

# Yoshihiko Tsumura

## List of Publications by Year in descending order

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221  
papers

6,456  
citations

53660

45  
h-index

106150

65  
g-index

223  
all docs

223  
docs citations

223  
times ranked

3818  
citing authors

#	ARTICLE	IF	CITATIONS
1	Diversity and inheritance of inter-simple sequence repeat polymorphisms in Douglas-fir ( <i>Pseudotsuga</i> ) Tj ETQq1 1 0,784314 rgBT /Overl	1.8	228
2	Phylogenetic Relationships of Eurasian Pines ( <i>Pinus</i> , Pinaceae) Based on Chloroplast <i>rbcl</i> , <i>matK</i> , <i>rpl20-rps18</i> Spacer, and <i>trnV</i> Intron Sequences. <i>American Journal of Botany</i> , 1999, 86, 1742.	0.8	193
3	Molecular phytoeny of conifers using RFLP analysis of PCR-amplified specific chloroplast genes. <i>Theoretical and Applied Genetics</i> , 1995, 91, 1222-1236.	1.8	189
4	Intraspecific variation and phylogeographic patterns of <i>Fagus crenata</i> (Fagaceae) mitochondrial DNA. <i>American Journal of Botany</i> , 1998, 85, 629-636.	0.8	120
5	Phylogenetic relationships in Taxodiaceae and Cupressaceae sensu stricto based on <i>matK</i> gene, <i>chlL</i> gene, <i>trnL-trnF</i> IGS region, and <i>trnL</i> intron sequences. <i>American Journal of Botany</i> , 2000, 87, 1480-1488.	0.8	115
6	Estimation of gene flow in the tropical-rainforest tree <i>Neobalanocarpus heimii</i> (Dipterocarpaceae), inferred from paternity analysis. <i>Molecular Ecology</i> , 2000, 9, 1843-1852.	2.0	114
7	DNA sequence from a fossil pollen of <i>Abies</i> spp. from Pleistocene peat.. <i>Genes and Genetic Systems</i> , 1996, 71, 145-149.	0.2	107
8	The population demography of <i>Betula maximowicziana</i> , a cool-temperate tree species in Japan, in relation to the last glacial period: its admixture-like genetic structure is the result of simple population splitting not admixing. <i>Molecular Ecology</i> , 2015, 24, 1403-1418.	2.0	101
9	Prospects for genomic selection in conifer breeding: a simulation study of <i>Cryptomeria japonica</i> . <i>Tree Genetics and Genomes</i> , 2011, 7, 747-758.	0.6	100
10	18S rRNA Gene Variation among Common Airborne Fungi, and Development of Specific Oligonucleotide Probes for the Detection of Fungal Isolates. <i>Applied and Environmental Microbiology</i> , 2003, 69, 5389-5397.	1.4	92
11	Genetic diversity in <i>Fagus crenata</i> (Japanese beech): influence of the distributional shift during the late-Quaternary. <i>Heredity</i> , 1997, 78, 241-251.	1.2	91
12	Molecular phylogeny of Dipterocarpaceae in Southeast Asia using RFLP of PCR-amplified chloroplast genes. <i>Theoretical and Applied Genetics</i> , 1996, 93-93, 22-29.	1.8	87
13	Genetic Diversity and Outcrossing Rate between Undisturbed and Selectively Logged Forests of <i>Shorea curtisii</i> (Dipterocarpaceae) Using Microsatellite DNA Analysis. <i>International Journal of Plant Sciences</i> , 2002, 163, 151-158.	0.6	86
14	Development and polymorphism of simple sequence repeat DNA markers for <i>Shorea curtisii</i> and other Dipterocarpaceae species. <i>Heredity</i> , 1998, 81, 422-428.	1.2	83
15	Sequence-tagged-sites (STSs) of cDNA clones in <i>Cryptomeria japonica</i> and their evaluation as molecular markers in conifers. <i>Theoretical and Applied Genetics</i> , 1997, 94, 764-772.	1.8	78
16	Genome Scan to Detect Genetic Structure and Adaptive Genes of Natural Populations of <i>Cryptomeria japonica</i> . <i>Genetics</i> , 2007, 176, 2393-2403.	1.2	77
17	Microsatellite markers reveal high allelic variation in natural populations of <i>Cryptomeria japonica</i> near refugial areas of the last glacial period. <i>Journal of Plant Research</i> , 2005, 118, 83-90.	1.2	75
18	DNA Variation in a Conifer, <i>Cryptomeria japonica</i> (Cupressaceae sensu lato). <i>Genetics</i> , 2003, 164, 1547-1559.	1.2	71

