

Kenta Shirasawa

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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|--------------------|-------------------------|----------------|-----------------|
| 149 papers | 6,339 citations | 37 h-index | 78 g-index |
| 175 ext. papers | 8,195 ext. citations | 4.6 avg, IF | 6.64 L-index |

| # | Paper | IF | Citations |
|-----|--|------|-----------|
| 149 | The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012 , 485, 635-41 | 50.4 | 2138 |
| 148 | The genome sequences of <i>Arachis duranensis</i> and <i>Arachis ipaensis</i> , the diploid ancestors of cultivated peanut. <i>Nature Genetics</i> , 2016 , 48, 438-46 | 36.3 | 498 |
| 147 | The genome sequence of segmental allotetraploid peanut <i>Arachis hypogaea</i> . <i>Nature Genetics</i> , 2019 , 51, 877-884 | 36.3 | 211 |
| 146 | Draft genome sequence of eggplant (<i>Solanum melongena</i> L.): the representative solanum species indigenous to the old world. <i>DNA Research</i> , 2014 , 21, 649-60 | 4.5 | 180 |
| 145 | Dissection of the octoploid strawberry genome by deep sequencing of the genomes of <i>Fragaria</i> species. <i>DNA Research</i> , 2014 , 21, 169-81 | 4.5 | 174 |
| 144 | Accumulation of glycinebetaine in rice plants that overexpress choline monooxygenase from spinach and evaluation of their tolerance to abiotic stress. <i>Annals of Botany</i> , 2006 , 98, 565-71 | 4.1 | 138 |
| 143 | The genome sequence of sweet cherry (<i>Prunus avium</i>) for use in genomics-assisted breeding. <i>DNA Research</i> , 2017 , 24, 499-508 | 4.5 | 136 |
| 142 | Draft sequences of the radish (<i>Raphanus sativus</i> L.) genome. <i>DNA Research</i> , 2014 , 21, 481-90 | 4.5 | 134 |
| 141 | Integrated consensus map of cultivated peanut and wild relatives reveals structures of the A and B genomes of <i>Arachis</i> and divergence of the legume genomes. <i>DNA Research</i> , 2013 , 20, 173-84 | 4.5 | 99 |
| 140 | Sequence analysis of the genome of carnation (<i>Dianthus caryophyllus</i> L.). <i>DNA Research</i> , 2014 , 21, 231-41 | 4.5 | 98 |
| 139 | In silico polymorphism analysis for the development of simple sequence repeat and transposon markers and construction of linkage map in cultivated peanut. <i>BMC Plant Biology</i> , 2012 , 12, 80 | 5.3 | 93 |
| 138 | Survey of genome sequences in a wild sweet potato, <i>Ipomoea trifida</i> (H. B. K.) G. Don. <i>DNA Research</i> , 2015 , 22, 171-9 | 4.5 | 88 |
| 137 | Identification of the carotenoid modifying gene PALE YELLOW PETAL 1 as an essential factor in xanthophyll esterification and yellow flower pigmentation in tomato (<i>Solanum lycopersicum</i>). <i>Plant Journal</i> , 2014 , 79, 453-65 | 6.9 | 87 |
| 136 | Genome-wide survey of artificial mutations induced by ethyl methanesulfonate and gamma rays in tomato. <i>Plant Biotechnology Journal</i> , 2016 , 14, 51-60 | 11.6 | 83 |
| 135 | SNP discovery and linkage map construction in cultivated tomato. <i>DNA Research</i> , 2010 , 17, 381-91 | 4.5 | 81 |
| 134 | An interspecific linkage map of SSR and intronic polymorphism markers in tomato. <i>Theoretical and Applied Genetics</i> , 2010 , 121, 731-9 | 6 | 81 |
