Giovanni G Vendramin

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2356989/publications.pdf

Version: 2024-02-01

201 papers

14,421 citations

59 h-index 24258 110 g-index

207 all docs

207 docs citations

times ranked

207

12674 citing authors

#	Article	IF	CITATIONS
1	Glacial Refugia: Hotspots But Not Melting Pots of Genetic Diversity. Science, 2003, 300, 1563-1565.	12.6	1,569
2	The GenTree Dendroecological Collection, tree-ring and wood density data from seven tree species across Europe. Scientific Data, 2020, 7, 1.	5.3	830
3	INVITED REVIEW: Comparative organization of chloroplast, mitochondrial and nuclear diversity in plant populations. Molecular Ecology, 2004, 14, 689-701.	3.9	790
4	A new scenario for the Quaternary history of European beech populations: palaeobotanical evidence and genetic consequences. New Phytologist, 2006, 171, 199-221.	7.3	757
5	Polymorphic simple sequence repeat regions in chloroplast genomes: applications to the population genetics of pines Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 7759-7763.	7.1	453
6	Chloroplast DNA variation and postglacial recolonization of common ash (Fraxinus excelsior L.) in Europe. Molecular Ecology, 2004, 13, 3437-3452.	3.9	248
7	Can Population Genetic Structure Be Predicted from Lifeâ€History Traits?. American Naturalist, 2007, 169, 662-672.	2.1	235
8	Imprints of glacial refugia in the modern genetic diversity of Pinus sylvestris. Global Ecology and Biogeography, 2006, 15, 271-282.	5.8	218
9	The distribution of <i>Quercus suber</i> chloroplast haplotypes matches the palaeogeographical history of the western Mediterranean. Molecular Ecology, 2007, 16, 5259-5266.	3.9	193
10	A consensus list of microsatellite markers for olive genotyping. Molecular Breeding, 2009, 24, 213-231.	2.1	188
11	Molecular Footprints of Local Adaptation in Two Mediterranean Conifers. Molecular Biology and Evolution, 2011, 28, 101-116.	8.9	172
12	Limited genetic variability and phenotypic plasticity detected for cavitation resistance in a <scp>M</scp> editerranean pine. New Phytologist, 2014, 201, 874-886.	7.3	170
13	Tree endurance on the Tibetan Plateau marks the world's highest known tree line of the Last Glacial Maximum. New Phytologist, 2010, 185, 332-342.	7. 3	163
14	Cross-species transferability and mapping of genomic and cDNA SSRs in pines. Theoretical and Applied Genetics, 2004, 109, 1204-1214.	3.6	153
15	High level of variation at Abies alba chloroplast microsatellite loci in Europe. Molecular Ecology, 1999, 8, 1117-1126.	3.9	147
16	Chloroplast microsatellites reveal population genetic diversity in red pine, Pinus resinosa Ait Molecular Ecology, 1998, 7, 307-316.	3.9	142
17	NUCLEAR MICROSATELLITES REVEAL CONTRASTING PATTERNS OF GENETIC STRUCTURE BETWEEN WESTERN AND SOUTHEASTERN EUROPEAN POPULATIONS OF THE COMMON ASH (FRAXINUS EXCELSIOR L.). Evolution; International Journal of Organic Evolution, 2004, 58, 976-988.	2.3	136
18	Genome–environment association study suggests local adaptation to climate at the regional scale in <i>Fagus sylvatica</i> . New Phytologist, 2016, 210, 589-601.	7.3	132