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19	Selfing and inbreeding depression in seeds and seedlings of <i>Neobalanocarpus heimii</i> (Dipterocarpaceae). <i>Journal of Plant Research</i> , 2005, 118, 423-430.	1.2	70
20	Density-dependent selfing and its effects on seed performance in a tropical canopy tree species, <i>Shorea acuminata</i> (Dipterocarpaceae). <i>Forest Ecology and Management</i> , 2008, 256, 375-383.	1.4	70
21	A second generation framework for the analysis of microsatellites in expressed sequence tags and the development of EST-SSR markers for a conifer, <i>Cryptomeria japonica</i> . <i>BMC Genomics</i> , 2012, 13, 136.	1.2	69
22	A Consensus Linkage Map for Sugi ( <i>Cryptomeria japonica</i> ) From Two Pedigrees, Based on Microsatellites and Expressed Sequence Tags. <i>Genetics</i> , 2003, 165, 1551-1568.	1.2	69
23	Expression analysis of ESTs derived from the inner bark of <i>Cryptomeria japonica</i> . <i>Plant Molecular Biology</i> , 2000, 43, 451-457.	2.0	68
24	Molecular Phylogeny of Dipterocarpaceae in Southeast Asia Based on Nucleotide Sequences of <i>matK</i> , <i>trnL</i> Intron, and <i>trnL-trnF</i> Intergenic Spacer Region in Chloroplast DNA. <i>Molecular Phylogenetics and Evolution</i> , 1998, 10, 202-209.	1.2	67
25	Development and characterization of microsatellite markers for <i>Cryptomeria japonica</i> D. Don. <i>Theoretical and Applied Genetics</i> , 2003, 106, 751-758.	1.8	61
26	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
27	Genome scanning for detecting adaptive genes along environmental gradients in the Japanese conifer, <i>Cryptomeria japonica</i> . <i>Heredity</i> , 2012, 109, 349-360.	1.2	61
28	A linkage map for sugi ( <i>Cryptomeria japonica</i> ) based on RFLP, RAPD, and isozyme loci. <i>Theoretical and Applied Genetics</i> , 1995, 90, 835-840.	1.8	58
29	Development and polymorphism of microsatellite markers for <i>Fagus crenata</i> and the closely related species, <i>F. japonica</i> . <i>Theoretical and Applied Genetics</i> , 1999, 99, 11-15.	1.8	58
30	The construction of a high-density linkage map for identifying SNP markers that are tightly linked to a nuclear-recessive major gene for male sterility in <i>Cryptomeria japonica</i> D. Don. <i>BMC Genomics</i> , 2012, 13, 95.	1.2	57
31	Chloroplast DNA Inversion Polymorphism in Populations of <i>Abies</i> and <i>Tsuga</i> . <i>Molecular Biology and Evolution</i> , 2000, 17, 1302-1312.	3.5	56
32	Differentiation of Mitochondrial DNA Polymorphisms in Populations of Five Japanese <i>Abies</i> Species. <i>Evolution; International Journal of Organic Evolution</i> , 1998, 52, 1031.	1.1	53
33	Population differentiation and gene flow within a metapopulation of a threatened tree, <i>Magnolia stellata</i> (Magnoliaceae). <i>American Journal of Botany</i> , 2007, 94, 128-136.	0.8	53
34	Effects of flowering tree density on the mating system and gene flow in <i>Shorea leprosula</i> (Dipterocarpaceae) in Peninsular Malaysia. <i>Journal of Plant Research</i> , 2007, 120, 413-420.	1.2	53
35	Evidence for cryptic northern refugia in the last glacial period in <i>Cryptomeria japonica</i> . <i>Annals of Botany</i> , 2014, 114, 1687-1700.	1.4	53
36	Development and characterization of microsatellite markers for <i>Fagus crenata</i> Blume. <i>Molecular Ecology Notes</i> , 2004, 4, 101-103.	1.7	52