| 133 | Mutant Selection from Progeny of Gamma-ray-irradiated Rice by DNA Heteroduplex Cleavage using Brassica Petiole Extract. <i>Breeding Science</i> , 2006 , 56, 179-183 | 2 | 74 |

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| 132 | Novel QTLs for photoperiodic flowering revealed by using reciprocal backcross inbred lines from crosses between japonica rice cultivars. <i>Theoretical and Applied Genetics</i> , 2008 , 117, 935-45 | 6 | 73 |
| 131 | Large-scale development of expressed sequence tag-derived simple sequence repeat markers and diversity analysis in <i>Arachis</i> spp. <i>Molecular Breeding</i> , 2012 , 30, 125-138 | 3-4 | 66 |
| 130 | SSR and EST-SSR-based genetic linkage map of cassava (<i>Manihot esculenta</i> Crantz). <i>Theoretical and Applied Genetics</i> , 2011 , 122, 1161-70 | 6 | 66 |
| 129 | Analytical workflow of double-digest restriction site-associated DNA sequencing based on empirical and in silico optimization in tomato. <i>DNA Research</i> , 2016 , 23, 145-53 | 4-5 | 63 |
| 128 | An EST-SSR linkage map of <i>Raphanus sativus</i> and comparative genomics of the Brassicaceae. <i>DNA Research</i> , 2011 , 18, 221-32 | 4-5 | 62 |
| 127 | Genome-wide association studies using single nucleotide polymorphism markers developed by re-sequencing of the genomes of cultivated tomato. <i>DNA Research</i> , 2013 , 20, 593-603 | 4-5 | 61 |
| 126 | Construction of an integrated high density simple sequence repeat linkage map in cultivated strawberry (<i>Fragaria ananassa</i>) and its applicability. <i>DNA Research</i> , 2013 , 20, 79-92 | 4-5 | 57 |
| 125 | Characterization of active miniature inverted-repeat transposable elements in the peanut genome. <i>Theoretical and Applied Genetics</i> , 2012 , 124, 1429-38 | 6 | 54 |
| 124 | Genome-wide SNP genotyping to infer the effects on gene functions in tomato. <i>DNA Research</i> , 2013 , 20, 221-33 | 4-5 | 50 |
| 123 | Dot-blot-SNP analysis for practical plant breeding and cultivar identification in rice. <i>Theoretical and Applied Genetics</i> , 2006 , 113, 147-55 | 6 | 48 |
| 122 | Development of gene-based markers and construction of an integrated linkage map in eggplant by using <i>Solanum</i> orthologous (SOL) gene sets. <i>Theoretical and Applied Genetics</i> , 2012 , 125, 47-56 | 6 | 46 |
| 121 | Development of <i>Capsicum</i> EST-SSR markers for species identification and in silico mapping onto the tomato genome sequence. <i>Molecular Breeding</i> , 2013 , 31, 101-110 | 3-4 | 45 |
| 120 | Tetrasomic recombination is surprisingly frequent in allotetraploid <i>Arachis</i> . <i>Genetics</i> , 2015 , 199, 1093-105 | 4 | 40 |
| 119 | Identification of RAN1 orthologue associated with sex determination through whole genome sequencing analysis in fig (<i>Ficus carica</i> L.). <i>Scientific Reports</i> , 2017 , 7, 41124 | 4-9 | 38 |
| 118 | De novo whole-genome assembly in <i>Chrysanthemum seticuspe</i> , a model species of <i>Chrysanthemums</i> , and its application to genetic and gene discovery analysis. <i>DNA Research</i> , 2019 , 26, 195-203 | 4-5 | 38 |
| 117 | Identification of QTLs for Rust Resistance in the Peanut Wild Species <i>Arachis magna</i> and the Development of KASP Markers for Marker-Assisted Selection. <i>G3: Genes, Genomes, Genetics</i> , 2015 , 5, 1403-13 | 3-2 | 38 |