#	Article	IF	CITATIONS
19	Chloroplast DNA phylogeography of European ashes, Fraxinus sp. (Oleaceae): roles of hybridization and life history traits. Molecular Ecology, 2006, 15, 2131-2140.	3.9	131
20	Range-wide phylogeography and gene zones in Pinus pinaster Ait. revealed by chloroplast microsatellite markers. Molecular Ecology, 2007, 16, 2137-2153.	3.9	129
21	Complete Chloroplast Genome of the Multifunctional Crop Globe Artichoke and Comparison with Other Asteraceae. PLoS ONE, 2015, 10, e0120589.	2.5	129
22	Chloroplast DNA variation, postglacial recolonization and hybridization in hazel, Corylus avellana. Molecular Ecology, 2002, 11, 1769-1779.	3.9	128
23	GENETICALLY DEPAUPERATE BUT WIDESPREAD: THE CASE OF AN EMBLEMATIC MEDITERRANEAN PINE. Evolution; International Journal of Organic Evolution, 2008, 62, 680-688.	2.3	128
24	The role of forest genetic resources in responding to biotic and abiotic factors in the context of anthropogenic climate change. Forest Ecology and Management, 2014, 333, 76-87.	3.2	125
25	Distribution of genetic diversity in Pinus pinaster Ait. as revealed by chloroplast microsatellites. Theoretical and Applied Genetics, 1998, 97, 456-463.	3.6	123
26	Combined analysis of nuclear and mitochondrial markers provide new insight into the genetic structure of North European Picea abies. Heredity, 2009, 102, 549-562.	2.6	121
27	Tandem repeats in plant mitochondrial genomes: application to the analysis of population differentiation in the conifer Norway spruce. Molecular Ecology, 2001, 10, 257-263.	3.9	110
28	Genomics of Fagaceae. Tree Genetics and Genomes, 2012, 8, 583-610.	1.6	109
29	Morphological and Molecular Differentiation between Quercus petraea(Matt.) Liebl. and Quercus pubescens Willd. (Fagaceae) in Northern and Central Italy. Annals of Botany, 2000, 85, 325-333.	2.9	108
30	Chloroplast DNA polymorphism reveals little geographical structure in Castanea sativa Mill. (Fagaceae) throughout southern European countries. Molecular Ecology, 2000, 9, 1495-1503.	3.9	106
31	Evolution-based approach needed for the conservation and silviculture of peripheral forest tree populations. Forest Ecology and Management, 2016, 375, 66-75.	3.2	97
32	Genetic effects of chronic habitat fragmentation revisited: Strong genetic structure in a temperate tree, <i>Taxus baccata</i> (Taxaceae), with great dispersal capability. American Journal of Botany, 2010, 97, 303-310.	1.7	94
33	Morphological and Molecular Diversity Among Italian Populations of Quercus petraea (Fagaceae). Annals of Botany, 2003, 91, 707-716.	2.9	92
34	High Rates of Gene Flow by Pollen and Seed in Oak Populations across Europe. PLoS ONE, 2014, 9, e85130.	2.5	92
35	Detection of haplotypic variation and natural hybridization inhalepensis-complex pine species using chloroplast simple sequence repeat (SSR) markers. Molecular Ecology, 1998, 7, 1633-1643.	3.9	90
36	Comparative phylogeography and population structure of European Betula species, with particular focus on B. pendula and B. pubescens. Journal of Biogeography, 2007, 34, 1601-1610.	3.0	88

#	Article	lF	CITATIONS
37	Genetic Biodiversity of Italian Olives (<i>Olea europaea</i>) Germplasm Analyzed by SSR Markers. Scientific World Journal, The, 2014, 2014, 1-12.	2.1	87
38	Genetic and Phylogeographic Structures of the Symbiotic Fungus Tuber magnatum. Applied and Environmental Microbiology, 2005, 71, 6584-6589.	3.1	84
39	Putative glacial refugia of <i>Cedrus atlantica</i> deduced from Quaternary pollen records and modern genetic diversity. Journal of Biogeography, 2009, 36, 1361-1371.	3.0	84
40	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 October 2009–30 November 2009. Molecular Ecology Resources, 2010, 10, 404-408.	4.8	84
41	Characterisation and inheritance of polymorphic plastid microsatellites in Abies. Genome, 1997, 40, 857-864.	2.0	81
42	Characterization of microsatellite markers in Fagus sylvatical. and Fagus orientalis Lipsky. Molecular Ecology Notes, 2003, 3, 76-78.	1.7	81
43	Analysis of spatial genetic structure in an expanding Pinus halepensis population reveals development of fine-scale genetic clustering over time. Molecular Ecology, 2006, 15, 3617-3630.	3.9	79
44	Molecular Proxies for Climate Maladaptation in a Long-Lived Tree (<i>Pinus pinaster</i> Aiton,) Tj ETQq0 0 0 rgBT	19verlock	2 10 Tf 50 46
45	Genetic variation at chloroplast microsatellites (cpSSRs) in Abies nebrodensis (Lojac.) Mattei and three neighboring Abies species. Theoretical and Applied Genetics, 2001, 102, 733-740.	3.6	72
46	Chloroplast DNA variation of white oaks in Italy. Forest Ecology and Management, 2002, 156, 103-114.	3.2	72
47	Plant phylogeography based on organelle genes: an introduction. , 2007, , 23-97.		72
48	Genetic diversity and differentiation in European beech (Fagus sylvatica L.) stands varying in management history. Forest Ecology and Management, 2007, 247, 98-106.	3.2	71
49	Geography determines genetic relationships between species of mountain pine (<i>Pinus mugo</i>) Tj ETQq $1\ 1$	0.784314 3.0	rgBT /Overlo
50	Spatial genetic structure in continuous and fragmented populations of <i>Pinus pinaster</i> Aiton. Molecular Ecology, 2009, 18, 4564-4576.	3.9	69
51	<i>InÂsitu</i> genetic association for serotiny, a fireâ€related trait, in Mediterranean maritime pine (<i>Pinus pinaster</i>). New Phytologist, 2014, 201, 230-241.	7.3	69
52	Spatial genetic structure of Taxus baccata L. in the western Mediterranean Basin: Past and present limits to gene movement over a broad geographic scale. Molecular Phylogenetics and Evolution, 2010, 55, 805-815.	2.7	67
53	Multispecies genetic structure and hybridization in the <i>Betula</i> genus across Eurasia. Molecular Ecology, 2017, 26, 589-605.	3.9	67
54	Bridging the gap between ecophysiological and genetic knowledge to assess the adaptive potential of European beech. Ecological Modelling, 2008, 216, 333-353.	2.5	66

