List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Genetic diversity and differentiation among populations of the pedunculate oak (Quercus robur) at the eastern margin of its range based on a new set of 95 SNP loci. Journal of Forestry Research, 2021, 32, 2237-2243.	3.6	4
2	Development of D-Loop mitochondrial markers for amplification of prey DNA from wolf scat. Conservation Genetics Resources, 2021, 13, 1-4.	0.8	2
3	Development of new SNP and INDEL loci for the valuable African timber species Lophira alata. Conservation Genetics Resources, 2021, 13, 85-87.	0.8	2
4	Applying targeted genotyping by sequencing with a new set of nuclear and plastid SNP and indel loci for Quercus robur and Quercus petraea. Conservation Genetics Resources, 2021, 13, 345-347.	0.8	11
5	When does habitat fragmentation lead to changes in populations gene pool of pedunculate oak (Quercus robur L.)?. Forest Ecology and Management, 2021, 499, 119617.	3.2	4
6	Genetic comparison of planted and natural <i>Quercus robur</i> stands in Russia. Silvae Genetica, 2021, 70, 1-8.	0.8	3
7	Impact of Gene Flow and Introgression on the Range Wide Genetic Structure of Quercus robur (L.) in Europe. Forests, 2021, 12, 1425.	2.1	13
8	Nuclear and plastid SNP markers for tracing Cedrela timber in the tropics. Conservation Genetics Resources, 2020, 12, 239-244.	0.8	4
9	Development of SNP markers for the African timber species Nauclea diderrichii. Conservation Genetics Resources, 2020, 12, 357-359.	0.8	0
10	Development of nuclear SNP markers for Mahogany (Swietenia spp.). Conservation Genetics Resources, 2020, 12, 585-587.	0.8	1
11	SNP Markers as a Successful Molecular Tool for Assessing Species Identity and Geographic Origin of Trees in the Economically Important South American Legume Genus <i>Dipteryx</i> . Journal of Heredity, 2020, 111, 346-356.	2.4	6
12	Development of new SNPs loci on Quercus robur and Quercus petraea for genetic studies covering the whole species' distribution range. Conservation Genetics Resources, 2020, 12, 597-600.	0.8	8
13	Nuclear and plastidial SNP and INDEL markers for genetic tracking studies of Jacaranda copaia. Conservation Genetics Resources, 2019, 11, 341-343.	0.8	7
14	Genetic diversity and differentiation among the species of African mahogany (Khaya spp.) based on a large SNP array. Conservation Genetics, 2019, 20, 1035-1044.	1.5	7
15	Development of nuclear and plastid SNP and INDEL markers for population genetic studies and timber traceability of Carapa species. Conservation Genetics Resources, 2019, 11, 337-339.	0.8	4
16	Nuclear and chloroplastic SNP markers for genetic studies of timber origin for Hymenaea trees. Conservation Genetics Resources, 2019, 11, 329-331.	0.8	8
17	Development of nuclear and plastid SNP markers for genetic studies of Dipteryx tree species in Amazonia. Conservation Genetics Resources, 2019, 11, 333-336.	0.8	11
18	Genetic differentiation of <i>Quercus robur</i> in the South-Ural. Silvae Genetica, 2019, 68, 111-115.	0.8	10

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19	Short note: Development of a new set of SNP markers to measure genetic diversity and genetic differentiation of Mongolian oak (Quercus monÂgolica Fisch. ex Ledeb.) in the Far East of Russia. Silvae Genetica, 2019, 68, 85-91.	0.8	2
20	Assessing the Ability of Chloroplast and Nuclear DNA Gene Markers to Verify the Geographic Origin of Jatoba (Hymenaea courbaril L.) Timber. Journal of Heredity, 2018, 109, 543-552.	2.4	11
21	Development of a set of SNP markers for population genetics studies of Ipe (Handroanthus sp.), a valuable tree genus from Latin America. Conservation Genetics Resources, 2018, 10, 779-781.	0.8	13
22	A set of SNP markers for timber tracking of Larix spp. in Europe and Russia. Forestry, 2018, 91, 614-628.	2.3	20
23	Complete Chloroplast Genome Sequences of Four Meliaceae Species and Comparative Analyses. International Journal of Molecular Sciences, 2018, 19, 701.	4.1	37
24	Development of nuclear SNP markers for the timber tracking of the African tree species Sapelli, Entandrophragma cylindricum. Conservation Genetics Resources, 2018, 10, 539-541.	0.8	10
25	A nearest neighbour approach by genetic distance to the assignment of individual trees to geographic origin. Forensic Science International: Genetics, 2017, 27, 132-141.	3.1	16
26	DNA taxonomy in the timber genus Milicia: evidence of unidirectional introgression in the West African contact zone. Tree Genetics and Genomes, 2017, 13, 1.	1.6	8
27	Opportunities for Improved Transparency in the Timber Trade through Scientific Verification. BioScience, 2016, 66, 990-998.	4.9	60
28	Development of Molecular Markers for Determining Continental Origin of Wood from White Oaks (Quercus L. sect. Quercus). PLoS ONE, 2016, 11, e0158221.	2.5	34
29	Revealing hidden species diversity in closely related species using nuclear SNPs, SSRs and DNA sequences – a case study in the tree genus Milicia. BMC Evolutionary Biology, 2016, 16, 259.	3.2	36
30	Development of nuclear, chloroplast and mitochondrial SNP markers for Khaya sp Conservation Genetics Resources, 2016, 8, 283-297.	0.8	13
31	Genetics and Tropical Forests. , 2016, , 885-920.		1
32	Forensic timber identification: It's time to integrate disciplines to combat illegal logging. Biological Conservation, 2015, 191, 790-798.	4.1	176
33	Genetics and Tropical Forests. , 2014, , 1-30.		16
34	Development of DNA-based methods to identify CITES-protected timber species: a case study in the Meliaceae family. Holzforschung, 2012, 66, .	1.9	14
35	Mating patterns and pollen dispersal in four contrasting wild cherry populations (Prunus avium L.). European Journal of Forest Research, 2012, 131, 1055-1069.	2.5	13
36	Spatial genetic structure in wild cherry (Prunus avium L.): I. variation among natural populations of different density. Tree Genetics and Genomes, 2011, 7, 271-283.	1.6	18

