <i>Agricultural Research</i> , 2021, 10, 369-377.	0.9	5

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2437	Genetic characterization and association mapping in near-isogenic lines of waxy maize using seed characteristics and SSR markers. <i>Genes and Genomics</i> , 2021, 43, 79-90.	0.5	10
2438	Globally Important Wheat Diseases: Status, Challenges, Breeding and Genomic Tools to Enhance Resistance Durability. , 2021, , 59-128.		12
2439	The development of SSR markers based on RNA-sequencing and its validation between and within <i>Carex L.</i> species. <i>BMC Plant Biology</i> , 2021, 21, 17.	1.6	15
2440	Genetic characterization of Cape gooseberry (<i>Physalis peruviana L.</i>) accessions in selected counties in Kenya using SSR markers. <i>African Journal of Plant Science</i> , 2021, 15, 28-38.	0.4	1
2441	Genetic diversity and structure of 2 indigenous sheep breeds (Kotel and Teteven) in Bulgaria using microsatellite markers. <i>Biotechnology and Biotechnological Equipment</i> , 2021, 35, 576-585.	0.5	10
2442	Heterotic grouping of tropical maize inbred lines and their hybrid performance under stem borer infestation and low soil nitrogen condition in West and Central Africa. <i>Euphytica</i> , 2021, 217, 1.	0.6	7
2443	Development of 23 novel microsatellite markers of <i>Amomum tsao-ko</i> (Zingiberaceae) based on restriction-site-associated DNA sequencing. <i>Molecular Biology Reports</i> , 2021, 48, 1943-1949.	1.0	7
2444	Analysis of Genetic Diversity among <i>Brassica juncea</i> Genotypes using Morpho-physiological and SSR Markers. <i>International Journal of Current Microbiology and Applied Sciences</i> , 2021, 10, 1108-1117.	0.0	8
2445	Measurement of Genetic Mobility Using a Transposon-Based Marker System in Sorghum. <i>Methods in Molecular Biology</i> , 2021, 2250, 195-205.	0.4	0
2446	Molecular characterization of elite maize (<i>Zea mays L.</i>) inbreds using markers associated with iron and zinc transporter genes. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 1545-1556.	0.8	5
2447	Development of new cowpea (<i>Vigna unguiculata</i>) mutant genotypes, analysis of their agromorphological variation, genetic diversity and population structure. <i>Biocell</i> , 2021, 45, 345-362.	0.4	3
2448	Genome-Wide Association Study of Tan Spot Resistance in a Hexaploid Wheat Collection From Kazakhstan. <i>Frontiers in Genetics</i> , 2020, 11, 581214.	1.1	24
2449	RAD sequencing for the development of microsatellite markers for identification of Malaysian taro cultivars. <i>Biotechnology and Biotechnological Equipment</i> , 2021, 35, 1284-1290.	0.5	2
2450	Development and characterization of Simple Sequence Repeat (SSR) markers from the genomic sequence of sweet potato [<i>Ipomoea batatas L. (Lam)</i>]. <i>Biocell</i> , 2021, 45, 1095-1105.	0.4	1
2451	Structure and genetic diversity of <i>Theobroma speciosum</i> (Malvaceae) and implications for Brazilian Amazon conservation. <i>Rodriguesia</i> , 0, 72, .	0.9	0
2452	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.	0.3	0
2453	Identification of zygotic and nucellar seedling of Harumanis mango through molecular markers and morphological approach. <i>African Journal of Biotechnology</i> , 2021, 20, 92-99.	0.3	1

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2454	Functional gene assessment of bread wheat: breeding implications in Ningxia Province. <i>BMC Plant Biology</i> , 2021, 21, 103.	1.6	4
2455	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.	1.2	18
2456	Development of sub-tropically adapted diverse provitamin-A rich maize inbreds through marker-assisted pedigree selection, their characterization and utilization in hybrid breeding. <i>PLoS ONE</i> , 2021, 16, e0245497.	1.1	24
2457	Detecting Genetic Mobility Using a Transposon-Based Marker System in Gamma-Ray Irradiated Soybean Mutants. <i>Plants</i> , 2021, 10, 373.	1.6	8
2458	Genotyping variability of computationally categorized peach microsatellite markers. <i>Acta Horticulturae</i> , 2021, , 107-112.	0.1	0
2459	A worldwide maize panel revealed new genetic variation for cold tolerance. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1083-1094.	1.8	17
2460	Analyses of genetic diversity and population structure of anchote (<i>Coccinia abyssinica</i> (Lam.) Cogn.) using newly developed EST-SSR markers. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 2337-2350.	0.8	5
2461	Genetic characterization of the orphan crop tef [<i>Eragrostis tef</i> (Zucc.) Trotter] accessions using simple sequence repeat markers. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 2143-2155.	0.8	0
2462	Insight into morphological and molecular variations across Iranian spinach landraces. <i>Molecular Biology Reports</i> , 2021, 48, 1567-1578.	1.0	0
2463	Development and use of miRNA-derived SSR markers for the study of genetic diversity, population structure, and characterization of genotypes for breeding heat tolerant wheat varieties. <i>PLoS ONE</i> , 2021, 16, e0231063.	1.1	25
2464	Transcriptomic and genome-wide association study reveal long noncoding RNAs responding to nitrogen deficiency in maize. <i>BMC Plant Biology</i> , 2021, 21, 93.	1.6	18
2465	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.	0.4	7
2466	Mining favorable alleles for rice sheath blight resistance by association mapping. <i>Plant Growth Regulation</i> , 2021, 94, 61-72.	1.8	2
2467	EST-SSR marker development based on transcriptome sequencing and genetic analyses of <i>Phoebe bournei</i> (Lauraceae). <i>Molecular Biology Reports</i> , 2021, 48, 2201-2208.	1.0	9
2468	Assessment of diversity in tropical soybean (<i>Glycine max</i> (L.) Merr.) varieties and elite breeding lines using single nucleotide polymorphism markers. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2021, 19, 20-28.	0.4	5
2470	Genetic diversity and population structure of early and extra-early maturing maize germplasm adapted to sub-Saharan Africa. <i>BMC Plant Biology</i> , 2021, 21, 96.	1.6	20
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2476	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.	1.3	20
2477	Developing a new genic SSR primer database in faba bean (<i>Vicia faba</i> L.). <i>Journal of Applied Genetics</i> , 2021, 62, 373-387.	1.0	2
2478	Characterization of Some Registered Chickpea (<i>Cicer arietinum</i> L.) Varieties with Simple Sequence Reiterations (SSRs) Markers. <i>Journal of the Institute of Science and Technology</i> , 0, , 732-742.	0.3	0
2479	Molecular Characterization of Some Soybean (<i>Glycine max</i> L.) Varieties. <i>Yuzuncu Yil University Journal of Agricultural Sciences</i> , 2021, 31, 11-18.	0.1	3
2480	Genetic diversity assessment and population structure analysis of pomegranate cultivars from different countries and Himalayan wild accessions. <i>Journal of Horticultural Science and Biotechnology</i> , 2021, 96, 614-623.	0.9	10
2481	Species delimitation with distinct methods based on molecular data to elucidate species boundaries in the <i>Cycas taiwaniana</i> complex (Cycadaceae). <i>Taxon</i> , 2021, 70, 477-491.	0.4	8
2482	Genetic relationship, population structure analysis and pheno-molecular characterization of rice (<i>Oryza sativa</i> L.) cultivars for bacterial leaf blight resistance and submergence tolerance using trait specific STS markers. <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 543-562.	1.4	2
2483	Genetic Diversity and Population Structure of Soybean Lines Adapted to Sub-Saharan Africa Using Single Nucleotide Polymorphism (SNP) Markers. <i>Agronomy</i> , 2021, 11, 604.	1.3	17
2484	Genetic Diversity of Purple Passion Fruit, <i>Passiflora edulis</i> f. <i>edulis</i> , Based on Single-Nucleotide Polymorphism Markers Discovered through Genotyping by Sequencing. <i>Diversity</i> , 2021, 13, 144.	0.7	3
2485	Population genetic structure and association mapping for iron toxicity tolerance in rice. <i>PLoS ONE</i> , 2021, 16, e0246232.	1.1	20
2486	Single nucleotide polymorphisms of leptin gene in five Ethiopian indigenous cattle breeds and the Korean Hanwoo breed. <i>Tropical Animal Health and Production</i> , 2021, 53, 202.	0.5	2
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2490	Morphological and microsatellite characterization of improved Lablab <i>purpureus</i> genotypes. <i>Journal of Plant Breeding and Crop Science</i> , 2021, 13, 23-34.	0.8	7
2491	Genetic Diversity and Population Assessment of <i>Musa</i> L. (Musaceae) Employing CDDP Markers. <i>Plant Molecular Biology Reporter</i> , 2021, 39, 801-820.	1.0	15
2492	Genetic characterization of novel polymorphic microsatellite markers for <i>Epilobium nankotaizanense</i> (Onagraceae), an endemic and threatened herb in Taiwan. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2021, 19, 275-278.	0.4	0

