

Kenta Shirasawa

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/1379887/kenta-shirasawa-publications-by-year.pdf>

Version: 2024-04-09

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

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	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
148	Genetic diversity among the varieties exhibiting early heading date in rice. <i>Euphytica</i> , 2022 , 218, 1	2.1	1
147	Cherry Blossom Forecast Based on Transcriptome of Floral Organs Approaching Blooming in the Flowering Cherry (<i>Prunus</i>) Cultivar 'Somei-Yoshino'.. <i>Frontiers in Plant Science</i> , 2022 , 13, 802203	6.2	1
146	Recent Advances in Genetics, Genomics, and Breeding for Nutritional Quality in Groundnut 2022 , 111-137		0
145	Mapping of Nematode Resistance in Hexaploid Sweetpotato Using an Next-Generation Sequencing-Based Association Study.. <i>Frontiers in Plant Science</i> , 2022 , 13, 858747	6.2	0
144	Fine-scale genetic structure of the rice landrace population in Japan.. <i>Molecular Genetics and Genomics</i> , 2022 , 1	3.1	1
143	Quantitative Trait Loci Analysis Based on High-Density Mapping of Single-Nucleotide Polymorphisms by Genotyping-by-Sequencing Against Pine Wilt Disease in Japanese Black Pine (<i>Pinus</i>).. <i>Frontiers in Plant Science</i> , 2022 , 13, 850660	6.2	1
142	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
141	Artificial selection in the expansion of rice cultivation. <i>Theoretical and Applied Genetics</i> , 2021 , 135, 291	6	1
140	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
139	A chromosome-level genome sequence of <i>Chrysanthemum seticuspe</i> , a model species for hexaploid cultivated chrysanthemum. <i>Communications Biology</i> , 2021 , 4, 1167	6.7	1
138	Genome features of common vetch (<i>Vicia</i>) in natural habitats. <i>Plant Direct</i> , 2021 , 5, e352	3.3	1
137	Genome sequence of <i>Hydrangea macrophylla</i> and its application in analysis of the double flower phenotype. <i>DNA Research</i> , 2021 , 28,	4.5	1
136	Genomic Selection for F Hybrid Breeding in Strawberry (<i>Fragaria</i>). <i>Frontiers in Plant Science</i> , 2021 , 12, 645111	6.2	2
135	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
134	Genomic insight into the developmental history of southern highbush blueberry populations. <i>Heredity</i> , 2021 , 126, 194-205	3.6	5
133	Chromosome-level genome assemblies of over 100 plant species. <i>Breeding Science</i> , 2021 , 71, 117-124	2	3

132	Population Genomics of Peanut. <i>Population Genomics</i> , 2021 , 1	1.4	2
131	Chromosome-scale genome assembly of Japanese pear (<i>Pyrus pyrifolia</i>) variety 'Nijisseiki'. <i>DNA Research</i> , 2021 , 28,	4.5	6
130	Chromosome-scale genome assembly of the transformation-amenable common wheat cultivar 'Fielder'. <i>DNA Research</i> , 2021 , 28,	4.5	9
129	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
128	Chromosome-level genome assembly of Japanese chestnut (<i>Castanea crenata</i> Sieb. et Zucc.) reveals conserved chromosomal segments in woody rosids. <i>DNA Research</i> , 2021 , 28,	4.5	1
127	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
126	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
125	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
124	De novo genome assembly of two tomato ancestors, <i>Solanum pimpinellifolium</i> and <i>Solanum lycopersicum</i> var. <i>cerasiforme</i> , by long-read sequencing. <i>DNA Research</i> , 2021 , 28,	4.5	5
123	Comparative QTL mapping for male sterility of cultivated strawberry (<i>F. Duch.</i>) using different reference genome sequences.. <i>Breeding Science</i> , 2021 , 71, 456-466	2	
122	DNA marker for resistance to in chrysanthemum (Ramat.) "Southern Pegasus". <i>Breeding Science</i> , 2021 , 71, 261-267	2	0
121	Translation of continuous artificial selection on phenotype into genotype during rice breeding programs. <i>Breeding Science</i> , 2021 , 71, 125-133	2	2
120	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
119	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
118	Root-knot nematode genetic diversity associated with host compatibility to sweetpotato cultivars. <i>Molecular Plant Pathology</i> , 2020 , 21, 1088-1098	5.7	5
117	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
116	Identification of genome-wide single-nucleotide polymorphisms among geographically diverse radish accessions. <i>DNA Research</i> , 2020 , 27,	4.5	5
115	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

114	QTL analysis and GWAS of agronomic traits in sweetpotato (L.) using genome wide SNPs. <i>Breeding Science</i> , 2020 , 70, 283-291	2	3
113	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
112	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
111	Advances of Whole Genome Sequencing in Strawberry with NGS Technologies. <i>Horticulture Journal</i> , 2020 , 89, 108-114	1.1	2
110	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
109	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
108	Genomics on plant breeding programs. <i>Ikushugaku Kenkyu</i> , 2020 , 22, 68-74	0.1	
107	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
106	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
105	QTL analysis for flowering time in carnation (<i>Dianthus caryophyllus</i> L.). <i>Scientia Horticulturae</i> , 2020 , 262, 109053	4.1	5
104	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
103	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
102	Transgressive segregation and gene regions controlling thermotolerance of fruit set and pollen germination in <i>Capsicum chinense</i> . <i>Euphytica</i> , 2020 , 216, 1	2.1	
101	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
100	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
99	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
98	Hayai-Annotation Plants: an ultra-fast and comprehensive functional gene annotation system in plants. <i>Bioinformatics</i> , 2019 , 35, 4427-4429	7.2	8
97	The genome sequence of segmental allotetraploid peanut <i>Arachis hypogaea</i> . <i>Nature Genetics</i> , 2019 , 51, 877-884	36.3	211

