

Nakao Kubo

List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	Genetic diversity among Japanese local populations of an edible and medicinal coastal plant <i>Glehnia littoralis</i> F. Schmidt ex Miq.. <i>Genetic Resources and Crop Evolution</i> , 2022, 69, 85-97.	1.6	7
2	Control of clubroot disease on Hanana (flower nabana) using dry seaweed powders. <i>Proceedings of the Kansai Plant Protection Society</i> , 2021, 63, 13-20.	0.1	0
3	Combination of genetic analysis and ancient literature survey reveals the divergence of traditional <i>Brassica rapa</i> varieties from Kyoto, Japan. <i>Horticulture Research</i> , 2021, 8, 132.	6.3	9
4	Parentage analysis of tea cultivars in Japan based on simple sequence repeat markers. <i>Breeding Science</i> , 2021, 71, 594-600.	1.9	2
5	Morphological and Genetic Diversities of <i>Habenaria radiata</i> (Orchidaceae) in the Kinki Area, Japan. <i>International Journal of Molecular Sciences</i> , 2021, 22, 311.	4.1	2
6	Quantitative Trait Locus Analysis in Squash (<i>Cucurbita moschata</i>) Based on Simple Sequence Repeat Markers and Restriction Site-Associated DNA Sequencing Analysis. <i>Horticulturae</i> , 2020, 6, 71.	2.8	3
7	Classification of "nabana" (<i>Brassica rapa</i>) cultivars and landraces based on simple sequence repeat markers. <i>Breeding Science</i> , 2019, 69, 179-185.	1.9	6
8	Genetic Relationships of Heirloom Turnip (<i>Brassica rapa</i>) Cultivars in Shiga Prefecture and Other Regions of Japan. <i>Horticulture Journal</i> , 2019, 88, 471-480.	0.8	8
9	Classification of tea (<i>Camellia sinensis</i>) landraces and cultivars in Kyoto, Japan and other regions, based on simple sequence repeat markers and restriction site-associated DNA sequencing analysis. <i>Genetic Resources and Crop Evolution</i> , 2019, 66, 441-451.	1.6	8
10	Life Cycle and Genetic Diversity of <i>Symplocarpus nipponicus</i> (Araceae), an Endangered Species in Japan. <i>Plants</i> , 2018, 7, 73.	3.5	2
11	Molecular phylogeny and postharvest morphology of petals in two major <i>Nelumbo nucifera</i> cultivars in Thailand. <i>Agriculture and Natural Resources</i> , 2018, 52, 45-52.	0.1	2
12	Development and characterization of simple sequence repeat markers for genetic analyses of <i>Sargassum horneri</i> (Sargassaceae, Phaeophyta) populations in Kyoto, Japan. <i>Journal of Applied Phycology</i> , 2017, 29, 1729-1733.	2.8	12
13	A <i>GLABRA1</i> ortholog on LG A9 controls trichome number in the Japanese leafy vegetables Mizuna and Mibuna (<i>Brassica rapa</i> L. subsp. <i>nipposinica</i> L. H. Bailey): evidence from QTL analysis. <i>Journal of Plant Research</i> , 2017, 130, 539-550.	2.4	11
14	Development of simple sequence repeat markers for the classification of the clubroot pathogen <i>Plasmodiophora brassicae</i> . <i>European Journal of Plant Pathology</i> , 2017, 149, 733-738.	1.7	4
15	Classification of flowering lotus cultivars in Japan, including "Ogura-ike group cultivars", based on SSR markers. <i>Ikushugaku Kenkyu</i> , 2015, 17, 45-54.	0.3	1
16	Detection of quantitative trait loci for heading traits in <i>Brassica rapa</i> using different heading types of Chinese cabbage. <i>Journal of Horticultural Science and Biotechnology</i> , 2015, 90, 311-317.	1.9	9
17	Construction of a chromosome-assigned, sequence-tagged linkage map for the radish, <i>Raphanus sativus</i> L. and QTL analysis of morphological traits. <i>Breeding Science</i> , 2013, 63, 218-226.	1.9	18
18	An SSR-based genetic map of pepper (<i>Capsicum annum</i> L.) serves as an anchor for the alignment of major pepper maps. <i>Breeding Science</i> , 2012, 62, 93-98.	1.9	81