#	Article	IF	CITATIONS
55	Patterns of polymorphism resulting from longâ€range colonization in the Mediterranean conifer Aleppo pine. New Phytologist, 2009, 184, 1016-1028.	7.3	66
56	Genetic diversity and differentiation of two Mediterranean pines (Pinus halepensis Mill. and Pinus) Tj ETQq $000r$ Distributions, 2005, $11, 257-263$.	gBT /Overlo 4.1	ock 10 Tf 50 65
57	Is <i>Cupressus sempervirens</i> native in Italy? An answer from genetic and palaeobotanical data. Molecular Ecology, 2009, 18, 2276-2286.	3.9	65
58	Permanent Genetic Resources added to Molecular Ecology Resources database 1 January 2009–30 April 2009. Molecular Ecology Resources, 2009, 9, 1375-1379.	4.8	64
59	Evidence of divergent selection for drought and cold tolerance at landscape and local scales in <i>Abies alba</i> Mill. in the French Mediterranean Alps. Molecular Ecology, 2016, 25, 776-794.	3.9	64
60	The Strait of Gibraltar as a major biogeographic barrier in Mediterranean conifers: a comparative phylogeographic survey. Molecular Ecology, 2010, 19, 5452-5468.	3.9	63
61	Adapting through glacial cycles: insights from a longâ€lived tree (<i>Taxus baccata</i>). New Phytologist, 2015, 208, 973-986.	7.3	63
62	Allozyme, chloroplast DNA and RAPD markers for determining genetic relationships between Abies alba and the relic population of Abies nebrodensis. Theoretical and Applied Genetics, 1995, 90, 1012-1018.	3.6	61
63	Delineation of genetic zones in the European Norway spruce natural range: preliminary evidence. Molecular Ecology, 2000, 9, 923-934.	3.9	61
64	A RAPD, AFLP and SSR linkage map, and QTL analysis in European beech (Fagus sylvatica L.). Theoretical and Applied Genetics, 2004, 108, 433-441.	3.6	61
65	First insights into the transcriptome and development of new genomic tools of a widespread circumâ€Mediterranean tree species, <i>Pinus halepensis</i> Mill. Molecular Ecology Resources, 2014, 14, 846-856.	4.8	61
66	Detecting short spatial scale local adaptation and epistatic selection in climateâ€related candidate genes in <scp>E</scp> uropean beech (<i><scp>F</scp>agus sylvatica</i>) populations. Molecular Ecology, 2014, 23, 4696-4708.	3.9	61
67	Population estimators or progeny tests: what is the best method to assess null allele frequencies at SSR loci?. Conservation Genetics, 2009, 10, 1343-1347.	1.5	59
68	Genetic stability and uniformity of Foeniculum vulgare Mill. regenerated plants through organogenesis and somatic embryogenesis. Plant Science, 2004, 166, 221-227.	3.6	58
69	Transcriptome versus Genomic Microsatellite Markers: Highly Informative Multiplexes for Genotyping Abies alba Mill. and Congeneric Species. Plant Molecular Biology Reporter, 2014, 32, 750-760.	1.8	57
70	Global to local genetic diversity indicators of evolutionary potential in tree species within and outside forests. Forest Ecology and Management, 2014, 333, 35-51.	3.2	57
71	The eastern part of the Fertile Crescent concealed an unexpected route of olive (Olea europaea L.) differentiation. Annals of Botany, 2017, 119, 1305-1318.	2.9	57
72	Comparison of pollen gene flow among four European beech (Fagus sylvatica L.) populations characterized by different management regimes. Heredity, 2012, 108, 322-331.	2.6	56