96	Impact of Genomics on Capsicum Breeding. <i>Compendium of Plant Genomes</i> , 2019 , 209-219	0.8	0
95	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
94	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
93	Phased genome sequence of an interspecific hybrid flowering cherry, 'Somei-Yoshino' (<i>Cerasus</i> × <i>yedoensis</i>). <i>DNA Research</i> , 2019 , 26, 379-389	4.5	21
92	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
91	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
90	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
89	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
88	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
87	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
86	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
85	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
84	Current Status of Octoploid Strawberry (<i>Fragaria ×ananassa</i>) Genome Study. <i>Compendium of Plant Genomes</i> , 2018 , 129-137	0.8	3
83	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
82	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
81	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
80	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
79	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

78	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
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	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
75	Genetic Maps and Whole Genome Sequences of Radish. <i>Compendium of Plant Genomes</i> , 2017 , 31-42	0.8	5
74	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
73	Sequence analysis of cultivated strawberry (F Duch.) using microdissected single somatic chromosomes. <i>Plant Methods</i> , 2017 , 13, 91	5.8	3
72	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
71	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
70	Challenges to genome sequence dissection in sweetpotato. <i>Breeding Science</i> , 2017 , 67, 35-40	2	13
69	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
68	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
67	Genomics research and development of genome-based breeding technologies in vegetable crops. <i>Ikushugaku Kenkyu</i> , 2016 , 18, 124-129	0.1	
66	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
65	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
64	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
63	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
62	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
61	Draft genome sequence of subterranean clover, a reference for genus <i>Trifolium</i> . <i>Scientific Reports</i> , 2016 , 6, 30358	4.9	25

60	A simulation-based breeding design that uses whole-genome prediction in tomato. <i>Scientific Reports</i> , 2016 , 6, 19454	4.9	37
59	Tetrasomic recombination is surprisingly frequent in allotetraploid <i>Arachis</i> . <i>Genetics</i> , 2015 , 199, 1093-105	4.1	40
58	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
57	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
56	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
55	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
54	A novel tomato mutant, <i>Solanum lycopersicum</i> elongated fruit1 (Slelf1), 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
53	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
52	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
51	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
50	Sequence analysis of the genome of carnation (<i>Dianthus caryophyllus</i> L.). <i>DNA Research</i> , 2014 , 21, 231-41	4.5	98
49	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
48	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
47	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
46	Kazusa Marker DataBase: a database for genomics, genetics, and molecular breeding in plants. <i>Breeding Science</i> , 2014 , 64, 264-71	2	19
45	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
44	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
43	Draft sequences of the radish (<i>Raphanus sativus</i> L.) genome. <i>DNA Research</i> , 2014 , 21, 481-90	4.5	134

42	Detection of genome donor species of neglected tetraploid crop <i>Vigna reflexo-pilosa</i> (crable 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
41	Marker-Assisted Backcrossing Selection for High O/L Ratio in Cultivated Peanut 2013 , 177-191		2
40	Analysis of a tomato introgression line, IL8-3, with increased Brix content. <i>Scientia Horticulturae</i> , 2013 , 153, 103-108	4.1	21
39	Development of Capsicum 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
38	DNA marker applications to molecular genetics and genomics in tomato. <i>Breeding Science</i> , 2013 , 63, 21-30		29
37	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
36	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
35	Structural analyses of the tomato genome. <i>Plant Biotechnology</i> , 2013 , 30, 257-263	1.3	2
34	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
33	Genome-wide SNP genotyping to infer the effects on gene functions in tomato. <i>DNA Research</i> , 2013 , 20, 221-33	4.5	50
32	Construction of an integrated high density simple sequence repeat linkage map in cultivated strawberry (<i>Fragaria lananassa</i>) and its applicability. <i>DNA Research</i> , 2013 , 20, 79-92	4.5	57
31	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
30	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012 , 485, 635-41	50.4	2138
29	Characterization of active miniature inverted-repeat transposable elements in the peanut genome. <i>Theoretical and Applied Genetics</i> , 2012 , 124, 1429-38	6	54
28	Development of gene-based markers and construction of an integrated linkage map in eggplant by using <i>Solanum orthologous</i> (SOL) gene sets. <i>Theoretical and Applied Genetics</i> , 2012 , 125, 47-56	6	46
27	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
26	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
25	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

24	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
23	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
22	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
21	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
20	SNP discovery and linkage map construction in cultivated tomato. <i>DNA Research</i> , 2010 , 17, 381-91	4.5	81
19	An interspecific linkage map of SSR and intronic polymorphism markers in tomato. <i>Theoretical and Applied Genetics</i> , 2010 , 121, 731-9	6	81
18	Improvement of the dot-blot-SNP technique for efficient and cost-effective genotyping. <i>Molecular Breeding</i> , 2010 , 25, 179-185	3.4	26
17	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
16	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	17.6	29
15	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
14	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
13	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
12	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
11	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
10	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
9	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
8	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
7	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

6	A chromosome-scale draft genome sequence of horsegram (<i>Macrotyloma uniflorum</i>). <i>GigaByte</i> , 2021, 1-23	3
5	Genomic region associated with pod color variation in pea (<i>Pisum sativum</i>)	2
4	Hayai-Annotation Plants: an ultra-fast and comprehensive gene annotation system in plants	1
3	De novo whole-genome assembly in interspecific hybrid table grape, Shine Muscat	3
2	Genome features of common vetch (<i>Vicia sativa</i>) in natural habitats	1
1	A Chromosome-scale draft genome sequence of horsegram (<i>Macrotyloma uniflorum</i>)	1