| 116 | Detection of genome donor species of neglected tetraploid crop <i>Vigna reflexo-pilosa</i> (crôle bean), and genetic structure of diploid species based on newly developed EST-SSR markers from azuki bean (<i>Vigna angularis</i>). <i>PLoS ONE</i> , 2014 , 9, e104990 | 3-7 | 38 |
| 115 | A high-density SNP genetic map consisting of a complete set of homologous groups in autohexaploid sweetpotato (<i>Ipomoea batatas</i>). <i>Scientific Reports</i> , 2017 , 7, 44207 | 4-9 | 37 |

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| 114 | A simulation-based breeding design that uses whole-genome prediction in tomato. <i>Scientific Reports</i> , 2016 , 6, 19454 | 4.9 | 37 |
| 113 | Mapping of a novel clubroot resistance QTL using ddRAD-seq in Chinese cabbage (<i>Brassica rapa</i> L.). <i>BMC Plant Biology</i> , 2019 , 19, 13 | 5.3 | 37 |
| 112 | Mapping of important taxonomic and productivity traits using genic and non-genic transposable element markers in peanut (<i>Arachis hypogaea</i> L.). <i>PLoS ONE</i> , 2017 , 12, e0186113 | 3.7 | 32 |
| 111 | QTL mapping for late leaf spot and rust resistance using an improved genetic map and extensive phenotypic data on a recombinant inbred line population in peanut (<i>Arachis hypogaea</i> L.). <i>Euphytica</i> , 2016 , 209, 147-156 | 2.1 | 32 |
| 110 | Genome-wide comparative analysis of 20 miniature inverted-repeat transposable element families in <i>Brassica rapa</i> and <i>B. oleracea</i> . <i>PLoS ONE</i> , 2014 , 9, e94499 | 3.7 | 30 |
| 109 | DNA marker applications to molecular genetics and genomics in tomato. <i>Breeding Science</i> , 2013 , 63, 21-30 | 3.0 | 29 |
| 108 | Identification of gene for rice (<i>Oryza sativa</i>) seed lipoxygenase-3 involved in the generation of stale flavor and development of SNP markers for lipoxygenase-3 deficiency. <i>Breeding Science</i> , 2008 , 58, 169-176 | 2.6 | 29 |
| 107 | Single nucleotide polymorphisms in randomly selected genes among japonica rice (<i>Oryza sativa</i> L.) varieties identified by PCR-RF-SSCP. <i>DNA Research</i> , 2004 , 11, 275-83 | 4.5 | 29 |
| 106 | Improvement of the dot-blot-SNP technique for efficient and cost-effective genotyping. <i>Molecular Breeding</i> , 2010 , 25, 179-185 | 3.4 | 26 |
| 105 | Draft genome sequence of subterranean clover, a reference for genus <i>Trifolium</i> . <i>Scientific Reports</i> , 2016 , 6, 30358 | 4.9 | 25 |
| 104 | The persimmon genome reveals clues to the evolution of a lineage-specific sex determination system in plants. <i>PLoS Genetics</i> , 2020 , 16, e1008566 | 6 | 23 |
| 103 | Marker-assisted backcrossing to develop foliar disease-resistant genotypes in TMV 2 variety of peanut (<i>Arachis hypogaea</i> L.). <i>Plant Breeding</i> , 2017 , 136, 948-953 | 2.4 | 22 |
| 102 | Development of EST-SSR markers and construction of a linkage map in faba bean (<i>Vicia faba</i>). <i>Breeding Science</i> , 2014 , 64, 252-63 | 2 | 22 |
| 101 | Phased genome sequence of an interspecific hybrid flowering cherry, 'Somei-Yoshino' (<i>Cerasus</i> sp. <i>yedoensis</i>). <i>DNA Research</i> , 2019 , 26, 379-389 | 4.5 | 21 |
| 100 | Analysis of a tomato introgression line, IL8-3, with increased Brix content. <i>Scientia Horticulturae</i> , 2013 , 153, 103-108 | 4.1 | 21 |