#	Article	IF	CITATIONS
73	Geographic distribution of chloroplast variation in Italian populations of beech (Fagus sylvatica L.). Theoretical and Applied Genetics, 2004, 109, 1-9.	3. 6	55
74	Genetic consequences of past climate and human impact on eastern Mediterranean Cedrus libani forests. Implications for their conservation. Conservation Genetics, 2008, 9, 85-95.	1.5	55
75	Introgression from modern hybrid varieties into landrace populations of maize (<i>Zea mays</i> ssp.) Tj ETQq1 1	. 0,784314	rgBT /Ove <mark>rlo</mark>
76	Variation in chloroplast single-sequence repeats in Portuguese maritime pine (Pinus pinaster Ait.). Theoretical and Applied Genetics, 2001, 102, 97-103.	3.6	54
77	A new set of mono- and dinucleotide chloroplast microsatellites in Fagaceae. Molecular Ecology Notes, 2004, 4, 259-261.	1.7	54
78	Comparative mapping in the Fagaceae and beyond with EST-SSRs. BMC Plant Biology, 2012, 12, 153.	3.6	54
79	Population structure of Cynara cardunculus complex and the origin of the conspecific crops artichoke and cardoon. Annals of Botany, 2013, 112, 855-865.	2.9	54
80	The extent and meaning of hybridization and introgression between Siberian spruce (<i>Picea) Tj ETQq0 0 0 rgB Molecular Ecology, 2016, 25, 2773-2789.</i>	T /Overlock 3.9	10 Tf 50 462 54
81	Comparison of direct and indirect genetic methods for estimating seed and pollen dispersal in Fagus sylvatica and Fagus crenata. Forest Ecology and Management, 2010, 259, 2151-2159.	3.2	53
82	A Reference Genome Sequence for the European Silver Fir (<i>Abies alba</i> Mill.): A Community-Generated Genomic Resource. G3: Genes, Genomes, Genetics, 2019, 9, 2039-2049.	1.8	53
83	Chloroplast microsatellites and mitochondrial nad1 intron 2 sequences indicate congruent phylogenetic relationships among Swiss stone pine (Pinus cembra), Siberian stone pine (Pinus sibirica), and Siberian dwarf pine (Pinus pumila). Molecular Ecology, 2001, 10, 1489-1497.	3.9	52
84	Natural hybridisation between <i>Quercus petraea </i> (Matt.) Liebl. and <i>Quercus pubescens </i> Willd. within an Italian stand as revealed by microsatellite fingerprinting. Plant Biology, 2009, 11, 758-765.	3.8	52
85	Chloroplast microsatellite analysis reveals the presence of population subdivision in Norway spruce (<i>Picea abies</i> K.). Genome, 2000, 43, 68-78.	2.0	52
86	Genetic evidence for a Janzen-Connell recruitment pattern in reproductive offspring of Pinus halepensis trees. Molecular Ecology, 2011, 20, 4152-4164.	3.9	50
87	Genetic resources in maritime pine (Pinus pinaster Aiton): molecular and quantitative measures of genetic variation and differentiation among maternal lineages. Forest Ecology and Management, 2004, 197, 103-115.	3.2	49
88	Molecular genetic diversity of Punica granatum L. (pomegranate) as revealed by microsatellite DNA markers (SSR). Gene, 2012, 493, 105-112.	2.2	49
89	Contrasting patterns of nucleotide diversity for four conifers of Alpine European forests. Evolutionary Applications, 2012, 5, 762-775.	3.1	49
90	Genomic data provide new insights on the demographic history and the extent of recent material transfers in Norway spruce. Evolutionary Applications, 2019, 12, 1539-1551.	3.1	49

#	Article	IF	Citations
91	Standardizing for microsatellite length in comparisons of genetic diversity. Molecular Ecology, 2005, 14, 885-890.	3.9	48
92	Assessing the genetic divergence of Pinus leucodermis Ant. endangered populations: use of molecular markers for conservation purposes. Theoretical and Applied Genetics, 1997, 95, 1138-1146.	3.6	47
93	Adaptive evolution of Mediterranean pines. Molecular Phylogenetics and Evolution, 2013, 68, 555-566.	2.7	46
94	Effects of seed dispersal, adult tree and seedling density on the spatial genetic structure of regeneration at fine temporal and spatial scales. Tree Genetics and Genomes, 2011, 7, 37-48.	1.6	45
95	Postglacial recolonization routes for Picea abies K. in Italy as suggested by the analysis of sequence-characterized amplified region (SCAR) markers. Molecular Ecology, 2000, 9, 699-708.	3.9	44
96	Variation in the chloroplast DNA of Swiss stone pine (<i>Pinus cembra</i> L.) reflects contrasting postâ∈glacial history of populations from the Carpathians and the Alps. Journal of Biogeography, 2009, 36, 1798-1806.	3.0	44
97	Identification and characterization of nuclear microsatellite loci in Abies alba Mill Molecular Ecology Notes, 2006, 6, 374-376.	1.7	43
98	The influence of forest management on beech (Fagus sylvatica L.) stand structure and genetic diversity. Forest Ecology and Management, 2012, 284, 34-44.	3.2	43
99	Allozyme and chloroplast DNA variation in Italian and Greek populations of Pinus leucodermis. Heredity, 1994, 73, 284-290.	2.6	41
100	Clinal Variation at Phenology-Related Genes in Spruce: Parallel Evolution in FTL2 and Gigantea?. Genetics, 2014, 197, 1025-1038.	2.9	41
101	Analysis of Hypervariable Chloroplast Microsatellites in Pinus Halepensis Reveals a Dramatic Genetic Bottleneck., 1998,, 407-412.		41
102	Development of microsatellite markers in Abies nordmanniana (Stev.) Spach and cross-species amplification in the Abies genus. Molecular Ecology Notes, 2005, 5, 784-787.	1.7	40
103	Introgressive Hybridization in <i>Pinus montezumae</i> Lamb and <i>Pinus pseudostrobus</i> Lindl. (Pinaceae): Morphological and Molecular (cpSSR) Evidence. International Journal of Plant Sciences, 2007, 168, 861-875.	1.3	40
104	Spatial vs. temporal effects on demographic and genetic structures: the roles of dispersal, masting and differential mortality on patterns of recruitment in <i>Fagus sylvatica</i> . Molecular Ecology, 2011, 20, 1997-2010.	3.9	40
105	Large-scale phylogeography of the disjunct Neotropical tree species Schizolobium parahyba (Fabaceae-Caesalpinioideae). Molecular Phylogenetics and Evolution, 2012, 65, 174-182.	2.7	40
106	Microsatellite markers for Pinus pinaster Ait Annals of Forest Science, 2001, 58, 203-206.	2.0	39
107	Isolation and characterization of polymorphic nuclear microsatellite loci in Taxus baccata L Conservation Genetics, 2008, 9, 1665-1668.	1.5	39
108	Unexpected scenarios from Mediterranean refugial areas: disentangling complex demographic dynamics along the Apennine distribution of silver fir. Journal of Biogeography, 2017, 44, 1547-1558.	3.0	38