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19	Genetic diversity of the endangered coastal violet <i>Viola grayi</i> Franchet et Savatier (Violaceae) and its genetic relationship to the species in subsection <i>Rostratae</i> . <i>Conservation Genetics</i> , 2012, 13, 837-848.	1.5	13
20	Development of genomic and EST-SSR markers in radish (<i>Raphanus sativus</i> L.). <i>Breeding Science</i> , 2011, 61, 413-419.	1.9	17
21	QTL mapping of clubroot resistance in radish (<i>Raphanus sativus</i> L.). <i>Theoretical and Applied Genetics</i> , 2010, 120, 1021-1027.	3.6	48
22	Genetic diversity and phylogenetic relationships of the endangered species <i>Vaccinium sieboldii</i> and <i>Vaccinium ciliatum</i> (Ericaceae). <i>Plant Systematics and Evolution</i> , 2010, 287, 75-84.	0.9	10
23	Detection of quantitative trait loci controlling morphological traits in <i>Brassica rapa</i> L.. <i>Breeding Science</i> , 2010, 60, 164-171.	1.9	34
24	Discovery of the <i>rpl10</i> Gene in Diverse Plant Mitochondrial Genomes and Its Probable Replacement by the Nuclear Gene for Chloroplast RPL10 in Two Lineages of Angiosperms. <i>DNA Research</i> , 2010, 17, 1-9.	3.4	52
25	Mapping of a novel locus regulating anthocyanin pigmentation in <i>Brassica rapa</i> . <i>Breeding Science</i> , 2010, 60, 76-80.	1.9	22
26	Classification and diversity of sacred and American <i>Nelumbo</i> species: the genetic relationships of flowering lotus cultivars in Japan using SSR markers. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2009, 7, 260-270.	0.8	19
27	Development and characterization of simple sequence repeat (SSR) markers in the water lotus (<i>Nelumbo nucifera</i>). <i>Aquatic Botany</i> , 2009, 90, 191-194.	1.6	38
28	Transfer of rice mitochondrial ribosomal protein L6 gene to the nucleus: acquisition of the 5'-untranslated region via a transposable element. <i>BMC Evolutionary Biology</i> , 2008, 8, 314.	3.2	7
29	Development of 101 novel SSR markers and construction of an SSR-based genetic linkage map in cucumber (<i>Cucumis sativus</i> L.). <i>Breeding Science</i> , 2008, 58, 475-483.	1.9	26
30	Mapping of QTLs controlling root shape and red pigmentation in radish, <i>Raphanus sativus</i> L.. <i>Breeding Science</i> , 2008, 58, 55-61.	1.9	41
31	An Integrated High-density Linkage Map of Soybean with RFLP, SSR, STS, and AFLP Markers Using A Single F2 Population. <i>DNA Research</i> , 2007, 14, 257-269.	3.4	99
32	Isolation and characterization of the pea cytochrome c oxidase Vb gene. <i>Genome</i> , 2006, 49, 1481-1489.	2.0	4
33	Construction of a Molecular Linkage Map of Radish (<i>Raphanus sativus</i> L.), Based on AFLP and Brassica-SSR Markers. <i>Breeding Science</i> , 2005, 55, 107-111.	1.9	28
34	Involvement of N-terminal region in mitochondrial targeting of rice RPS10 and RPS14 proteins. <i>Plant Science</i> , 2003, 164, 1047-1055.	3.6	9
35	Rpp16 and Rpp17, from a Common Origin, have Different Protein Characteristics but Both Genes are Predominantly Expressed in Rice Phloem Tissues. <i>Plant and Cell Physiology</i> , 2002, 43, 668-674.	3.1	18
36	Mitochondrial sequence migrated downstream to a nuclear V-ATPase B gene is transcribed but non-functional. <i>Gene</i> , 2001, 271, 193-201.	2.2	12

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37	The Gene Encoding Mitochondrial Succinate Dehydrogenase Subunit 4 Has Been Successfully Transferred to the Nuclear Genome in Pea, while Leaving an Original Sequence as a Pseudogene in the Mitochondrial Genome.. Plant Biotechnology, 2001, 18, 283-287.	1.0	2
38	Involvement of 5' flanking sequence for specifying RNA editing sites in plant mitochondria. FEBS Letters, 1997, 413, 40-44.	2.8	20
39	A ribosomal protein L2 gene is transcribed, spliced, and edited at one site in rice mitochondria. Plant Molecular Biology, 1996, 31, 853-862.	3.9	26
40	A promiscuous chloroplast DNA fragment is transcribed in plant mitochondria but the encoded RNA is not edited. Plant Molecular Biology, 1996, 31, 647-656.	3.9	24
41	Creation of an initiation codon by RNA editing in the coxI transcript from tomato mitochondria. Current Genetics, 1995, 28, 415-422.	1.7	25