| 99 | Conversion of AFLP markers to sequence-specific markers for closely related lines in rice by use of the rice genome sequence. <i>Molecular Breeding</i> , 2004 , 14, 283-292 | 3.4 | 21 |
| 98 | Availability of Micro-Tom mutant library combined with TILLING in molecular breeding of tomato fruit shelf-life. <i>Breeding Science</i> , 2012 , 62, 202-8 | 2 | 20 |
| 97 | A novel tomato mutant, <i>Solanum lycopersicum</i> elongated fruit1 (<i>Slelf1</i>), exhibits an elongated fruit shape caused by increased cell layers in the proximal region of the ovary. <i>Molecular Genetics and Genomics</i> , 2014 , 289, 399-409 | 3.1 | 19 |

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| 96 | Transcriptome-based single nucleotide polymorphism markers for genome mapping in Japanese pear (<i>Pyrus pyrifolia</i> Nakai). <i>Tree Genetics and Genomes</i> , 2014 , 10, 853-863 | 2.1 | 19 |
| 95 | Kazusa Marker DataBase: a database for genomics, genetics, and molecular breeding in plants. <i>Breeding Science</i> , 2014 , 64, 264-71 | 2 | 19 |
| 94 | Development of AhMITE1 markers through genome-wide analysis in peanut (<i>Arachis hypogaea</i> L.). <i>BMC Research Notes</i> , 2018 , 11, 10 | 2.3 | 18 |
| 93 | Development of NILs from heterogeneous inbred families for validating the rust resistance QTL in peanut (<i>Arachis hypogaea</i> L.). <i>Plant Breeding</i> , 2014 , 133, 80-85 | 2.4 | 17 |
| 92 | Construction of an SSR and RAD Marker-Based Genetic Linkage Map for Carnation (<i>Dianthus caryophyllus</i> L.). <i>Plant Molecular Biology Reporter</i> , 2017 , 35, 110-117 | 1.7 | 17 |
| 91 | Comparative Genetic Mapping and Discovery of Linkage Disequilibrium Across Linkage Groups in White Clover (<i>Trifolium repens</i> L.). <i>G3: Genes, Genomes, Genetics</i> , 2012 , 2, 607-17 | 3.2 | 17 |
| 90 | The number of genes having different alleles between rice cultivars estimated by SNP analysis. <i>Theoretical and Applied Genetics</i> , 2007 , 115, 1067-74 | 6 | 17 |
| 89 | Target Amplicon Sequencing for Genotyping Genome-Wide Single Nucleotide Polymorphisms Identified by Whole-Genome Resequencing in Peanut. <i>Plant Genome</i> , 2016 , 9, plantgenome2016.06.0052 | 4.4 | 17 |
| 88 | Sequencing Analysis of Genetic Loci for Resistance for Late Leaf Spot and Rust in Peanut (L.). <i>Frontiers in Plant Science</i> , 2018 , 9, 1727 | 6.2 | 16 |
| 87 | SNP discovery of Korean short day onion inbred lines using double digest restriction site-associated DNA sequencing. <i>PLoS ONE</i> , 2018 , 13, e0201229 | 3.7 | 15 |
| 86 | Identification of the chromosomal region responsible for high-temperature stress tolerance during the grain-filling period in rice. <i>Molecular Breeding</i> , 2013 , 32, 223-232 | 3.4 | 15 |
| 85 | Rapid identification of candidate genes for resistance to tomato late blight disease using next-generation sequencing technologies. <i>PLoS ONE</i> , 2017 , 12, e0189951 | 3.7 | 15 |
| 84 | Discrimination of candidate subgenome-specific loci by linkage map construction with an S population of octoploid strawberry (<i>Fragaria ×ananassa</i>). <i>BMC Genomics</i> , 2017 , 18, 374 | 4.5 | 14 |
| 83 | Challenges to genome sequence dissection in sweetpotato. <i>Breeding Science</i> , 2017 , 67, 35-40 | 2 | 13 |