#	Article	IF	CITATIONS
109	Phylogeography of a species complex of lowland Neotropical rain forest trees (<i>Carapa</i> ,) Tj ETQq1 1 0.7843	.4.gBT /0	Overlock 10
110	Nucleotide diversity and linkage disequilibrium at 58 stress response and phenology candidate genes in a European beech (Fagus sylvatica L.) population from southeastern France. Tree Genetics and Genomes, 2014, 10, 15-26.	1.6	36
111	Selection against inbreds in early life-cycle phases in Pinus leucodermis Ant Heredity, 1993, 70, 622-627.	2.6	34
112	High genetic diversity with moderate differentiation in Juniperus excelsa from Lebanon and the eastern Mediterranean region. AoB PLANTS, 2011, 2011, plr003.	2.3	34
113	Local Adaptation in European Firs Assessed through Extensive Sampling across Altitudinal Gradients in Southern Europe. PLoS ONE, 2016, 11, e0158216.	2.5	34
114	High genetic variation in marginal fragmented populations at extreme climatic conditions of the Patagonian Cypress Austrocedrus chilensis. Molecular Phylogenetics and Evolution, 2010, 54, 941-949.	2.7	32
115	Novel polymorphic nuclear microsatellite markers for Pinus sylvestris L Conservation Genetics Resources, 2012, 4, 231-234.	0.8	31
116	Cryptic species and phylogeographical structure in the tree <i>Cedrela odorata</i> L. throughout the Neotropics. Journal of Biogeography, 2013, 40, 732-746.	3.0	31
117	Title is missing!. Conservation Genetics, 2002, 3, 145-153.	1.5	30
118	Population genetic structure of the relict Serbian spruce, Picea omorika, inferred from plastid DNA. Plant Systematics and Evolution, 2008, 271, 1-7.	0.9	30
119	Forests at the limit: evolutionary — genetic consequences of environmental changes at the receding (xeric) edge of distribution. Report from a research workshop. Annals of Forest Science, 2009, 66, 800-800.	2.0	29
120	Development and characterization of SSR markers for pomegranate (Punica granatum L.) using an enriched library. Conservation Genetics Resources, 2010, 2, 283-285.	0.8	28
121	Within-Population Genetic Structure in Beech (Fagus sylvatica L.) Stands Characterized by Different Disturbance Histories: Does Forest Management Simplify Population Substructure?. PLoS ONE, 2013, 8, e73391.	2.5	28
122	Characterization of highly polymorphic nuclear microsatellite loci in Juniperus communis L Molecular Ecology Notes, 2006, 6, 346-348.	1.7	27
123	Gradual decline in genetic diversity in Swiss stone pine populations (Pinus cembra) across Switzerland suggests postglacial re-colonization into the Alps from a common eastern glacial refugium. Botanica Helvetica, 2009, 119, 13-22.	1.1	27
124	Characterization of variable EST SSR markers for Norway spruce (Picea abies L.). BMC Research Notes, 2011, 4, 401.	1.4	27
125	Increased fire frequency promotes stronger spatial genetic structure and natural selection at regional and local scales in Pinus halepensis Mill. Annals of Botany, 2017, 119, 1061-1072.	2.9	27
126	Micro- and Macro-Geographic Scale Effect on the Molecular Imprint of Selection and Adaptation in Norway Spruce. PLoS ONE, 2014, 9, e115499.	2.5	27