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2499	Genetic Diversity and Relationships of Terebinth (<i>Pistacia terebinthus</i> L.) Genotypes Growing Wild in Turkey. Agronomy, 2021, 11, 671.	1.3	5
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2507	Deconstructing molecular phylogenetic relationship among cultivated and wild <i>Brassica</i> species. Genetic Resources and Crop Evolution, 2021, 68, 2281-2288.	0.8	1
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2509	Genetic diversity and kinship relationships in one of the largest South American fur seal (<i>Arctocephalus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.8	3
2510	Genetic Diversity and Population Differentiation of <i>Pinus koraiensis</i> in China. Horticulturae, 2021, 7, 104.	1.2	10
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2518	Microsatellite and morphological characterization of three Rostrato di Val Chiavenna (Sondrio, Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 50	0.8	6
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2520	Morphophysiological and molecular characterization of millet (<i>Panicum miliaceum</i> L.) varieties for crop improvement in Western Europe. <i>CABI Agriculture and Bioscience</i> , 2021, 2, .	1.1	2
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2524	Genetic variation and association mapping in the F2 population of the Perilla crop (<i>Perilla frutescens</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 50	0.6	11
2525	Genetic Variability of Nile Tilapia Strains as Determined by Microsatellite DNA Markers. <i>North American Journal of Aquaculture</i> , 2021, 83, 177-183.	0.7	1
2526	Genetic differentiation and restricted gene flow in rice landraces from Yunnan, China: effects of isolation-by-distance and isolation-by-environment. <i>Rice</i> , 2021, 14, 54.	1.7	8
2527	The origin of the A/G single nucleotide polymorphism of <i>starch synthase IIa</i> in rice and its relation to gelatinization temperature. <i>Cereal Chemistry</i> , 2022, 99, 275-285.	1.1	3
2528	GENETIC ANALYSIS OF 38 DOUBLE-FLOWERED AMARYLLIS (<i>Hippeastrum hybridum</i>) CULTIVARS BASED ON SRAP MARKERS. <i>Acta Scientiarum Polonorum, Hortorum Cultus</i> , 2021, 20, 15-25.	0.3	1
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2534	Variability for Seed-based Economic Traits and Genetic Diversity Analysis in <i>Mucuna pruriens</i> Population of Northeast India. <i>Agricultural Research</i> , 2022, 11, 1-11.	0.9	4
2535	Genetic Diversity among Some Walnut (<i>Juglans regia</i> L.) Genotypes by SSR Markers. <i>Sustainability</i> , 2021, 13, 6830.	1.6	23
2536	Association analysis and evaluation of genetic diversity in wheat genotypes using SSR markers. <i>Biologia Futura</i> , 2021, 72, 441-452.	0.6	7
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2539	Development of 50 InDel-based barcode system for genetic identification of tartary buckwheat resources. <i>PLoS ONE</i> , 2021, 16, e0250786.	1.1	4
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2543	Development of GBTS and KASP Panels for Genetic Diversity, Population Structure, and Fingerprinting of a Large Collection of Broccoli (<i>Brassica oleracea</i> L. var. <i>italica</i>) in China. <i>Frontiers in Plant Science</i> , 2021, 12, 655254.	1.7	20
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2547	Allelic variation in <i>sugary1</i> gene affecting kernel sweetness among diverse-mutant and -wild-type maize inbreds. <i>Molecular Genetics and Genomics</i> , 2021, 296, 1085-1102.	1.0	5
2548	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.	1.0	10
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2553	Genetic relationship and parentages of historical peaches revealed by microsatellite markers. <i>Tree Genetics and Genomes</i> , 2021, 17, 1.	0.6	3
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2557	Genetic diversity assessment and gene expression analysis of prolonged shelf-life genes in Mangalore melon (<i>Cucumis melo</i> ssp. <i>agrestis</i> var. <i>acidulus</i>). <i>Euphytica</i> , 2021, 217, 1.	0.6	1
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2565	Molecular characterization of China aster (<i>Callistephus chinensis</i> (L.) Nees) genotypes using SSR markers. <i>Israel Journal of Plant Sciences</i> , 2021, 68, 287-296.	0.3	2
2566	Chloroplastic and nuclear diversity of endemic <i>Prunus armeniaca</i> L. species in the oasis agroecosystems. <i>Genetica</i> , 2021, 149, 239-251.	0.5	2
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2573	Diversity, population structure, and linkage disequilibrium among cowpea accessions. <i>Plant Genome</i> , 2021, 14, e20113.	1.6	11
2574	Evaluation of Genetic Diversity and Population Structure Analysis among Germplasm of <i>Agaricus bisporus</i> by SSR Markers. <i>Mycobiology</i> , 2021, 49, 376-384.	0.6	2
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2576	Genetic Diversity of a Natural Population of <i>Akebia trifoliata</i> (Thunb.) Koidz and Extraction of a Core Collection Using Simple Sequence Repeat Markers. <i>Frontiers in Genetics</i> , 2021, 12, 716498.	1.1	9
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2580	Association analysis for agronomic traits in wheat under terminal heat stress. <i>Saudi Journal of Biological Sciences</i> , 2021, 28, 7404-7415.	1.8	6
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2582	Development of polymorphic simple sequence repeat markers in <i>Juglans regia</i> L.. <i>Acta Horticulturae</i> , 2021, , 45-50.	0.1	0
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2588	Genome-Wide Analysis and Polymorphism Evaluation of Microsatellites Involved in Photoperiodic Flowering-time Genes in Kenaf (<i>Hibiscus Cannabinus</i> L.). <i>Journal of Natural Fibers</i> , 0, , 1-13.	1.7	0