| 82 | Mapping of Micro-Tom BAC-End Sequences to the Reference Tomato Genome Reveals Possible Genome Rearrangements and Polymorphisms. <i>International Journal of Plant Genomics</i> , 2012 , 2012, 437026 | | 12 |
| 81 | Genome sequence and analysis of a Japanese radish (<i>Raphanus sativus</i>) cultivar named 'Sakurajima Daikon' possessing giant root. <i>DNA Research</i> , 2020 , 27, | 4.5 | 11 |
| 80 | Genome-Wide Association Studies (GWAS) for Yield and Weevil Resistance in Sweet potato (<i>Ipomoea batatas</i> (L.) Lam). <i>Plant Cell Reports</i> , 2019 , 38, 1383-1392 | 5.1 | 11 |
| 79 | S genotyping and S screening utilizing SFB gene polymorphism in Japanese plum and sweet cherry by dot-blot analysis. <i>Molecular Breeding</i> , 2008 , 21, 339-349 | 3.4 | 11 |

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| 78 | Bayesian QTL mapping using genome-wide SSR markers and segregating population derived from a cross of two commercial F hybrids of tomato. <i>Theoretical and Applied Genetics</i> , 2017 , 130, 1601-1616 | 6 | 10 |
| 77 | A System for Distinguishing Octoploid Strawberry Cultivars Using High-Throughput SNP Genotyping. <i>Tropical Plant Biology</i> , 2017 , 10, 68-76 | 1.6 | 10 |
| 76 | Genome-wide association study overcomes the genome complexity in autohexaploid chrysanthemum and tags SNP markers onto the flower color genes. <i>Scientific Reports</i> , 2019 , 9, 13947 | 4.9 | 10 |
| 75 | Genome-wide structural mutations among the lines resulting from genetic instability in peanut (<i>Arachis hypogaea</i> L.). <i>Plant Gene</i> , 2018 , 13, 1-7 | 3.1 | 10 |
| 74 | Current status in whole genome sequencing and analysis of <i>Ipomoea</i> spp. <i>Plant Cell Reports</i> , 2019 , 38, 1365-1371 | 5.1 | 9 |
| 73 | Chromosome-scale genome assembly of the transformation-amenable common wheat cultivar 'Fielder'. <i>DNA Research</i> , 2021 , 28, | 4.5 | 9 |
| 72 | Hayai-Annotation Plants: an ultra-fast and comprehensive functional gene annotation system in plants. <i>Bioinformatics</i> , 2019 , 35, 4427-4429 | 7.2 | 8 |
| 71 | Characterization of Egyptian <i>Phytophthora infestans</i> population using simple sequence repeat markers. <i>Journal of General Plant Pathology</i> , 2018 , 84, 104-107 | 1 | 8 |
| 70 | Development of molecular markers associated with resistance to <i>Meloidogyne incognita</i> by performing quantitative trait locus analysis and genome-wide association study in sweetpotato. <i>DNA Research</i> , 2019 , 26, 399-409 | 4.5 | 8 |
| 69 | Construction of genetic linkage map and identification of a novel major locus for resistance to pine wood nematode in Japanese black pine (<i>Pinus thunbergii</i>). <i>BMC Plant Biology</i> , 2019 , 19, 424 | 5.3 | 7 |
| 68 | Climate Clever Clovers: New Paradigm to Reduce the Environmental Footprint of Ruminants by Breeding Low Methanogenic Forages Utilizing Haplotype Variation. <i>Frontiers in Plant Science</i> , 2017 , 8, 1463 | 6.2 | 7 |
| 67 | Identification of a Seed Phospholipase D Null Allele in Rice (<i>Oryza sativa</i> L.) and Development of SNP Markers for Phospholipase D Deficiency. <i>Crop Science</i> , 2011 , 51, 2113-2118 | 2.4 | 7 |