#	Article	IF	CITATIONS
127	Chloroplast microsatellite variation in Abies nordmanniana and simulation of causes for low differentiation among populations. Tree Genetics and Genomes, 2005, 1, 116-123.	1.6	26
128	Imprints of glacial refugia in the modern genetic diversity of Pinus sylvestris. Global Ecology and Biogeography, 2006, 15, 271-282.	5.8	26
129	Development and characterization of eight polymorphic microsatellite loci from <i>Pistacia lentiscus</i> L. (Anacardiaceae). Molecular Ecology Resources, 2008, 8, 904-906.	4.8	26
130	High genetic diversity and distinct origin of recently fragmented Scots pine (Pinus sylvestris L.) populations along the Carpathians and the Pannonian Basin. Tree Genetics and Genomes, 2017, 13, 1.	1.6	26
131	Amazon diversification and crossâ€Andean dispersal of the widespread Neotropical tree species <i>Journal of Biogeography, 2013, 40, 707-719.</i>	3.0	25
132	Genomic exploration and molecular marker development in a large and complex conifer genome using RADseq and mRNAseq. Molecular Ecology Resources, 2015, 15, 601-612.	4.8	25
133	Genetic diversity and phylogeographic analysis of <i>Pinus leiophylla</i> : a postâ€glacial range expansion. Journal of Biogeography, 2009, 36, 1807-1820.	3.0	24
134	Recent population decline and selection shape diversity of taxolâ€related genes. Molecular Ecology, 2012, 21, 3006-3021.	3.9	24
135	Fine- and local- scale genetic structure of Dysoxylum malabaricum, a late-successional canopy tree species in disturbed forest patches in the Western Ghats, India. Conservation Genetics, 2017, 18, 1-15.	1.5	24
136	Genomic and phenotypic divergence unveil microgeographic adaptation in the Amazonian hyperdominant tree <i>Eperua falcata</i> Aubl. (Fabaceae). Molecular Ecology, 2021, 30, 1136-1154.	3.9	24
137	Inferring selection in instances of longâ€range colonization: The Aleppo pine (<i>Pinus halepensis</i>) in the Mediterranean Basin. Molecular Ecology, 2018, 27, 3331-3345.	3.9	22
138	A multiscale approach to detect selection in nonmodel tree species: Widespread adaptation despite population decline in Taxus baccata L. Evolutionary Applications, 2020, 13, 143-160.	3.1	22
139	Isolation and characterization of nuclear microsatellite loci in Pinus pinaster Ait. Molecular Ecology Notes, 2005, 5, 57-59.	1.7	21
140	Habitat features and genetic integrity of wild grapevine Vitis vinifera L. subsp. sylvestris (C.C. Gmel.) Hegi populations: A case study from Sicily. Flora: Morphology, Distribution, Functional Ecology of Plants, 2013, 208, 538-548.	1.2	21
141	Polygenic adaptation and negative selection across traits, years and environments in a longâ€ived plant species (<i>Pinus pinaster</i> i> Ait., Pinaceae). Molecular Ecology, 2022, 31, 2089-2105.	3.9	21
142	Halfway encounters: Meeting points of colonization routes among the southern beeches Nothofagus pumilio and N. antarctica. Molecular Phylogenetics and Evolution, 2015, 85, 197-207.	2.7	20
143	Hyrcanian forestsâ€"Stable rearâ€edge populations harbouring high genetic diversity of <i>Fraxinus excelsior,</i> a common European tree species. Diversity and Distributions, 2018, 24, 1521-1533.	4.1	20
144	Genetic signatures of divergent selection in European beech (<i>Fagus sylvatica</i> L.) are associated with the variation in temperature and precipitation across its distribution range. Molecular Ecology, 2021, 30, 5029-5047.	3.9	20