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37	Variation of paternal contribution in a seed orchard of <i>Cryptomeria japonica</i> determined using microsatellite markers. <i>Canadian Journal of Forest Research</i> , 2004, 34, 1683-1690.	0.8	52
38	AFLP and CAPS linkage maps of <i>Cryptomeria japonica</i> . <i>Theoretical and Applied Genetics</i> , 2000, 100, 825-831.	1.8	50
39	Development and characteristics of microsatellite markers for sugi ( <i>Cryptomeria japonica</i> D. Don) derived from microsatellite-enriched libraries. <i>Annals of Forest Science</i> , 2004, 61, 569-575.	0.8	50
40	Cleaved amplified polymorphic sequence markers in sugi, <i>Cryptomeria japonica</i> D. Don, and their locations on a linkage map. <i>Theoretical and Applied Genetics</i> , 2001, 103, 881-895.	1.8	49
41	Phylogeographic study based on intraspecific sequence variation of chloroplast DNA for the conservation of genetic diversity in the Japanese endangered species <i>Primula sieboldii</i> . <i>Biological Conservation</i> , 2004, 120, 211-220.	1.9	49
42	Paternity analysis-based inference of pollen dispersal patterns, male fecundity variation, and influence of flowering tree density and general flowering magnitude in two dipterocarp species. <i>Annals of Botany</i> , 2009, 104, 1421-1434.	1.4	48
43	Isolation and characterization of 20 microsatellite loci for an important tropical tree <i>Shorea leprosula</i> (Dipterocarpaceae) and their applicability to <i>S. parvifolia</i> . <i>Molecular Ecology Notes</i> , 2004, 4, 222-225.	1.7	47
44	Gene flow and mating system in five <i>Cryptomeria japonica</i> D. Don seed orchards as revealed by analysis of microsatellite markers. <i>Tree Genetics and Genomes</i> , 2005, 1, 174-183.	0.6	47
45	Molecular Phylogenetic Position of Japanese <i>Abies</i> (Pinaceae) Based on Chloroplast DNA Sequences. <i>Molecular Phylogenetics and Evolution</i> , 2000, 16, 271-277.	1.2	46
46	Spatial genetic structure among and within populations of <i>Primula sieboldii</i> growing beside separate streams. <i>Molecular Ecology</i> , 2004, 14, 149-157.	2.0	46
47	Genetic Differentiation and Evolutionary Adaptation in <i>Cryptomeria japonica</i> . <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 2389-2402.	0.8	46
48	Range shifts of <i>Potentilla fruticosa</i> on the Qinghai-Tibetan Plateau during glacial and interglacial periods revealed by chloroplast DNA sequence variation. <i>Heredity</i> , 2010, 104, 534-542.	1.2	45
49	Molecular Evolution of Nuclear Genes in Cupressaceae, a Group of Conifer Trees. <i>Molecular Biology and Evolution</i> , 2002, 19, 736-747.	3.5	44
50	Demonstration of Genome-Wide Association Studies for Identifying Markers for Wood Property and Male Strobili Traits in <i>Cryptomeria japonica</i> . <i>PLoS ONE</i> , 2013, 8, e79866.	1.1	44
51	Comparative Analysis of Expressed Sequence Tags of Conifers and Angiosperms Reveals Sequences Specifically Conserved in Conifers. <i>Plant Molecular Biology</i> , 2005, 59, 895-907.	2.0	42
52	Nuclear gene sequences and DNA variation of <i>Cryptomeria japonica</i> samples from the postglacial period. <i>Molecular Ecology</i> , 2003, 12, 859-868.	2.0	41
53	Microsatellite markers derived from <i>Quercus mongolica</i> var. <i>crispula</i> (Fagaceae) inner bark expressed sequence tags. <i>Genes and Genetic Systems</i> , 2008, 83, 179-187.	0.2	41
54	Genetic Differentiation and Genetic Diversity of <i>Castanopsis</i> (Fagaceae), the Dominant Tree Species in Japanese Broadleaved Evergreen Forests, Revealed by Analysis of EST-Associated Microsatellites. <i>PLoS ONE</i> , 2014, 9, e87429.	1.1	41