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2590	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.	1.0	16
2591	Association analysis, genetic diversity and population structure of barley (<i>Hordeum vulgare</i> L.) under heat stress conditions using SSR and ISSR markers linked to primary and secondary metabolites. <i>Molecular Biology Reports</i> , 2021, 48, 6673-6694.	1.0	6
2592	Virulence and SSR Diversity of Brown Planthopper (<i>Nilaparvata lugens</i>) Adapted on Differential Rice Host Varieties. <i>HAYATI Journal of Biosciences</i> , 2021, 28, 293-303.	0.1	1
2593	Transcriptomic analysis of salt tolerance-associated genes and diversity analysis using indel markers in yardlong bean (<i>Vigna unguiculata</i> ssp. <i>sesquipedialis</i>). <i>BMC Genomic Data</i> , 2021, 22, 34.	0.7	5
2594	Haplotype and diversity analysis of indigenous rice for salinity tolerance in early-stage seedling using simple sequence repeat markers. <i>Biotechnology Reports (Amsterdam, Netherlands)</i> , 2021, 31, e00666.	2.1	3
2595	Utilization of Whole Genome Re-Sequencing for Large-InDel Markers Development in Malting Barley. <i>Han'guk Yukchong Hakhoe Chi</i> , 2021, 53, 266-276.	0.2	0
2597	Development of Genome-wide SSR Markers for Physical Map Construction with PCR-based Polymorphic SSRs in Jute (<i>Corchorus</i> Spp.). <i>Tropical Plant Biology</i> , 0, , 1.	1.0	2
2598	Genetic Diversity and Primary Core Collection Construction of Turnip (<i>Brassica rapa</i> L. ssp. <i>rapifera</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.3	3
2599	Morpho-molecular characterization and genetic diversity analysis across wild apple (<i>Malus baccata</i>) accessions using simple sequence repeat markers. <i>South African Journal of Botany</i> , 2022, 145, 378-385.	1.2	7
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2602	Genetic Diversity Analysis and Molecular Screening for Salinity Tolerance in Wheat Germplasm. <i>Plant Breeding and Biotechnology</i> , 2021, 9, 185-198.	0.3	4
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2606	Novel Expressed Sequence Tag-Derived and Other Genomic Simple Sequence Repeat Markers Revealed Genetic Diversity in Ethiopian Finger Millet Landrace Populations and Cultivars. <i>Frontiers in Plant Science</i> , 2021, 12, 735610.	1.7	4
2607	Development of Genome-Wide Functional Markers Using Draft Genome Assembly of Guava (<i>Psidium</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 708332.	1.7	8

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2608	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.	0.4	3
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2612	Revealing the coexistence of differentiation and communication in an endemic hare, <i>Lepus yarkandensis</i> (Mammalia, Leporidae) using specific-length amplified fragment sequencing. <i>Frontiers in Zoology</i> , 2021, 18, 50.	0.9	2
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2620	Genetic diversity in spring faba bean (<i>Vicia faba</i> L.) genotypes as revealed by high-throughput KASP SNP markers. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 1971-1986.	0.8	9
2621	Identifying SSR markers associated with seed characteristics in <i>Perilla</i> (<i>Perilla frutescens</i> L.). <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 93-105.	1.4	13
2622	Cross-transferability-based identification and validation of simple sequence repeat (SSR) markers in oaks of western Himalayas. <i>Silvae Genetica</i> , 2021, 70, 108-116.	0.4	3
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2625	Characterization of EST-SSR markers in <i>Curcuma kwangsiensis</i> S. K. Lee & C. F. Liang based on RNA sequencing and its application for phylogenetic relationship analysis and core collection construction. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 1503-1516.	0.8	6

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2802	ISAG-recommended Microsatellite Marker Analysis Among Five Korean Native Chicken Lines. <i>Journal of Animal Science and Technology</i> , 2012, 54, 401-409.	0.8	9
2803	The <i>DCAT1</i> gene <i>K232A</i> mutation is associated with milk fat content, milk yield and milk somatic cell count in cattle (Short) <i>Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf 50</i>	0.0	18
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2808	Assessment of Genetic Diversity and Population Structure in a Selected Germplasm Collection of 292 Jute Genotypes by Microsatellite (SSR) Markers. <i>Molecular Plant Breeding</i> , 0, , .	0.0	8
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2938	Genetic Markers in Tobacco, Usage for Map Development, Diversity Studies, and Quantitative Trait Loci Analysis. Compendium of Plant Genomes, 2020, , 43-49.	0.3	0
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2941	Genetic Variation of Common Millet (<i>Panicum miliaceum</i> L.) Collected from East Asia Based on Simple Sequence Repeats (SSRs). Plant Breeding and Biotechnology, 2020, 8, 186-195.	0.3	0
2942	Comparison of SRAP markers and pedigree data in assessing genetic relatedness among chrysanthemum cultivars. Acta Horticulturae, 2020, , 71-82.	0.1	0
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2947	Genetic diversity and population structure analysis for morphological traits in upland cotton (<i>Gossypium hirsutum</i> L.). Journal of Applied Genetics, 2022, 63, 87-101.	1.0	6
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2951	Genetic Characteristics of Brook Trout <i>Salvelinus fontinalis</i> (Mitchill, 1848) Broodstocks from Hatcheries in Bosnia and Herzegovina. Ribarstvo, Croatian Journal of Fisheries, 2020, 78, 183-194.	0.2	1
2952	Development and technical application of SSR-based individual identification system for <i>Chamaecyparis taiwanensis</i> Against illegal logging convictions. Scientific Reports, 2020, 10, 22095.	1.6	6
2953	Microsatellite marker-based genetic diversity of tropical-adapted <i>shrunken-2</i> maize inbred lines and its relationship with normal endosperm inbred lines of known heterotic classification. Plant Genetic Resources: Characterisation and Utilisation, 2020, 18, 454-461.	0.4	2

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2975	Genetic Variation of Native Germplasms Collected from South Korea Using Simple Sequence Repeat (SSR) Markers and Morphological Characteristics. <i>Plants</i> , 2021, 10, .	1.6	0