#	Article	IF	CITATIONS
145	Maternally and paternally inherited molecular markers elucidate population patterns and inferred dispersal processes on a small scale within a subalpine stand of Norway spruce (Picea abies [L.] Karst.). Forest Ecology and Management, 2008, 255, 3806-3812.	3.2	19
146	Local effects drive heterozygosity–fitness correlations in an outcrossing long-lived tree. Proceedings of the Royal Society B: Biological Sciences, 2015, 282, 20152230.	2.6	19
147	Differentiation of Seiridium species associated with virulent cankers on cypress in the Mediterraneanregion by PCR-SSCP. Plant Pathology, 2000, 49, 774-781.	2.4	17
148	Sicily represents the Italian reservoir of chloroplast DNA diversity of Quercus ilex L. (Fagaceae). Annals of Forest Science, 2005, 62, 79-84.	2.0	17
149	Estimating exotic gene flow into native pine stands: zygotic vs. gametic components. Molecular Ecology, 2014, 23, 5435-5447.	3.9	17
150	Estimation of mating system parameters in two Italian natural populations of Fagussylvatica. Canadian Journal of Forest Research, 1996, 26, 1187-1192.	1.7	16
151	Isolation and characterization of polymorphic nuclear microsatellite loci in <i>Pinus cembra</i> L Molecular Ecology Resources, 2009, 9, 858-861.	4.8	16
152	Chloroplast microsatellites reveal that metallicolous populations of the Mediterranean shrub Cistus ladanifer L have multiple origins. Plant and Soil, 2010, 334, 161-174.	3.7	16
153	Aquaporins in the wild: natural genetic diversity and selective pressure in the PIP gene family in five Neotropical tree species. BMC Evolutionary Biology, 2010, 10, 202.	3.2	16
154	Looking for Local Adaptation: Convergent Microevolution in Aleppo Pine (Pinus halepensis). Genes, 2019, 10, 673.	2.4	16
155	Mating system analysis in Pinus leucodermis Ant.: detection of self-fertilization in natural populations. Heredity, 1991, 67, 197-203.	2.6	15
156	Novel polymorphic nuclear microsatellites in Cupressus sempervirens L Molecular Ecology Notes, 2005, 5, 393-394.	1.7	15
157	Isolation of microsatellite markers for the common Mediterranean shrub <i>Myrtus communis</i> (Myrtaceae). American Journal of Botany, 2010, 97, e23-5.	1.7	15
158	Recent phylogeographic structure in a widespread â€~weedy' Neotropical tree species, <i>Cordia alliodora</i> (Boraginaceae). Journal of Biogeography, 2013, 40, 693-706.	3.0	15
159	Effective gene flow in a historically fragmented area at the southern edge of silver fir (Abies alba) Tj ETQq1 1 0.78	4314 rgBT 1.6	/ <mark>O</mark> verlock
160	Evolutionary rate and genetic load in an emblematic Mediterranean tree following an ancient and prolonged population collapse. Molecular Ecology, 2020, 29, 4797-4811.	3.9	15
161	Spatiotemporal mating pattern variation in a windâ€pollinated Mediterranean shrub. Molecular Ecology, 2009, 18, 5195-5206.	3.9	14
162	Nuclear microsatellites for <i>Pinus pinea</i> (Pinaceae), a genetically depauperate tree, and their transferability to <i>P. halepensis</i> American Journal of Botany, 2012, 99, e362-5.	1.7	14

#	Article	IF	Citations
163	RAPD-derived, PCR-based mitochondrial markers for Larix species and their usefulness in phylogeny. Conservation Genetics, 2006, 7, 621-625.	1.5	13
164	A landscape genetics approach reveals ecological-based differentiation in populations of holm oak (Quercus ilex L.) at the northern limit of its range. Biological Journal of the Linnean Society, 2012, 107, 458-467.	1.6	13
165	Recent, Late Pleistocene fragmentation shaped the phylogeographic structure of the European black pine (Pinus nigra Arnold). Tree Genetics and Genomes, 2019, 15, 1.	1.6	13
166	Using reduced representation libraries sequencing methods to identify cpDNA polymorphisms in European beech (Fagus sylvatica L). Tree Genetics and Genomes, 2019, 15, 1.	1.6	13
167	Molecular and Quantitative Genetics of Stone Pine (Pinus pinea). Sustainable Development and Biodiversity, 2019, , 61-84.	1.7	13
168	Genetic diversity and differentiation of Fagus orientalis Lipsky in Hyrcanian forests revealed by nuclear and chloroplast microsatellite markers. Conservation Genetics, 2010, 11, 2321-2331.	1.5	12
169	The effect of silvicultural management on the genetic diversity of a mixed Nothofagus forest in LanÃn Natural Reserve, Argentina. Forest Ecology and Management, 2016, 363, 11-20.	3.2	12
170	Chloroplast DNA phylogeography of the shrub <i>Cistus ladanifer</i> L. (Cistaceae) in the highly diverse Western Mediterranean region. Plant Biology, 2011, 13, 391-400.	3.8	11
171	Genetic structure in the <i>Genista ephedroides </i> complex (Fabaceae) and implications for its present distribution. Botanical Journal of the Linnean Society, 2015, 177, 607-618.	1.6	11
172	Assessing early fitness consequences of exotic gene flow in the wild: a field study with Iberian pine relicts. Evolutionary Applications, 2016, 9, 367-380.	3.1	11
173	Mid-Pleistocene and Holocene demographic fluctuation of Scots pine (Pinus sylvestris L.) in the Carpathian Mountains and the Pannonian Basin: Signs of historical expansions and contractions. Quaternary International, 2019, 504, 202-213.	1.5	11
174	Fineâ€scale spatial genetic structure across the species range reflects recent colonization of high elevation habitats in silver fir (<i>Abies alba</i> Mill.). Molecular Ecology, 2021, 30, 5247-5265.	3.9	11
175	Genetic diversity and divergence at the Arbutus unedo L. (Ericaceae) westernmost distribution limit. PLoS ONE, 2017, 12, e0175239.	2.5	11
176	Cross transferability of SSRs to five species of Araucariaceae: a useful tool for population genetic studies in Araucaria araucana. Forest Systems, 2011, 20, 303.	0.3	11
177	Individual reproductive success in Norway spruce natural populations depends on growth rate, age and sensitivity to temperature. Heredity, 2020, 124, 685-698.	2.6	10
178	Evolutionary relevance of lineages in the European black pine (Pinus nigra) in the transcriptomic era. Tree Genetics and Genomes, 2020, 16 , 1 .	1.6	10
179	NUCLEAR MICROSATELLITES REVEAL CONTRASTING PATTERNS OF GENETIC STRUCTURE BETWEEN WESTERN AND SOUTHEASTERN EUROPEAN POPULATIONS OF THE COMMON ASH (FRAXINUS EXCELSIOR L). Evolution; International Journal of Organic Evolution, 2004, 58, 976.	2.3	9
180	Isolation of SSR markers for two African tropical tree species, <i>Erythrophleum suaveolens</i> and <i>E. ivorense</i> (Caesalpinioideae). American Journal of Botany, 2011, 98, e106-8.	1.7	9