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55	Segregation distortion for AFLP markers in <i>Cryptomeria japonica</i> . <i>Genes and Genetic Systems</i> , 1999, 74, 55-59.	0.2	40
56	Effect of flowering phenology on pollen flow distance and the consequences for spatial genetic structure within a population of <i>Primula sieboldii</i> (Primulaceae). <i>American Journal of Botany</i> , 2006, 93, 226-233.	0.8	40
57	Comparison of the fine-scale genetic structure of three dipterocarp species. <i>Heredity</i> , 2004, 92, 323-328.	1.2	38
58	Molecular database for classifying <i>Shorea</i> species (Dipterocarpaceae) and techniques for checking the legitimacy of timber and wood products. <i>Journal of Plant Research</i> , 2011, 124, 35-48.	1.2	37
59	Genetic structure within a Japanese stone pine ( <i>Pinus pumila</i> regel) population on Mt. Aino-dake in central Honshu, Japan. <i>Journal of Plant Research</i> , 1998, 111, 7-15.	1.2	36
60	Genetic diversity of <i>Cryptomeria japonica</i> using co-dominant DNA markers based on sequenced-tagged sites. <i>Theoretical and Applied Genetics</i> , 1999, 98, 396-404.	1.8	36
61	Heterogeneous genetic structure in a <i>Fagus crenata</i> population in an old-growth beech forest revealed by microsatellite markers. <i>Molecular Ecology</i> , 2004, 13, 1241-1250.	2.0	36
62	Regeneration system and genetic diversity of <i>Cryptomeria japonica</i> growing at different altitudes. <i>Canadian Journal of Forest Research</i> , 1997, 27, 447-452.	0.8	35
63	Genetic structure of island populations of <i>Prunus lannesiana</i> var. <i>speciosa</i> revealed by chloroplast DNA, AFLP and nuclear SSR loci analyses. <i>Journal of Plant Research</i> , 2011, 124, 11-23.	1.2	35
64	Genetic structure of geographical marginal populations of <i>Cryptomeria japonica</i> . <i>Canadian Journal of Forest Research</i> , 1993, 23, 859-863.	0.8	34
65	Half-sib family structure of <i>Fagus crenata</i> saplings in an old-growth beech-dwarf bamboo forest. <i>Molecular Ecology</i> , 2005, 14, 2565-2575.	2.0	34
66	Extended Linkage Disequilibrium in Noncoding Regions in a Conifer, <i>Cryptomeria japonica</i> . <i>Genetics</i> , 2012, 190, 1145-1148.	1.2	34
67	Phylogenetic relationships of Eurasian pines ( <i>Pinus</i> , Pinaceae) based on chloroplast <i>rbcl</i> , <i>MATK</i> , <i>RPL20-RPS18</i> spacer, and <i>TRNV</i> intron sequences. <i>American Journal of Botany</i> , 1999, 86, 1742-53.	0.8	34
68	A cline of allozyme variation in <i>Abies mariesii</i> . <i>Journal of Plant Research</i> , 1997, 110, 219-226.	1.2	33
69	A high-density linkage map with 2560 markers and its application for the localization of the male-sterile genes <i>ms3</i> and <i>ms4</i> in <i>Cryptomeria japonica</i> D. Don. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	33
70	Nuclear and chloroplast DNA phylogeography reveals Pleistocene divergence and subsequent secondary contact of two genetic lineages of the tropical rainforest tree species <i>Shorea leprosula</i> (Dipterocarpaceae) in Southeast Asia. <i>Molecular Ecology</i> , 2013, 22, 2264-2279.	2.0	32
71	Genetic diversity and differentiation of <i>Taxodium</i> in the south-eastern United States using cleaved amplified polymorphic sequences. <i>Heredity</i> , 1999, 83, 229-238.	1.2	31
72	Microsatellite Analysis of the Breeding System and Seed Dispersal in <i>Shorea leprosula</i> (Dipterocarpaceae). <i>International Journal of Plant Sciences</i> , 2001, 162, 155-159.	0.6	31