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2977	Microsatellite-based association mapping for agronomic traits in mungbean (<i>Vigna radiata</i> L. Wilczek). <i>Journal of Genetics</i> , 2021, 100, 1.	0.4	6
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2981	Genetic variability and population structure of Ethiopian chickpea (<i>Cicer arietinum</i> L.) germplasm. <i>PLoS ONE</i> , 2021, 16, e0260651.	1.1	2
2982	Population structure, gene flow and genetic diversity analyses based on agro-morphological traits and microsatellite markers within cultivated and wild germplasms of okra [<i>Abelmoschus esculentus</i> (L.) Moench.]. <i>Genetic Resources and Crop Evolution</i> , 2022, 69, 771-791.	0.8	5
2983	Predictive genotype-phenotype relations using genetic diversity in African yam bean (<i>Sphenostylis</i> Tj ETQq1 1 0.784314 rgBT ₃ /Overlap 10 TFS	1.6	3
2984	Comparison of selection methods for the establishment of a core collection using SSR markers for hazelnut (<i>Corylus avellana</i> L.) accessions from European germplasm repositories. <i>Tree Genetics and Genomes</i> , 2021, 17, 1.	0.6	11
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2988	Estimation of genetic diversity and its exploitation in plant breeding. <i>Botanical Review, The</i> , 2022, 88, 413-435.	1.7	6
2989	Structure of genetic diversity and genome-wide association studies of bean fly (<i>Ophiomyia</i>) Tj ETQq1 1 0.784314 rgBT ₃ /Overlap 10 TFS	0.6	3
2990	Genetic Variability of <i>Klebsiella Variicola</i> by RAPD-PCR Technique and Bioremoval of Pb ²⁺ and Cd ²⁺ from Simulated Contaminated Soils. <i>Soil and Sediment Contamination</i> , 2022, 31, 770-784.	1.1	1
2991	Genome-wide association analysis of chickpea germplasms differing for salinity tolerance based on DArTseq markers. <i>PLoS ONE</i> , 2021, 16, e0260709.	1.1	19
2992	Genome structure and diversity among <i>Cynanchum wilfordii</i> accessions. <i>BMC Plant Biology</i> , 2022, 22, 4.	1.6	2
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2995	Phenotypic and Molecular Assessment for Genetic Diversity of Egyptian Wheat Varieties. <i>Egyptian Journal of Agronomy</i> , 2020, .	0.3	0
2996	Diallel Analysis of Different Rice Genotypes under Water Deficiency Conditions and Assessing Genetic Diversity Using SSR Markers. <i>Journal of Plant Production</i> , 2020, 11, 1319-1332.	0.0	2
2997	Genetic diversity among tropical maize inbred lines as revealed by SSR markers. <i>Australian Journal of Crop Science</i> , 2020, , 2010-2019.	0.1	0
2998	Genetic Variation of Native <i>Perilla</i> Germplasms Collected from South Korea Using Simple Sequence Repeat (SSR) Markers and Morphological Characteristics. <i>Plants</i> , 2021, 10, 1764.	1.6	4
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3002	Development and application of novel InDel markers in flax (<i>Linum usitatissimum</i> L.) through whole-genome re-sequencing. <i>Genetic Resources and Crop Evolution</i> , 2022, 69, 1471-1483.	0.8	4
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3005	The Build-Up of Population Genetic Divergence along the Speciation Continuum during a Recent Adaptive Radiation of Rhagoletis Flies. <i>Genes</i> , 2022, 13, 275.	1.0	4
3006	A chromosome-scale reference genome assembly of yellow mangrove (<i>Bruguiera parviflora</i>) reveals a whole genome duplication event associated with the Rhizophoraceae lineage. <i>Molecular Ecology Resources</i> , 2022, 22, 1939-1953.	2.2	13
3007	Genetic diversity and population structure analysis to study the evolution of herbicide resistance in <i>Echinochloa colona</i> ecotypes in Australia. <i>Acta Physiologiae Plantarum</i> , 2022, 44, 1.	1.0	3
3008	Genetic diversity and population structure of <i>Curcuma alismatifolia</i> Gagnep. accessions revealed by SSR markers. <i>Genetic Resources and Crop Evolution</i> , 2022, 69, 1661-1669.	0.8	2
3009	Genetic relationship of pigmented rice (<i>Oryza sativa</i> L.) collected from Eastern Indonesia based on morpho-agronomical traits and SSR markers. <i>AIP Conference Proceedings</i> , 2022, , .	0.3	2
3010	Classification and Association Analysis of <i>Gerbera</i> (<i>Gerbera hybrida</i>) Flower Color Traits. <i>Frontiers in Plant Science</i> , 2021, 12, 779288.	1.7	10
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3013	Genome-wide development of lncRNA-derived-SSR markers for Dongxiang wild rice (<i>Oryza</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 1007	0.4	2
3014	Developing and deploying an efficient genotyping workflow for accelerating maize improvement in developing countries. <i>Gates Open Research</i> , 0, 6, 3.	2.0	0
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3016	Molecular diversity comparison in local rice accessions originated from Kalimantan and other islands of Indonesia. <i>AIP Conference Proceedings</i> , 2022, , .	0.3	0
3017	Insights into the genetic diversity of an underutilized Indian legume, <i>Vigna stipulacea</i> (Lam.) Kuntz., using morphological traits and microsatellite markers. <i>PLoS ONE</i> , 2022, 17, e0262634.	1.1	6
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3019	Genome-wide SSR markers in bottle gourd: development, characterization, utilization in assessment of genetic diversity of National Genebank of India and synteny with other related cucurbits. <i>Journal of Applied Genetics</i> , 2022, 63, 237-263.	1.0	5
3020	Genetic diversity of Sesame (<i>Sesamum indicum</i> L) using high throughput diversity array technology. <i>Journal of Crop Science and Biotechnology</i> , 2022, 25, 359-371.	0.7	4
3021	Molecular Characterization of Almond Cultivars Using Simple Sequence Repeat Markers. <i>Erwerbs-Obstbau</i> , 0, , 1.	0.5	2
3022	Genetic variation among the salinity tolerant breeding lines identified from two multi-parent advanced generation introgression line populations in rice (<i>Oryza sativa</i>). <i>Journal of Agronomy and Crop Science</i> , 2022, 208, 295-313.	1.7	4
3023	Analysis of parental genetic diversity and its impact on grain yield and quality of japonica hybrid rice in northern China. <i>Crop Journal</i> , 2022, 10, 904-910.	2.3	3
3024	Population Genetic Structure Analysis Reveals Significant Genetic Differentiation of the Endemic Species <i>Camellia chekiangoleosa</i> Hu. with a Narrow Geographic Range. <i>Forests</i> , 2022, 13, 234.	0.9	7
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3028	Identifying Traits Associated With Terminal Drought Tolerance in Sesame (<i>Sesamum indicum</i> L.) Genotypes. <i>Frontiers in Plant Science</i> , 2021, 12, 739896.	1.7	14
3029	Construction of a core collection of native <i>Perilla</i> germplasm collected from South Korea based on SSR markers and morphological characteristics. <i>Scientific Reports</i> , 2021, 11, 23891.	1.6	11

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3031	Candidate screening of blast resistance donors for rice breeding. <i>Journal of Genetics</i> , 2019, 98, .	0.4	0
3032	Narrow gene pool can threaten the survival of <i>R. R. Fernald & Dey</i> : a highly, endemic dioecious rattan species in the Western Ghats of India. <i>Journal of Genetics</i> , 2019, 98, .	0.4	0
3033	High-throughput single nucleotide polymorphism genotyping reveals population structure and		

