Nakao Kubo

List of Publications by Year
in descending order

41 papers	779 citations	516710 16 h-index	526287 27 g-index
41 all docs	41 docs citations	41 times ranked	791 citing authors

#	Article	IF	Citations
1	An Integrated High-density Linkage Map of Soybean with RFLP, SSR, STS, and AFLP Markers Using A Single F2 Population. DNA Research, 2007, 14, 257-269.	3.4	99
2	An SSR-based genetic map of pepper (<i>Capsicum annuum</i> L.) serves as an anchor for the alignment of major pepper maps. Breeding Science, 2012, 62, 93-98.	1.9	81
3	Discovery of the rpl10 Gene in Diverse Plant Mitochondrial Genomes and Its Probable Replacement by the Nuclear Gene for Chloroplast RPL10 in Two Lineages of Angiosperms. DNA Research, 2010, 17, 1-9.	3.4	52
4	QTL mapping of clubroot resistance in radish (Raphanus sativus L.). Theoretical and Applied Genetics, 2010, 120, 1021-1027.	3.6	48
5	Mapping of QTLs controlling root shape and red pigmentation in radish, Raphanus sativus L.. Breeding Science, 2008, 58, 55-61.	1.9	41
6	Development and characterization of simple sequence repeat (SSR) markers in the water lotus (Nelumbo nucifera). Aquatic Botany, 2009, 90, 191-194.	1.6	38
7	Detection of quantitative trait loci controlling morphological traits in Brassica rapa L.. Breeding Science, 2010, 60, 164-171.	1.9	34
8	Construction of a Molecular Linkage Map of Radish (Raphanus sativus L.), Based on AFLP and Brassica-SSR Markers. Breeding Science, 2005, 55, 107-111.	1.9	28
9	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
10	Development of 101 novel SSR markers and construction of an SSR-based genetic linkage map in cucumber (<i>Cucumis sativus</i> L.). Breeding Science, 2008, 58, 475-483.	1.9	26
11	Creation of an initiation codon by RNA editing in the coxI transcript from tomato mitochondria. Current Genetics, 1995, 28, 415-422.	1.7	25
12	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
13	Mapping of a novel locus regulating anthocyanin pigmentation in Brassica rapa. Breeding Science, 2010, 60, 76-80.	1.9	22
14	Involvement of 5â€² flanking sequence for specifying RNA editing sites in plant mitochondria. FEBS Letters, 1997, 413, 40-44.	2.8	20
15	Classification and diversity of sacred and American Nelumbo species: the genetic relationships of flowering lotus cultivars in Japan using SSR markers. Plant Genetic Resources: Characterisation and Utilisation, 2009, 7, 260-270.	0.8	19
16	Rpp16 and Rpp17, from a Common Origin, have Different Protein Characteristics but Both Genes are Predominantly Expressed in Rice Phloem Tissues. Plant and Cell Physiology, 2002, 43, 668-674.	3.1	18
17	Construction of a chromosome-assigned, sequence-tagged linkage map for the radish, <i>Raphanus sativus</i> L. and QTL analysis of morphological traits. Breeding Science, 2013, 63, 218-226.	1.9	18
18	Development of genomic and EST-SSR markers in radish (Raphanus sativus L.). Breeding Science, 2011, 61, 413-419.	1.9	17