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73	Climate, not Aboriginal landscape burning, controlled the historical demography and distribution of fire-sensitive conifer populations across Australia. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2013, 280, 20132182.	1.2	31
74	Detection of quantitative trait loci for juvenile growth, flower bearing and rooting ability based on a linkage map of sugi ( <i>Cryptomeria japonica</i> D. Don). <i>Theoretical and Applied Genetics</i> , 1998, 97, 45-50.	1.8	30
75	DIFFERENTIATION OF MITOCHONDRIAL DNA POLYMORPHISMS IN POPULATIONS OF FIVE JAPANESE <i>ABIES</i> SPECIES. <i>Evolution; International Journal of Organic Evolution</i> , 1998, 52, 1031-1042.	1.1	30
76	Gene flow and inbreeding depression inferred from fine-scale genetic structure in an endangered heterostylous perennial, <i>Primula sieboldii</i> . <i>Molecular Ecology</i> , 2005, 14, 983-990.	2.0	30
77	Tracing the origins of stocks of the endangered species <i>Primula sieboldii</i> using nuclear microsatellites and chloroplast DNA. <i>Conservation Genetics</i> , 2008, 9, 1139-1147.	0.8	30
78	Recent distribution changes affect geographic clines in genetic diversity and structure of <i>Pinus densiflora</i> natural populations in Japan. <i>Forest Ecology and Management</i> , 2013, 304, 407-416.	1.4	30
79	Genetic Relationship among East and South Asian Melon ( <i>Cucumis melo</i> L.) Revealed by AFLP Analysis. <i>Breeding Science</i> , 2005, 55, 197-206.	0.9	29
80	Genetic diversity and the genetic structure of natural populations of <i>Chamaecyparis obtusa</i> : implications for management and conservation. <i>Heredity</i> , 2007, 99, 161-172.	1.2	28
81	Size-related flowering and fecundity in the tropical canopy tree species, <i>Shorea acuminata</i> (Dipterocarpaceae) during two consecutive general flowerings. <i>Journal of Plant Research</i> , 2008, 121, 33-42.	1.2	28
82	Population Genetic Diversity and Structure of Ancient Tree Populations of <i>Cryptomeria japonica</i> var. <i>sinensis</i> Based on RAD-seq Data. <i>Forests</i> , 2020, 11, 1192.	0.9	28
83	Genetic Variation and Population Differentiation in Natural Populations of <i>Cryptomeria japonica</i> . <i>Plant Species Biology</i> , 1994, 9, 191-199.	0.6	27
84	EVIDENCE FOR INTROGRESSIVE HYBRIDIZATION BASED ON CHLOROPLAST DNA POLYMORPHISMS AND MORPHOLOGICAL VARIATION IN WILD EVERGREEN AZALEA POPULATIONS OF THE KIRISHIMA MOUNTAINS, JAPAN. <i>Edinburgh Journal of Botany</i> , 2000, 57, 209-219.	0.4	27
85	Development of ten microsatellite markers for <i>Quercus mongolica</i> var. <i>crispula</i> by database mining. <i>Conservation Genetics</i> , 2008, 9, 1083-1085.	0.8	27
86	Development of microsatellite markers in <i>Primula sieboldii</i> E. Morren, a threatened Japanese perennial herb. <i>Conservation Genetics</i> , 2003, 4, 809-811.	0.8	26
87	Genetic structure of <i>Cerasus jamasakura</i> , a Japanese flowering cherry, revealed by nuclear SSRs: implications for conservation. <i>Journal of Plant Research</i> , 2009, 122, 367-375.	1.2	26
88	Evidence of intense chromosomal shuffling during conifer evolution. <i>Genome Biology and Evolution</i> , 2015, 7, evv185.	1.1	26
89	Geographical cline of chloroplast DNA variation in <i>Abies mariesii</i> . <i>Theoretical and Applied Genetics</i> , 1994, 89-89, 922-926.	1.8	25
90	The phylogeographic structure of Japanese coniferous species as revealed by genetic markers. <i>Taxon</i> , 2006, 55, 53-66.	0.4	25