#	Article	IF	Citations
181	Logging by selective extraction of best trees: Does it change patterns of genetic diversity? The case of Nothofagus pumilio. Forest Ecology and Management, 2016, 373, 81-92.	3.2	9
182	A New Set of Nuclear Microsatellites for an Ecologically and Economically Important Conifer: the European Black Pine (Pinus nigra Arn.). Plant Molecular Biology Reporter, 2017, 35, 379-388.	1.8	8
183	De novo assembly of English yew (Taxus baccata) transcriptome and its applications for intra- and inter-specific analyses. Plant Molecular Biology, 2018, 97, 337-345.	3.9	8
184	Molecular evidence for the natural production of homozygous Cupressus sempervirens L. lines by Cupressus dupreziana seed trees. Heredity, 2010, 104, 185-190.	2.6	7
185	A sample view of the pedunculate oak (Quercus robur) genome from the sequencing of hypomethylated and random genomic libraries. Tree Genetics and Genomes, 2011, 7, 1277-1285.	1.6	7
186	Portuguese Pinus nigra J.F. Arnold populations: genetic diversity, structure and relationships inferred by SSR markers. Annals of Forest Science, 2020, 77, 1.	2.0	7
187	Evolutionary history of the mediterranean Pinus halepensis-brutia species complex using gene-resequencing and transcriptomic approaches. Plant Molecular Biology, 2021, 106, 367-380.	3.9	7
188	Genomic Resources Notes Accepted 1 October 2014-30 November 2014. Molecular Ecology Resources, 2015, 15, 458-459.	4.8	6
189	Tracking the origin of silver fir plantations along the boundary between different genetic clusters in central Apennines: Implications for their management. Forest Ecology and Management, 2018, 408, 220-227.	3.2	6
190	A comprehensive, genus-level time-calibrated phylogeny of the tree flora of Mediterranean Europe and an assessment of its vulnerability. Botany Letters, 2020, 167, 276-289.	1.4	6
191	Staying close: short local dispersal distances on a managed forest of two Patagonian Nothofagus species. Forestry, 2020, 93, 652-661.	2.3	6
192	Eight novel microsatellite DNA markers in Rhodiola rosea L Conservation Genetics, 2009, 10, 1397-1399.	1.5	5
193	Development of highly polymorphic tetranucleotide microsatellite markers in <i>Austrocedrus chilensis</i> . Molecular Ecology Resources, 2008, 8, 887-889.	4.8	3
194	Microsatellite loci isolated from the tropical tree <i> Hymenaea courbaril</i> L. (Fabaceae). Molecular Ecology Resources, 2008, 8, 1020-1022.	4.8	3
195	Characterization of new microsatellite loci isolated from <i>Santiria trimera</i> (Burseraceae). American Journal of Botany, 2012, 99, e334-6.	1.7	3
196	The GenTree Platform: growth traits and tree-level environmental data in 12 European forest tree species. GigaScience, 2021, 10, .	6.4	3
197	High pollen immigration but no gene flow via-seed into a Genetic Conservation Unit of the endangered Picea omorika after disturbance. Forest Ecology and Management, 2022, 510, 120115.	3.2	3
198	Absence of Geographic Structure in European Populations of Rubus fruticosus L. Complex Using Chloroplast DNA Microsatellites. Journal of the American Society for Horticultural Science, 2006, 131, 616-621.	1.0	2

#	Article	IF	CITATIONS
199	Polymorphic microsatellite markers in the Neotropical forest tree Minquartia guianensis Aubl. (Olacaceae). Conservation Genetics Resources, 2010, 2, 185-187.	0.8	1
200	Population Genetics and Genomics of Aleppo Pine (Pinus halepensis). Managing Forest Ecosystems, 2021, , 19-32.	0.9	1
201	Imprints of selection in peripheral and ecologically marginal central-eastern European Scots pine populations. Gene, 2021, 779, 145509.	2.2	0