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37	Spatial genetic structure in wild cherry (Prunus avium L.): II. Effect of density and clonal propagation on spatial genetic structure based on simulation studies. Tree Genetics and Genomes, 2011, 7, 541-552.	1.6	11
38	Forest ecosystem genomics and adaptation: EVOLTREE conference report. Tree Genetics and Genomes, 2011, 7, 869-875.	1.6	7
39	Efficient Long-Distance Gene Flow into an Isolated Relict Oak Stand. Journal of Heredity, 2011, 102, 464-472.	2.4	82
40	Geographic Influence on Genetic Structure in the Widespread Neotropical Tree Simarouba amara (Simaroubaceae). Tropical Plant Biology, 2010, 3, 28-39.	1.9	22
41	Genetic variation for growth, morphological, and physiological traits in a wild population of the Neotropical shadeAtolerant rainforest tree Sextonia rubra (Mez) van der Werff (Lauraceae). Tree Genetics and Genomes, 2010, 6, 319-329.	1.6	14
42	A Very Small and Isolated Population of the Green Oak Leaf Roller, Tortrix viridana L., with High Genetic Diversity—How Does This Work?. Journal of Heredity, 2010, 101, 780-783.	2.4	5
43	Modelling exploration of the future of European beech (Fagus sylvatica L.) under climate change—Range, abundance, genetic diversity and adaptive response. Forest Ecology and Management, 2010, 259, 2213-2222.	3.2	206
44	Use of DNA-Fingerprints to Control the Origin of Forest Reproductive Material. Silvae Genetica, 2010, 59, 268-273.	0.8	9
45	High levels of pollen dispersal detected through paternity analysis from a continuous Symphonia globulifera population in the Brazilian Amazon. Forest Ecology and Management, 2009, 258, 1260-1266.	3.2	27
46	Spatial genetic structure in populations of the green oak leaf roller, Tortrix viridana L. (Lepidoptera,) Tj ETQq0 0 C) rgBT /Ovo 2.5	erlock 10 Tf 5
47	Modelling the long-term impacts of selective logging on genetic diversity and demographic structure of four tropical tree species in the Amazon forest. Forest Ecology and Management, 2008, 254, 335-349.	3.2	96
48	Genetic structure of the green oak leaf roller (Tortrix viridana L.) and one of its hosts, Quercus robur L Forest Ecology and Management, 2008, 256, 1270-1279.	3.2	15
49	Low Inbreeding and High Pollen Dispersal Distances in Populations of Two Amazonian Forest Tree Species. Biotropica, 2007, 39, 406-415.	1.6	20
50	Low Interannual Variation of Mating System and Gene Flow of Symphonia globulifera in the Brazilian Amazon. Biotropica, 2007, 39, 628-636.	1.6	29
51	An assessment of heterozygosity and fitness in Chir pine (Pinus roxburghii Sarg.) using isozymes. New Forests, 2007, 34, 153-162.	1.7	6
52	Fine-scale genetic structure and gene dispersal inferences in 10 Neotropical tree species. Molecular Ecology, 2005, 15, 559-571.	3.9	277
53	Effects of Animal Pollination on Pollen Dispersal, Selfing, and Effective Population Size of Tropical Trees: A Simulation Study. Biotropica, 2004, 36, 165-179.	1.6	32
54	Fine-scale spatial genetic structure of eight tropical tree species as analysed by RAPDs. Heredity, 2001, 87, 497-507.	2.6	58

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55	Comparative study of genetic variation and differentiation of two pedunculate oak (Quercus robur) stands using microsatellite and allozyme loci. Heredity, 1999, 83, 597-603.	2.6	48
56	Large-scale genetic structure of <i>Quercus robur</i> in its eastern distribution range enables assignment of unknown seed sources. Forestry, 0, , .	2.3	0
57	<i>Khaya</i> revisited: Genetic markers and morphological analysis reveal six species in the widespread taxon <i>K.Âanthotheca</i> . Taxon, 0, , .	0.7	2