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3050	Unraveling the Genetic Basis of Key Agronomic Traits of Wrinkled Vining Pea (<i>Pisum sativum</i> L.) for Sustainable Production. <i>Frontiers in Plant Science</i> , 2022, 13, 844450.	1.7	6
3051	Genetic dissection of false smut resistance in rice through Genome Wide Association Mapping. <i>Journal of Phytopathology</i> , 2022, 170, 282-299.	0.5	0
3052	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.	0.7	2
3053	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.	1.2	7
3054	Population Structure Analysis and Association Mapping for Turicum Leaf Blight Resistance in Tropical Maize Using SSR Markers. <i>Genes</i> , 2022, 13, 618.	1.0	9
3055	Genetic Diversity and Population Structure Analysis in Indian Mustard Germplasm Using Phenotypic Traits and SSR Markers. <i>Plant Molecular Biology Reporter</i> , 2022, 40, 579-594.	1.0	5
3056	Genotyping-by-Sequencing Based Molecular Genetic Diversity of Pakistani Bread Wheat (<i>Triticum</i>) Tj ETQq1 1 0.784314 rgBT ₁ /Overlook	1.1	1
3057	Two Main Routes of Spore Migration Contributing to the Occurrence of Wheat Stripe Rust in the Jiangsu and Zhejiang Coastal Sporadic Epidemiological Region in 2019, Based on Phenotyping and Genotyping Analyses. <i>Plant Disease</i> , 2022, 106, 2948-2957.	0.7	6
3058	Construction of a core germplasm bank of upland cotton (<i>Gossypium hirsutum</i> L.) based on phenotype, genotype and favorable alleles. <i>Genetic Resources and Crop Evolution</i> , 2022, 69, 2399-2411.	0.8	6
3059	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.	1.0	4
3060	Molecular markers dataset to assess the genetic diversity of oriental plane trees from historical sites in Lazio (central Italy). <i>Data in Brief</i> , 2022, 42, 108100.	0.5	1
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3062	Genetic diversity analysis of sorghum [<i>Sorghum bicolor</i> (L.) Moench] races in Ethiopia using simple sequence repeats (SSR) markers. <i>African Journal of Biotechnology</i> , 2021, 20, 431-439.	0.3	4
3063	Genome-Wide Analysis of Simple Sequence Repeats in Cabbage (<i>Brassica oleracea</i> L.). <i>Frontiers in Plant Science</i> , 2021, 12, 726084.	1.7	6
3064	Development of Whole Genome Sequence-based Novel SSR Markers in <i>Astragalus membranaceus</i> (Fisch.). <i>Korean Journal of Medicinal Crop Science</i> , 2021, 29, 418-424.	0.1	1
3065	Genetic Diversity, QTL Mapping, and Marker-Assisted Selection Technology in Cotton (<i>Gossypium</i> spp.). <i>Frontiers in Plant Science</i> , 2021, 12, 779386.	1.7	29
3066	Agro-morphological and molecular diversity in different maturity groups of Indian cauliflower (<i>Brassica oleracea</i> var. <i>botrytis</i> L.). <i>PLoS ONE</i> , 2021, 16, e0260246.	1.1	7

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3068	Genetic diversity and population structure analysis of rice false smut pathogen in North India using molecular markers. <i>Journal of Phytopathology</i> , 2022, 170, 124-140.	0.5	0
3069	Identification of Candidate Genes and Genomic Regions Associated with Adult Plant Resistance to Stripe Rust in Spring Wheat. <i>Agronomy</i> , 2021, 11, 2585.	1.3	11
3070	Genetic Diversity, Structure, and Selective Sweeps in <i>Spinacia turkestanica</i> Associated With the Domestication of Cultivated Spinach. <i>Frontiers in Genetics</i> , 2021, 12, 740437.	1.1	4
3071	Morphological and Genetic Characterization of Local Maize Accessions from Emilia Romagna Region, Italy. <i>Sustainability</i> , 2022, 14, 91.	1.6	3
3072	Genetic Diversity of Turkish Cultivated Emmer (<i>Triticum dicoccum</i> Schrank) Revealed by Microsatellite Markers. <i>Journal of the Institute of Science and Technology</i> , 0, , 3119-3127.	0.3	0
3073	Phenotypic and Molecular Characterization of Rice Genotypesâ€™ Tolerance to Cold Stress at the Seedling Stage. <i>Sustainability</i> , 2022, 14, 4871.	1.6	3
3074	Evaluation of genetic diversity in rice (<i>Oryza sativa</i> L. ssp. <i>Indica</i>) accessions using SSR marker. <i>Vegetos</i> , 2022, 35, 961-968.	0.8	6
3075	De novo transcriptome assembly and development of EST-SSR markers for <i>Pterocarpus santalinus</i> L. f. (Red sanders), a threatened and endemic tree of India. <i>Genetic Resources and Crop Evolution</i> , 2022, 69, 2469-2484.	0.8	3
3265	Populations of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> in Winter Spore Production Regions Spread from Southwestern Overwintering Areas in China. <i>Plant Disease</i> , 2022, 106, 2856-2865.	0.7	4
3267	Molecular Characterization of Sixty Local Mango Germplasm of Chapainawabganj. <i>Agricultural Sciences</i> , 2022, 13, 580-590.	0.2	1
3269	Morphological and molecular characterization of some pumpkin (<i>Cucurbita pepo</i> L.) genotypes collected from Erzincan province of Turkey. <i>Scientific Reports</i> , 2022, 12, 6814.	1.6	2
3270	Development of Novel Polymorphic Microsatellite Markers and Their Application for Closely Related <i>Camellia</i> (Theaceae) Species. <i>Russian Journal of Genetics</i> , 2022, 58, 404-412.	0.2	1
3271	Genetic stability of cryopreserved ornamental <i>Lilium</i> germplasm. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 0, , 1-3.	0.4	1
3272	Genetic Diversity Study on Geographical Populations of the Multipurpose Species <i>Elsholtzia stauntonii</i> Using Transferable Microsatellite Markers. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	2
3273	Development of novel polymorphic microsatellite markers for <i>Picea brachytyla</i> . <i>Molecular Biology Reports</i> , 2022, , .	1.0	1
3274	Genetic Structure and Triazole Antifungal Susceptibilities of <i>Alternaria alternata</i> from Greenhouses in Kunming, China. <i>Microbiology Spectrum</i> , 2022, 10, e0038222.	1.2	2
3275	Allelic Variation in <i>Zmfatb</i> Gene Defines Variability for Fatty Acids Composition Among Diverse Maize Genotypes. <i>Frontiers in Nutrition</i> , 2022, 9, .	1.6	8

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3276	Delineation of Bangladeshi coastal rice germplasm based on qualitative phenotypic traits. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 0, , 1-7.	0.4	0
3277	Genetic Diversity and Streptomycin Sensitivity in <i>Xanthomonas axonopodis</i> pv. <i>punicae</i> Causing Oily Spot Disease in Pomegranates. <i>Horticulturae</i> , 2022, 8, 441.	1.2	3
3278	Empirical Evidence on Enhanced Mutation Rates of 19 RM-YSTRs for Differentiating Paternal Lineages. <i>Genes</i> , 2022, 13, 946.	1.0	0
3279	Development and Application of Fruit Color-Related Expressed Sequence Tag-Simple Sequence Repeat Markers in <i>Abelmoschus esculentus</i> on the Basis of Transcriptome Sequencing. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	2
3280	Genetic Diversity Analysis of <i>Sapindus</i> in China and Extraction of a Core Germplasm Collection Using EST-SSR Markers. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	4
3281	Rice landraces from haor areas of Bangladesh possess greater genetic diversity as revealed by morpho-molecular approaches along with grain quality traits. <i>Cogent Food and Agriculture</i> , 2022, 8, .	0.6	4
3282	Genome-wide identification and development of InDel markers in tobacco (<i>Nicotiana tabacum</i> L.) using RAD-seq. <i>Physiology and Molecular Biology of Plants</i> , 2022, 28, 1077-1089.	1.4	4
3283	Genetic diversity of Ethiopian potato (<i>Plectranthus edulis</i> (Vatke) Agnew) genotypes using simple sequence repeat markers. <i>Journal of Crop Improvement</i> , 0, , 1-26.	0.9	0
3284	Detection of Genomic Regions Controlling the Antioxidant Enzymes, Phenolic Content, and Antioxidant Activities in Rice Grain through Association Mapping. <i>Plants</i> , 2022, 11, 1463.	1.6	8
3286	Chromosome-level genome assembly of Indian mangrove (<i>Ceriops tagal</i>) revealed a genome-wide duplication event predating the divergence of Rhizophoraceae mangrove species. <i>Plant Genome</i> , 2022, 15, .	1.6	8
3287	Genetic diversity of Banat Naked Neck, indigenous chicken breed from Serbia, inferred from mitochondrial DNA D-loop sequence and microsatellite markers. <i>Animal Biotechnology</i> , 0, , 1-10.	0.7	0
3288	Sucrose-Specific Genic Microsatellites to Analyse the Genetic Structure Among the Commercial Hybrids and Clones of Interspecific and Intergeneric Origin in <i>Saccharum</i> Complex. <i>Sugar Tech</i> , 0, , .	0.9	0
3290	Unraveling the genomic regions controlling the seed vigour index, root growth parameters and germination per cent in rice. <i>PLoS ONE</i> , 2022, 17, e0267303.	1.1	8
3291	Developing and deploying an efficient genotyping workflow for accelerating maize improvement in developing countries. <i>Gates Open Research</i> , 0, 6, 3.	2.0	0
3292	Genetic diversity and population structure assessed through simple sequence repeat markers in <i>Saccharum</i> spp. hybrids from Pakistan and Sri Lanka. <i>Genetic Resources and Crop Evolution</i> , 2022, 69, 2889-2900.	0.8	3
3293	Revealing genetic diversity and population structure in Pistachio (<i>Pistacia vera</i> L.) by SSR markers. <i>Genetic Resources and Crop Evolution</i> , 2022, 69, 2875-2887.	0.8	6
3294	Genome-Wide Association Study of Kernel Traits Using a 35K SNP Array in Bread Wheat (<i>Triticum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.7	3
3295	Mutations in <i>PmUFGT3</i> contribute to color variation of fruit skin in Japanese apricot (<i>Prunus mume</i>) Tj ETQq1 1 0.784314 rgBT /Overlock	1.6	4