| 66 | A reference genetic linkage map of apomictic <i>Hieracium</i> species based on expressed markers derived from developing ovule transcripts. <i>Annals of Botany</i> , 2015 , 115, 567-80 | 4.1 | 6 |
| 65 | Marker-assisted breeding of a LOX-3-null rice line with improved storability and resistance to preharvest sprouting. <i>Theoretical and Applied Genetics</i> , 2015 , 128, 1421-30 | 6 | 6 |
| 64 | Construction of a framework linkage map and genetic dissection of drought- and yield-related QTLs in horsegram (<i>Macrotyloma uniflorum</i>). <i>Euphytica</i> , 2020 , 216, 1 | 2.1 | 6 |
| 63 | The <i>Ficus erecta</i> genome aids <i>Ceratocystis</i> canker resistance breeding in common fig (<i>F. carica</i>). <i>Plant Journal</i> , 2020 , 102, 1313-1322 | 6.9 | 6 |
| 62 | Regulatory change in cell division activity and genetic mapping of a tomato (<i>Solanum lycopersicum</i> L.) elongated-fruit mutant. <i>Plant Biotechnology</i> , 2014 , 31, 149-158 | 1.3 | 6 |
| 61 | Dot-blot Analysis for Identification of japonica Rice Cultivars and Genotyping of Recombinant Inbred Lines. <i>Breeding Science</i> , 2005 , 55, 187-192 | 2 | 6 |

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| 60 | DNA methylation and expression analyses reveal epialleles for the foliar disease resistance genes in peanut (<i>Arachis hypogaea</i> L.). <i>BMC Research Notes</i> , 2020 , 13, 20 | 2.3 | 6 |
| 59 | Chromosome-scale genome assembly of Japanese pear (<i>Pyrus pyrifolia</i>) variety 'Nijisseiki'. <i>DNA Research</i> , 2021 , 28, | 4.5 | 6 |
| 58 | Genetic Maps and Whole Genome Sequences of Radish. <i>Compendium of Plant Genomes</i> , 2017 , 31-42 | 0.8 | 5 |
| 57 | Genetic Mapping in Autohexaploid Sweet Potato with Low-Coverage NGS-Based Genotyping Data. <i>G3: Genes, Genomes, Genetics</i> , 2020 , 10, 2661-2670 | 3.2 | 5 |
| 56 | Root-knot nematode genetic diversity associated with host compatibility to sweetpotato cultivars. <i>Molecular Plant Pathology</i> , 2020 , 21, 1088-1098 | 5.7 | 5 |
| 55 | Identification of genome-wide single-nucleotide polymorphisms among geographically diverse radish accessions. <i>DNA Research</i> , 2020 , 27, | 4.5 | 5 |
| 54 | Leaf-punch method to prepare a large number of PCR templates from plants for SNP analysis. <i>Molecular Breeding</i> , 2009 , 23, 329-336 | 3.4 | 5 |
| 53 | QTL analysis for flowering time in carnation (<i>Dianthus caryophyllus</i> L.). <i>Scientia Horticulturae</i> , 2020 , 262, 109053 | 4.1 | 5 |
| 52 | Genomic insight into the developmental history of southern highbush blueberry populations. <i>Heredity</i> , 2021 , 126, 194-205 | 3.6 | 5 |
| 51 | De novo genome assembly of two tomato ancestors, <i>Solanum pimpinellifolium</i> and <i>Solanum</i> lycopersicum var. <i>cerasiforme</i> , by long-read sequencing. <i>DNA Research</i> , 2021 , 28, | 4.5 | 5 |
| 50 | Technical review of molecular markers and next-generation sequencing technology to manage plant pathogenic oomycetes. <i>African Journal of Biotechnology</i> , 2018 , 17, 369-379 | 0.6 | 4 |
| 49 | A pure line derived from a self-compatible <i>Chrysanthemum seticuspe</i> mutant as a model strain in the genus <i>Chrysanthemum</i> . <i>Plant Science</i> , 2019 , 287, 110174 | 5.3 | 4 |