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91	Management units of the endangered herb <i>Primula sieboldii</i> based on microsatellite variation among and within populations throughout Japan. <i>Conservation Genetics</i> , 2009, 10, 257-267.	0.8	25
92	Molecular phylogeny of Dipterocarpaceae in Southeast Asia using RFLP of PCR-amplified chloroplast genes*. <i>Theoretical and Applied Genetics</i> , 1996, 93, 22-29.	1.8	25
93	Provenance tests for survival and growth of 50-year-old Japanese larch ( <i>Larix kaempferi</i> ) trees related to climatic conditions in central Japan. <i>Tree Genetics and Genomes</i> , 2014, 10, 87-99.	0.6	23
94	Genetic diversity of nuclear and mitochondrial genomes in <i>Pinus parviflora</i> Sieb. & Zucc. (Pinaceae) populations. <i>Heredity</i> , 2003, 91, 510-518.	1.2	22
95	Development of microsatellite markers in <i>Magnolia stellata</i> (Magnoliaceae), a threatened Japanese tree. <i>Conservation Genetics</i> , 2005, 6, 317-320.	0.8	22
96	Effects of genetic and environmental factors on clonal reproduction in old-growth natural populations of <i>Cryptomeria japonica</i> . <i>Forest Ecology and Management</i> , 2013, 304, 10-19.	1.4	22
97	Establishment of a microsatellite panel covering the sugi ( <i>Cryptomeria japonica</i> ) genome, and its application for localization of a male-sterile gene ( <i>ms-2</i> ). <i>Molecular Breeding</i> , 2014, 33, 315-325.	1.0	22
98	Approximate Bayesian computation analysis of EST-associated microsatellites indicates that the broadleaved evergreen tree <i>Castanopsis sieboldii</i> survived the Last Glacial Maximum in multiple refugia in Japan. <i>Heredity</i> , 2019, 122, 326-340.	1.2	22
99	Analysis of Expressed Sequence Tags Derived from Developing Seed and Pollen Cones of <i>Cryptomeria japonica</i> . <i>Plant Biology</i> , 2003, 5, 600-607.	1.8	21
100	Genetic structure of <i>Miscanthus sinensis</i> ssp. <i>condensatus</i> (Poaceae) on Miyake Island: implications for revegetation of volcanically devastated sites. <i>Ecological Research</i> , 2005, 20, 233-238.	0.7	21
101	Single nucleotide polymorphisms in <i>Cryptomeria japonica</i> : their discovery and validation for genome mapping and diversity studies. <i>Tree Genetics and Genomes</i> , 2012, 8, 1213-1222.	0.6	21
102	Development of microsatellite markers in the tropical tree <i>Neobalanocarpus heimii</i> (Dipterocarpaceae). <i>Molecular Ecology</i> , 2000, 9, 1684-1685.	2.0	20
103	Adaptive and Slightly Deleterious Evolution in a Conifer, <i>Cryptomeria japonica</i> . <i>Journal of Molecular Evolution</i> , 2008, 67, 201-210.	0.8	20
104	Development of 14 EST-SSRs for <i>Betula maximowicziana</i> and their applicability to related species. <i>Conservation Genetics</i> , 2009, 10, 661-664.	0.8	20
105	Generation de marqueurs de séquences exprimées et développement de marqueurs microsatellites pour <i>Castanopsis sieboldii</i> var. <i>sieboldii</i> (Fagaceae). <i>Annals of Forest Science</i> , 2009, 66, 509-509.	0.8	20
106	Genetic diversity and structure of natural fragmented <i>Chamaecyparis obtusa</i> populations as revealed by microsatellite markers. <i>Journal of Plant Research</i> , 2010, 123, 689-699.	1.2	20
107	Identification and genetic diversity analysis of a male-sterile gene ( <i>MS1</i> ) in Japanese cedar ( <i>Cryptomeria</i> ) Tj ETQq1	1.0784314	20
108	Application of a simplified method of chloroplast enrichment to small amounts of tissue for chloroplast genome sequencing. <i>Applications in Plant Sciences</i> , 2017, 5, 1700002.	0.8	19