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19	Genetic diversity of the endangered coastal violet Viola grayi Franchet et Savatier (Violaceae) and its genetic relationship to the species in subsection Rostratae. Conservation Genetics, 2012, 13, 837-848.	1.5	13
20	Mitochondrial sequence migrated downstream to a nuclear V-ATPase B gene is transcribed but non-functional. Gene, 2001, 271, 193-201.	2.2	12
21	Development and characterization of simple sequence repeat markers for genetic analyses of Sargassum horneri (Sargassaceae, Phaeophyta) populations in Kyoto, Japan. Journal of Applied Phycology, 2017, 29, 1729-1733.	2.8	12
22	A GLABRA1 ortholog on LG A9 controls trichome number in the Japanese leafy vegetables Mizuna and Mibuna (Brassica rapa L. subsp. nipposinica L. H. Bailey): evidence from QTL analysis. Journal of Plant Research, 2017, 130, 539-550.	2.4	11
23	Genetic diversity and phylogenetic relationships of the endangered species Vaccinium sieboldii and Vaccinium ciliatum (Ericaceae). Plant Systematics and Evolution, 2010, 287, 75-84.	0.9	10
24	Involvement of N-terminal region in mitochondrial targeting of rice RPS10 and RPS14 proteins. Plant Science, 2003, 164, 1047-1055.	3.6	9
25	Detection of quantitative trait loci for heading traits inBrassica rapausing different heading types of Chinese cabbage. Journal of Horticultural Science and Biotechnology, 2015, 90, 311-317.	1.9	9
26	Combination of genetic analysis and ancient literature survey reveals the divergence of traditional Brassica rapa varieties from Kyoto, Japan. Horticulture Research, 2021, 8, 132.	6.3	9
27	Genetic Relationships of Heirloom Turnip (<i>Brassica rapa</i>) Cultivars in Shiga Prefecture and Other Regions of Japan. Horticulture Journal, 2019, 88, 471-480.	0.8	8
28	Classification of tea (Camellia sinensis) landraces and cultivars in Kyoto, Japan and other regions, based on simple sequence repeat markers and restriction site-associated DNA sequencing analysis. Genetic Resources and Crop Evolution, 2019, 66, 441-451.	1.6	8
29	Transfer of rice mitochondrial ribosomal protein L6 gene to the nucleus: acquisition of the 5'-untranslated region via a transposable element. BMC Evolutionary Biology, 2008, 8, 314.	3.2	7
30	Genetic diversity among Japanese local populations of an edible and medicinal coastal plant Glehnia littoralis F. Schmidt ex Miq.. Genetic Resources and Crop Evolution, 2022, 69, 85-97.	1.6	7
31	Classification of â€œnabanaâ€•(<i>Brassica rapa</i>) cultivars and landraces based on simple sequence repeat markers. Breeding Science, 2019, 69, 179-185.	1.9	6
32	Isolation and characterization of the pea cytochrome c oxidase Vb gene. Genome, 2006, 49, 1481-1489.	2.0	4
33	Development of simple sequence repeat markers for the classification of the clubroot pathogen Plasmodiophora brassicae. European Journal of Plant Pathology, 2017, 149, 733-738.	1.7	4
34	Quantitative Trait Locus Analysis in Squash (Cucurbita moschata) Based on Simple Sequence Repeat Markers and Restriction Site-Associated DNA Sequencing Analysis. Horticulturae, 2020, 6, 71.	2.8	3
35	Life Cycle and Genetic Diversity of Symplocarpus nipponicus (Araceae), an Endangered Species in Japan. Plants, 2018, 7, 73.	3.5	2
36	Molecular phylogeny and postharvest morphology of petals in two major Nelumbo nucifera cultivars in Thailand. Agriculture and Natural Resources, 2018, 52, 45-52.	0.1	2

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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	Parentage analysis of tea cultivars in Japan based on simple sequence repeat markers. Breeding Science, 2021, 71, 594-600.	1.9	2
39	Morphological and Genetic Diversities of Habenaria radiata (Orchidaceae) in the Kinki Area, Japan. International Journal of Molecular Sciences, 2021, 22, 311.	4.1	2
40	Classification of flowering lotus cultivars in Japan, including â€œOgura-ike group cultivarsâ€, based on SSR markers. Ikushugaku Kenkyu, 2015, 17, 45-54.	0.3	1
41	Control of clubroot disease on Hanana (flower nabana) using dry seaweed powders. Proceedings of the Kansai Plant Protection Society, 2021, 63, 13-20.	0.1	0