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3296	SSR-Based Molecular Identification and Population Structure Analysis for Forage Pea (<i>Pisum sativum</i>) Tj ETQq0 0 0 190 /Overlock 10 Tf		
3297	Comparative Genetic Diversity Analysis for Biomass Allocation and Drought Tolerance in <i>Wheat</i> . <i>Agronomy</i> , 2022, 12, 1457.	1.3	0
3298	Optimizing use of U.S. Ex-PVP inbred lines for enhancing agronomic performance of tropical <i>Striga</i> resistant maize inbred lines. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	3
3299	Identification of Putative SNP Markers Associated with Resistance to Egyptian Loose Smut Race(s) in Spring Barley. <i>Genes</i> , 2022, 13, 1075.	1.0	6
3300	An efficient ancestry informative SNPs panel for further discriminating East Asian populations. <i>Electrophoresis</i> , 2022, 43, 1774-1783.	1.3	2
3301	Genetic diversity and marker trait association for phytophthora resistance in chilli. <i>Molecular Biology Reports</i> , 0, , .	1.0	4
3302	Screening of salt-tolerant wheat (<i>Triticum aestivum</i> L.) through morphological and molecular markers. <i>Cereal Research Communications</i> , 2023, 51, 87-100.	0.8	2
3303	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

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3316	Genetic diversity and population structure of pigeonpea (<i>Cajanus cajan</i> [L.] Millspaugh) landraces grown in Benin revealed by Genotyping-By-Sequencing. PLoS ONE, 2022, 17, e0271565.	1.1	3
3317	Evaluation of black gram (<i>Vigna mungo</i>) gene pool against <i>Callosobruchus maculatus</i> and diversity analysis inter se. , 2022, 92, 915-919.		0
3318	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	0.9	4
3319	Population Dynamics of Wide Compatibility System and Evaluation of Intersubspecific Hybrids by indica-japonica Hybridization in Rice. Plants, 2022, 11, 1930.	1.6	3
3320	Development of markers using microsatellite loci of two rove beetle species, <i>Paederus fuscipes</i> Curtis and <i>Aleochara (Aleochara) curtula</i> Goeze (Coleoptera: Staphylinidae), followed by analyses of genetic diversity and population structure. Genes and Genomics, 0, , .	0.5	0
3321	Development and verification of SSR markers from drought stress-responsive miRNAs in Dongxiang wild rice (<i>Oryza rufipogon</i> Griff.). Functional and Integrative Genomics, 2022, 22, 1153-1157.	1.4	3
3322	Study on the Genetic Variation of <i>Triadica sebifera</i> (Linnaeus) Small Populations Based on SSR Markers. Forests, 2022, 13, 1330.	0.9	2
3323	Assessment of Genetic Diversity of Bread Wheat Genotypes for Drought Tolerance Using Canopy Reflectance-Based Phenotyping and SSR Marker-Based Genotyping. Sustainability, 2022, 14, 9818.	1.6	5
3324	Molecular characterization and genetic diversity analysis in Indian mustard (<i>Brassica juncea</i> L. Czern) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	1.1	8
3325	Developing and deploying an efficient genotyping workflow for accelerating maize improvement in developing countries. Gates Open Research, 0, 6, 3.	2.0	0
3326	Association mapping of lignin response to <i>Verticillium Wilt</i> through eight-way MAGIC population in upland cotton. Journal of Integrative Agriculture, 2022, , .	1.7	1
3327	Comprehensive Analyses of Simple Sequence Repeat (SSR) in Bamboo Genomes and Development of SSR Markers with Peroxidase Genes. Genes, 2022, 13, 1518.	1.0	4
3328	Genetic Diversity of Nanmu (<i>Phoebe zhennan</i> S. Lee. et F. N. Wei) Breeding Population and Extraction of Core Collection Using nSSR, cpSSR and Phenotypic Markers. Forests, 2022, 13, 1320.	0.9	4
3329	Identification and validation of novel loci associated with wheat quality through a genome-wide association study. Journal of Integrative Agriculture, 2022, 21, 3131-3147.	1.7	6
3330	Genetic diversity and structure of a core collection of Huangqi (<i>Astragalus</i> ssp.) developed using genomic simple sequence repeat markers. Genetic Resources and Crop Evolution, 2023, 70, 571-585.	0.8	4
3332	Disease Resistance and Molecular Variations in Irradiation Induced Mutants of Two Pea Cultivars. International Journal of Molecular Sciences, 2022, 23, 8793.	1.8	2
3334	Genetic diversity of DGAT1 gene linked to milk production in cattle populations of Ethiopia. BMC Genomic Data, 2022, 23, .	0.7	3