| 48 | Analysis of the lineage of <i>Phytophthora infestans</i> isolates using mating type assay, traditional markers, and next generation sequencing technologies. <i>PLoS ONE</i> , 2020 , 15, e0221604 | 3.7 | 4 |
| 47 | Four genetic loci control compact plant size with yellow pear-shaped fruit in ornamental tomato (<i>Solanum lycopersicum</i> L.). <i>Plant Genome</i> , 2020 , 13, e20017 | 4.4 | 4 |
| 46 | Genotyping-by-Sequencing Based Genetic Mapping Identified Major and Consistent Genomic Regions for Productivity and Quality Traits in Peanut. <i>Frontiers in Plant Science</i> , 2021 , 12, 668020 | 6.2 | 4 |
| 45 | QTL analysis and GWAS of agronomic traits in sweetpotato (L.) using genome wide SNPs. <i>Breeding Science</i> , 2020 , 70, 283-291 | 2 | 3 |
| 44 | Sequence analysis of cultivated strawberry (♂Duch.) using microdissected single somatic chromosomes. <i>Plant Methods</i> , 2017 , 13, 91 | 5.8 | 3 |
| 43 | Current Status of Octoploid Strawberry (<i>Fragaria ×ananassa</i>) Genome Study. <i>Compendium of Plant Genomes</i> , 2018 , 129-137 | 0.8 | 3 |

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| 42 | A chromosome-scale draft genome sequence of horsegram (<i>Macrotyloma uniflorum</i>). <i>GigaByte</i> , 2021, 1-23 | | 3 |
| 41 | De novo whole-genome assembly in interspecific hybrid table grape, B Shine Muscat | | 3 |
| 40 | Development of High-Density Genetic Linkage Maps and Identification of Loci for Chestnut Gall Wasp Resistance in spp. <i>Plants</i> , 2020, 9, | 4.5 | 3 |
| 39 | Chromosome-level genome assemblies of over 100 plant species. <i>Breeding Science</i> , 2021, 71, 117-124 | 2 | 3 |
| 38 | Genome-wide study on the polysomic genetic factors conferring plasticity of flower sexuality in hexaploid persimmon. <i>DNA Research</i> , 2020, 27, | 4.5 | 2 |
| 37 | Advances of Whole Genome Sequencing in Strawberry with NGS Technologies. <i>Horticulture Journal</i> , 2020, 89, 108-114 | 1.1 | 2 |
| 36 | Marker-Assisted Backcrossing Selection for High O/L Ratio in Cultivated Peanut 2013, 177-191 | | 2 |
| 35 | Structural analyses of the tomato genome. <i>Plant Biotechnology</i> , 2013, 30, 257-263 | 1.3 | 2 |
| 34 | Genetic analyses of anthocyanin content using polyploid GWAS followed by QTL detection in the sweetpotato (<i>Ipomoea batatas</i> L.) storage root. <i>Plant Root</i> , 2020, 14, 11-21 | 0.8 | 2 |
| 33 | Genomic region associated with pod color variation in pea (<i>Pisum sativum</i>) | | 2 |
| 32 | Foliar disease resistant and productive mutants from the introgression lines of peanut (<i>Arachis hypogaea</i>). <i>Plant Breeding</i> , 2020, 139, 148-155 | 2.4 | 2 |
| 31 | Genomic Selection for F Hybrid Breeding in Strawberry (). <i>Frontiers in Plant Science</i> , 2021, 12, 645111 | 6.2 | 2 |
| 30 | Enhancing oleic acid content in two commercially released peanut varieties through marker-assisted backcross breeding. <i>Crop Science</i> , 2021, 61, 2435 | 2.4 | 2 |
| 29 | Population Genomics of Peanut. <i>Population Genomics</i> , 2021, 1 | 1.4 | 2 |
| 28 | Whole-genome sequencing and analysis of two azaleas, <i>Rhododendron ripense</i> and <i>Rhododendron kiyosumense</i> . <i>DNA Research</i> , 2021, 28, | 4.5 | 2 |
| 27 | Genome-wide association study of individual sugar content in fruit of Japanese pear (<i>Pyrus</i> spp.). <i>BMC Plant Biology</i> , 2021, 21, 378 | 5.3 | 2 |