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109	Phylogenetic relationships in Taxodiaceae and Cupressaceae sensu stricto based on matK gene, chlL gene, trnL-trnF IGS region, and trnL intron sequences. <i>American Journal of Botany</i> , 2000, 87, 1480-8.	0.8	19
110	Genetic Control of Isozyme Variation in Needle Tissues of <i>Cryptomeria japonica</i> . <i>Journal of Heredity</i> , 1989, 80, 291-297.	1.0	18
111	Fine-scale spatial structure of genets and sexes in the dioecious plant <i>Dioscorea japonica</i> , which disperses by both bulbils and seeds. <i>Evolutionary Ecology</i> , 2010, 24, 1399-1415.	0.5	18
112	Scanning RNA-Seq and RAD-Seq approach to develop SNP markers closely linked to <i>MALE STERILITY 1</i> (<i>MS1</i>) in <i>Cryptomeria japonica</i>. <i>Breeding Science</i> , 2019, 69, 19-29.	0.9	18
113	Isolation and characterization of highly polymorphic microsatellites in the aquatic plant, <i>Nymphoides peltata</i> (Menyanthaceae). <i>Molecular Ecology Notes</i> , 2005, 5, 343-345.	1.7	17
114	Distribution of S-alleles in island populations of flowering cherry, <i>Prunus lannesiana</i> var. <i>speciosa</i> . <i>Genes and Genetic Systems</i> , 2007, 82, 65-75.	0.2	17
115	Enhanced hybridization rates in a <i>Larix gmelinii</i> var. <i>japonica</i> × <i>L. kaempferi</i> interspecific seed orchard with a single maternal clone revealed by cytoplasmic DNA markers. <i>Tree Genetics and Genomes</i> , 2008, 4, 637-645.	0.6	17
116	Population genetic structure and the effect of historical human activity on the genetic variability of <i>Cryptomeria japonica</i> core collection, in Japan. <i>Tree Genetics and Genomes</i> , 2014, 10, 1257-1270.	0.6	17
117	Development of EST-SSR markers for <i>Taxus cuspidata</i> from publicly available transcriptome sequences. <i>Biochemical Systematics and Ecology</i> , 2015, 63, 20-26.	0.6	17
118	TodoFirGene: Developing Transcriptome Resources for Genetic Analysis of <i>Abies sachalinensis</i> . <i>Plant and Cell Physiology</i> , 2018, 59, 1276-1284.	1.5	17
119	Genetic diversity and the origin of commercial plantation of Indonesian teak on Java Island. <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	0.6	17
120	Highly polymorphic microsatellite markers in <i>Chamaecyparis obtusa</i> . <i>Canadian Journal of Forest Research</i> , 2001, 31, 2248-2251.	0.8	16
121	Evaluation of cleaved amplified polymorphic sequence markers for <i>Chamaecyparis obtusa</i> based on expressed sequence tag information from <i>Cryptomeria japonica</i> . <i>Theoretical and Applied Genetics</i> , 2004, 110, 80-91.	1.8	16
122	Contrasting patterns of DNA variation in natural populations of two related conifers, <i>Cryptomeria japonica</i> and <i>Taxodium distichum</i> (Cupressaceae sensu lato). <i>Genes and Genetic Systems</i> , 2006, 81, 103-113.	0.2	16
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