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3336	Analysis of waxy maize germplasm resources in Southwest China based on SNP markers. Genetic Resources and Crop Evolution, 0, , .	0.8	0
3337	Phenotypic, chemical component and molecular assessment of genetic diversity and population structure of <i>Morinda officinalis</i> germplasm. BMC Genomics, 2022, 23, .	1.2	4
3338	Analysis of the genetic diversity and population structure of <i>Monochasma savatieri</i> Franch. ex Maxim using novel EST-SSR markers. BMC Genomics, 2022, 23, .	1.2	11
3339	Direct evidence demonstrates that <i>Puccinia striiformis</i> f. sp. <i>tritici</i> infects susceptible barberry to complete sexual cycle in autumn. Plant Disease, 0, , .	0.7	1
3340	Design and validation of a codominant molecular marker for fruit acidity in muskmelon (<i>Cucumis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.8	1
3341	Genetic Dissection of Grain Size Traits Through Genome-Wide Association Study Based on Genic Markers in Rice. Rice Science, 2022, 29, 462-472.	1.7	9
3342	Genetic data of 22 autosomal STR loci in Khyber-Pakhtunkhwa, Balochistan and Gilgit Baltistan population of Pakistan using PowerPlex® fusion system. Legal Medicine, 2022, 59, 102129.	0.6	1
3343	SSR and GBS based GWAS study for identification of QTLs associated with nutritional elemental in common bean (<i>Phaseolus vulgaris</i> L.). Scientia Horticulturae, 2022, 306, 111470.	1.7	6
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3346	Genetic diversity and population structure of <i>Bruguiera cylindrica</i> along coastal areas in Thailand. Aquatic Botany, 2022, 183, 103575.	0.8	3
3347	Morphological and molecular profiling of <i>Striga gesnerioides</i> on cowpea in Ghana. Ecological Genetics and Genomics, 2022, 25, 100141.	0.3	0
3348	Identification of arsenic-tolerant varieties and candidate genes of tolerance in spring wheat (<i>Triticum</i>) Tj ETQq1 1 0,784314 rgBT /Overlock	4.2	8
3349	Genetic Diversity and Population Structure of Sorghum [<i>Sorghum Bicolor</i> (L.) Moench] Genotypes in Ethiopia as Revealed by Microsatellite Markers. SSRN Electronic Journal, 0, , .	0.4	0
3350	Development of DNA molecular ID card in hog millet germplasm based on high motif SSR. Acta Agronomica Sinica(China), 2022, 48, 908-919.	0.1	0
3351	Genetic diversity analysis of Chinese fresh corn hybrids using SNP Chips. Acta Agronomica Sinica(China), 2022, 48, 1301-1311.	0.1	0
3352	Development and Characterization of Microsatellite Markers Based on the Chloroplast Genome of Tree Peony. Genes, 2022, 13, 1543.	1.0	2
3353	Changes in the Genetic Structure of Lithuania's Wild Boar (<i>Sus scrofa</i>) Population Following the Outbreak of African Swine Fever. Genes, 2022, 13, 1561.	1.0	4
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3356	Elucidation of the population structure and genetic diversity of <i>Bipolaris oryzae</i> associated with rice brown spot disease using SSR markers. <i>3 Biotech</i> , 2022, 12, .	1.1	1
3357	The Rediscovery of Traditional Maize Agrobiodiversity: A Study Case from Northern Italy. <i>Sustainability</i> , 2022, 14, 12110.	1.6	1
3358	Effects of Traditional Ethnic Minority Food Culture on Genetic Diversity in Rice Landraces in Guizhou Province, China. <i>Agronomy</i> , 2022, 12, 2308.	1.3	1
3359	Genome-wide association analysis to delineate high-quality SNPs for seed micronutrient density in chickpea (<i>Cicer arietinum</i> L.). <i>Scientific Reports</i> , 2022, 12, .	1.6	8
3362	Determining the Genetic Difference of Some World Cotton Genotypes Using iPbs (Inter-Primer Binding) Tj ETQq1 1,0,784314 1 rgBT /Ove	1.7	1
3363	Allelic variation in <i>shrunken2</i> gene affecting kernel sweetness in exotic-and indigenous-maize inbreds. <i>PLoS ONE</i> , 2022, 17, e0274732.	1.1	5
3364	Genetic Variation Among Tropical Maize Inbred Lines from NARS and CGIAR Breeding Programs. <i>Plant Molecular Biology Reporter</i> , 2023, 41, 209-217.	1.0	4
3365	Phenotypic variability and genetic diversity analysis of cultivated potatoes in China. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
3366	De novo transcriptome assembly, gene annotation, and EST-SSR marker development of an important medicinal and edible crop, <i>Amomum tsaoko</i> (Zingiberaceae). <i>BMC Plant Biology</i> , 2022, 22, .	1.6	3
3368	Genetic diversity and population structure of sorghum [<i>Sorghum bicolor</i> (L.) Moench] in Ethiopia as revealed by microsatellite markers. <i>Acta Agriculturae Scandinavica - Section B Soil and Plant Science</i> , 2022, 72, 873-884.	0.3	3
3369	Genetic diversity of wild rice accessions (<i>Oryza rufipogon</i> Griff.) in Guangdong and Hainan Provinces, China, and construction of a wild rice core collection. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
3370	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.	0.4	1
3371	Analysis of the complete plastomes and nuclear ribosomal DNAs from <i>Euonymus hamiltonianus</i> and its relatives sheds light on their diversity and evolution. <i>PLoS ONE</i> , 2022, 17, e0275590.	1.1	0
3372	Deciphering environmental factors and defense response of rice genotypes against sheath blight disease. <i>Physiological and Molecular Plant Pathology</i> , 2022, 122, 101916.	1.3	6
3374	Assessment of morpho-genetic diversity of guava (<i>Psidium guajava</i>) hybrids and genotypes. , 2021, 91, .		1
3375	Relationship between Phenolic Compounds and Antioxidant Activity in Berries and Leaves of Raspberry Genotypes and Their Genotyping by SSR Markers. <i>Antioxidants</i> , 2022, 11, 1961.	2.2	14
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3378	Development and Application of SNP-KASP Markers Based on Genes Related to Nitrogen Uptake, Assimilation and Allocation in Tea Plant (<i>Camellia sinensis</i> L.). <i>Agronomy</i> , 2022, 12, 2534.	1.3	3
3379	Genetic characterization and population structure analysis among different horticultural groups of muskmelon (<i>Cucumis melo</i> L.) using microsatellite markers. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 0, , 1-8.	0.4	0
3380	Assessment of the Genetic Diversity and Population Structure of <i>Rhizophora apiculata</i> Blume (<i>Rhizophoraceae</i>) in Thailand. <i>Biology</i> , 2022, 11, 1449.	1.3	4
3381	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.	1.3	2
3382	Genetic Diversity of Bosnian and Herzegovinian Autochthonous Dog Breed Bosnian Broken-Haired Hound "Barak". <i>Biochemical Genetics</i> , 0, , .	0.8	0
3383	Potential drivers for schistosomiasis persistence: Population genetic analyses from a cluster-randomized urogenital schistosomiasis elimination trial across the Zanzibar islands. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010419.	1.3	3
3384	Genetic Diversity and Population Structure of Normal Maize Germplasm Collected in South Sudan Revealed by SSR Markers. <i>Plants</i> , 2022, 11, 2787.	1.6	7
3385	Molecular characterization of Kinnow mutants. , 2021, 91, .		0
3386	Sui Generis Development of Molecular Markers from Transcriptome of <i>Crotalaria juncea</i> , a Fabaceae Family Bast Fiber Crop. <i>Journal of Natural Fibers</i> , 2023, 20, .	1.7	0
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3388	Genetic improvement of faba bean (<i>Vicia faba</i> L.) genotypes selected for resistance to chocolate spot disease. <i>Agronomia Colombiana</i> , 2022, 40, .	0.1	2
3389	Construction of an SNP fingerprinting database and population genetic analysis of 329 cauliflower cultivars. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	3
3390	Microsatellite analysis and polymorphic marker development based on the full-length transcriptome of <i>Camellia chekiangoleosa</i> . <i>Scientific Reports</i> , 2022, 12, .	1.6	0
3392	Population structure of sumac (<i>Rhus coriaria</i> L.) from TÃ¼rkiye based on transcriptome-developed SSR marker. <i>Genetic Resources and Crop Evolution</i> , 0, , .	0.8	0
3393	Inbreeding in Chinese Fir: Insight into the Rare Self-Fertilizing Event from a Genetic View. <i>Genes</i> , 2022, 13, 2105.	1.0	3
3394	Utilization of Novel <i>Perilla</i> SSR Markers to Assess the Genetic Diversity of Native <i>Perilla</i> Germplasm Accessions Collected from South Korea. <i>Plants</i> , 2022, 11, 2974.	1.6	4
3395	Genetic Characterization and Population Structure of Pea (<i>Pisum sativum</i> L.) by Molecular Markers against Rust (<i>Uromyces viciae-fabae</i>) in Newly Developed Genotypes. <i>Sustainability</i> , 2022, 14, 15082.	1.6	2