| 26 | Translation of continuous artificial selection on phenotype into genotype during rice breeding programs. <i>Breeding Science</i> , 2021, 71, 125-133 | 2 | 2 |
| 25 | Genome-wide structural and functional features of single nucleotide polymorphisms revealed from the whole genome resequencing of 179 accessions of <i>Arachis</i> .. <i>Physiologia Plantarum</i> , 2022, | 4.6 | 1 |

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| 24 | Genetic diversity among the varieties exhibiting early heading date in rice. <i>Euphytica</i> , 2022 , 218, 1 | 2.1 | 1 |
| 23 | Cherry Blossom Forecast Based on Transcriptome of Floral Organs Approaching Blooming in the Flowering Cherry () Cultivar 'Somei-Yoshino'.. <i>Frontiers in Plant Science</i> , 2022 , 13, 802203 | 6.2 | 1 |
| 22 | Artificial selection in the expansion of rice cultivation. <i>Theoretical and Applied Genetics</i> , 2021 , 135, 291 | 6 | 1 |
| 21 | A chromosome-level genome sequence of Chrysanthemum seticuspe, a model species for hexaploid cultivated chrysanthemum. <i>Communications Biology</i> , 2021 , 4, 1167 | 6.7 | 1 |
| 20 | Genome features of common vetch () in natural habitats. <i>Plant Direct</i> , 2021 , 5, e352 | 3.3 | 1 |
| 19 | Genome sequence of Hydrangea macrophylla and its application in analysis of the double flower phenotype. <i>DNA Research</i> , 2021 , 28, | 4.5 | 1 |
| 18 | Hayai-Annotation Plants: an ultra-fast and comprehensive gene annotation system in plants | | 1 |
| 17 | CURLED LATER1 encoding the largest subunit of the Elongator complex has a unique role in leaf development and meristem function in rice. <i>Plant Journal</i> , 2020 , 104, 351-364 | 6.9 | 1 |
| 16 | Genome features of common vetch (Vicia sativa) in natural habitats | | 1 |
| 15 | Chromosome-level genome assembly of Japanese chestnut (Castanea crenata Sieb. et Zucc.) reveals conserved chromosomal segments in woody rosids. <i>DNA Research</i> , 2021 , 28, | 4.5 | 1 |
| 14 | Analysis of the Segregation Distortion of Genotypes Based on Whole-Genome Resequencing of Fig (L.) Breeding Parents. <i>Frontiers in Plant Science</i> , 2021 , 12, 647599 | 6.2 | 1 |
| 13 | A Chromosome-scale draft genome sequence of horsegram (Macrotyloma uniflorum) | | 1 |
| 12 | Fine-scale genetic structure of the rice landrace population in Japan.. <i>Molecular Genetics and Genomics</i> , 2022 , 1 | 3.1 | 1 |
| 11 | Quantitative Trait Loci Analysis Based on High-Density Mapping of Single-Nucleotide Polymorphisms by Genotyping-by-Sequencing Against Pine Wilt Disease in Japanese Black Pine ().. <i>Frontiers in Plant Science</i> , 2022 , 13, 850660 | 6.2 | 1 |
| 10 | Impact of Genomics on Capsicum Breeding. <i>Compendium of Plant Genomes</i> , 2019 , 209-219 | 0.8 | 0 |
| 9 | Genome-Wide Identification of Loci Associated With Phenology-Related Traits and Their Adaptive Variations in a Highbush Blueberry Collection.. <i>Frontiers in Plant Science</i> , 2021 , 12, 793679 | 6.2 | 0 |
| 8 | Organelle genome assembly uncovers the dynamic genome reorganization and cytoplasmic male sterility associated genes in tomato. <i>Horticulture Research</i> , 2021 , 8, 250 | 7.7 | 0 |
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