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3397	Genetic diversity in Groundnut (<i>Arachis hypogaea</i> . L) genotypes varying in maturity duration. <i>Vegetos</i> , 0, , .	0.8	0
3400	Molecular Characterization of <i>Tinospora cordifolia</i> (Willd.) Miers Using Novel g-SSR Markers and Their Comparison with EST-SSR and SCoT Markers for Genetic Diversity Study. <i>Genes</i> , 2022, 13, 2042.	1.0	5
3401	Polymorphic Microsatellite Development, Genetic Diversity, Population Differentiation and Sexual State of <i>Phytophthora capsici</i> on Commercial Peppers in Three Provinces of Southwest China. <i>Applied and Environmental Microbiology</i> , 0, , .	1.4	1
3402	First evidence of multiple paternity in the blue shark (<i>Prionace glauca</i>). <i>Journal of Fish Biology</i> , 2023, 102, 528-531.	0.7	2
3403	Dissecting the Genetic Mechanisms of Hemicellulose Content in Rapeseed Stalk. <i>Agronomy</i> , 2022, 12, 2886.	1.3	1
3404	Genetic diversity and paternity analysis of <i>Mytilaria laosensis</i> hybrids using microsatellite markers provide insight into the breeding system. <i>Industrial Crops and Products</i> , 2023, 191, 115974.	2.5	1
3407	Reliable Propagation of Persian Walnut Varieties Using SSR Marker-based True-to-type Validation. <i>Hortscience: A Publication of the American Society for Horticultural Science</i> , 2023, 58, 64-66.	0.5	3
3408	Yield plasticity and molecular diversity analysis in chickpea (<i>Cicer arietinum</i>). , 2019, 89, .		0
3409	Morphological, biochemical and SSR marker based genetic diversity and identification of trait-specific accessions in exotic germplasm collection of tomato (<i>Solanum lycopersicum</i> L.). <i>Environment Conservation Journal</i> , 2022, 23, 113-121.	0.1	0
3410	Microsatellite Characterization and Panel Selection for Brown Bear (<i>Ursus arctos</i>) Population Assessment. <i>Genes</i> , 2022, 13, 2164.	1.0	1
3411	Molecular Markers Efficiency for Assessment of Genetic Structure in Barley Accessions. <i>Cytology and Genetics</i> , 2022, 56, 548-558.	0.2	1
3412	Association Mapping for Quantitative Trait Loci Controlling Superoxide Dismutase, Flavonoids, Anthocyanins, Carotenoids, Î ³ -Oryzanol and Antioxidant Activity in Rice. <i>Agronomy</i> , 2022, 12, 3036.	1.3	8
3413	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.	1.4	2
3415	Genetic Diversity and Population Structure Analysis of <i>Castanopsis hystrix</i> and Construction of a Core Collection Using Phenotypic Traits and Molecular Markers. <i>Genes</i> , 2022, 13, 2383.	1.0	9
3416	Population genetics analysis of Tolai hares (<i>Lepus tolai</i>) in Xinjiang, China using genome-wide SNPs from SLAF-seq and mitochondrial markers. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
3417	Differential gene expression associated with flower development of mango (<i>Mangifera indica</i> L.) varieties with different shelf-life. <i>Gene Expression Patterns</i> , 2023, 47, 119301.	0.3	0
3418	Agro-morphological traits and SSR markers reveal genetic variations in germplasm accessions of Indian mustard – An industrially important oilseed crop. <i>Heliyon</i> , 2022, 8, e12519.	1.4	4

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3420	Identification and characterization of <i>Pythium</i> , <i>Globisporangium</i> , and <i>Phytophthium</i> species present in floricultural crops from Long Island, New York. <i>Phytopathology</i> , 0, , .	1.1	0
3421	Correlation between the DNJ content and genetic diversity of SSR markers of 36 mulberry (<i>Morus</i> spp.) germplasm resources. <i>Genetic Resources and Crop Evolution</i> , 0, , .	0.8	0
3423	Diversity Analysis Using Agricultural Traits and SSR Markers of Wheat Germplasms. <i>Han'guk Yukchong Hakhoe Chi</i> , 2022, 54, 345-357.	0.2	1
3424	Development of Simple Sequence REPEAT Markers for Genetic Diversity Analysis Based on the cDNA Sequences of Chinese Yam (<i>Dioscorea</i> spp.). <i>Horticulturae</i> , 2022, 8, 1163.	1.2	1
3426	A superior gene allele involved in abscisic acid signaling enhances drought tolerance and yield in chickpea. <i>Plant Physiology</i> , 2023, 191, 1884-1912.	2.3	8
3427	Identification of Drought-Tolerance Genes in the Germination Stage of Soybean. <i>Biology</i> , 2022, 11, 1812.	1.3	5
3428	Molecular Analysis of Genetic Diversity and Structure of the Lablab (<i>Lablab purpureus</i> (L.) Sweet) Gene Pool Reveals Two Independent Routes of Domestication. <i>Plants</i> , 2023, 12, 57.	1.6	6
3430	Association Study for Drought Tolerance of Flint Maize Inbred Lines Using SSR Markers. <i>Plant Breeding and Biotechnology</i> , 2022, 10, 257-271.	0.3	2
3431	Diversity, classification, and EST-SSR-based association analysis of caladium ornamental traits. <i>Physiologia Plantarum</i> , 2023, 175, .	2.6	6
3432	Genetic Improvement in Plant Architecture, Maturity Duration and Agronomic Traits of Three Traditional Rice Landraces through Gamma Ray-Based Induced Mutagenesis. <i>Plants</i> , 2022, 11, 3448.	1.6	1
3433	Genetic diversity analysis of sorghum genotypes for sustainable genetic resource conservation and its implication for breeding program in ethiopia. <i>Genetic Resources and Crop Evolution</i> , 2023, 70, 1831-1852.	0.8	3
3434	Genome-wide association and RNA-seq analyses identify loci for pod orientation in rapeseed (<i>Brassica</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.7	0
3435	Establishment of DNA Molecular Fingerprint of Caladium Core Collections. <i>Agriculture (Switzerland)</i> , 2023, 13, 200.	1.4	0
3436	Genetic diversity and population structure assessment of Western Canadian barley cooperative trials. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
3437	Analysis of germplasm genetic diversity and construction of a core collection in <i>Camellia oleifera</i> C.Abel by integrating novel simple sequence repeat markers. <i>Genetic Resources and Crop Evolution</i> , 2023, 70, 1517-1530.	0.8	1
3438	Genetic diversity and population structure of sorghum [<i>Sorghum bicolor</i> (L.) Moench] genotypes in Ethiopia as revealed by microsatellite markers. <i>Heliyon</i> , 2023, 9, e12830.	1.4	5
3439	Scion/Rootstock Interaction Studies for Quality Traits in Mango (<i>Mangifera indica</i> L.) Varieties. <i>Agronomy</i> , 2023, 13, 204.	1.3	2

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3441	Development and Application of EST-SSR Markers Related to Lead Stress Responses in Kenaf Based on Transcriptome Sequencing Data. <i>Sustainability</i> , 2023, 15, 1514.	1.6	1
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