

Christophe Plomion

List of Publications by Year in descending order

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Version: 2024-02-01

186
papers

11,629
citations

22146

59
h-index

37202

96
g-index

202
all docs

202
docs citations

202
times ranked

10719
citing authors

#	ARTICLE	IF	CITATIONS
1	The GenTree Dendroecological Collection, tree-ring and wood density data from seven tree species across Europe. <i>Scientific Data</i> , 2020, 7, 1.	5.3	830
2	Wood Formation in Trees. <i>Plant Physiology</i> , 2001, 127, 1513-1523.	4.8	650
3	Oak genome reveals facets of long lifespan. <i>Nature Plants</i> , 2018, 4, 440-452.	9.3	303
4	Mapping QTLs controlling fruit quality in peach (<i>Prunus persica</i> (L.) Batsch). <i>Theoretical and Applied Genetics</i> , 1999, 98, 18-31.	3.6	226
5	Proteomics for genetic and physiological studies in plants. <i>Electrophoresis</i> , 1999, 20, 2013-2026.	2.4	203
6	Candidate genes and QTLs for sugar and organic acid content in peach [<i>Prunus persica</i> (L.) Batsch]. <i>Theoretical and Applied Genetics</i> , 2002, 105, 145-159.	3.6	199
7	"Contrasting Patterns of Selection at <i>Pinus pinaster</i> Ait. Drought Stress Candidate Genes as Revealed by Genetic Differentiation Analyses". <i>Molecular Biology and Evolution</i> , 2008, 25, 417-437.	8.9	198
8	Wood formation in trees. <i>Plant Physiology</i> , 2001, 127, 1513-23.	4.8	192
9	Genomic landscape of the global oak phylogeny. <i>New Phytologist</i> , 2020, 226, 1198-1212.	7.3	186
10	Limited genetic variability and phenotypic plasticity detected for cavitation resistance in a Mediterranean pine. <i>New Phytologist</i> , 2014, 201, 874-886.	7.3	170
11	Mapping the proteome of poplar and application to the discovery of drought-stress responsive proteins. <i>Proteomics</i> , 2006, 6, 6509-6527.	2.2	155
12	Cross-species transferability and mapping of genomic and cDNA SSRs in pines. <i>Theoretical and Applied Genetics</i> , 2004, 109, 1204-1214.	3.6	153
13	A fast and cost-effective approach to develop and map EST-SSR markers: oak as a case study. <i>BMC Genomics</i> , 2010, 11, 570.	2.8	144
14	LPmerge: an R package for merging genetic maps by linear programming. <i>Bioinformatics</i> , 2014, 30, 1623-1624.	4.1	140
15	Range-wide phylogeography and gene zones in <i>Pinus pinaster</i> Ait. revealed by chloroplast microsatellite markers. <i>Molecular Ecology</i> , 2007, 16, 2137-2153.	3.9	129
16	Uniform Selection as a Primary Force Reducing Population Genetic Differentiation of Cavitation Resistance across a Species Range. <i>PLoS ONE</i> , 2011, 6, e23476.	2.5	129
17	Genomics of growth traits in forest trees. <i>Current Opinion in Plant Biology</i> , 2009, 12, 148-156.	7.1	126
18	A genetic linkage map of <i>Quercus robur</i> L. (pedunculate oak) based on RAPD, SCAR, microsatellite, minisatellite, isozyme and 5S rDNA markers. <i>Theoretical and Applied Genetics</i> , 1998, 97, 1090-1103.	3.6	125

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19	Genetic parameters and QTL analysis of $\delta^{13}C$ and ring width in maritime pine. <i>Plant, Cell and Environment</i> , 2002, 25, 945-953.	5.7	119
20	Genetic diversity within and among <i>Pinus pinaster</i> populations: comparison between AFLP and microsatellite markers. <i>Heredity</i> , 2001, 86, 469-479.	2.6	117
21	Adaptive introgression as a driver of local adaptation to climate in European white oaks. <i>New Phytologist</i> , 2020, 226, 1171-1182.	7.3	117
22	Transcriptome analysis of bud burst in sessile oak (<i>Quercus petraea</i>). <i>New Phytologist</i> , 2006, 170, 723-738.	7.3	116
23	<i>De novo</i> assembly of maritime pine transcriptome: implications for forest breeding and biotechnology. <i>Plant Biotechnology Journal</i> , 2014, 12, 286-299.	8.3	115
24	Extensive recent secondary contacts between four European white oak species. <i>New Phytologist</i> , 2017, 214, 865-878.	7.3	113
25	Palaeogenomics of plants: synteny-based modelling of extinct ancestors. <i>Trends in Plant Science</i> , 2010, 15, 479-487.	8.8	111
26	A micromethod for high throughput RNA extraction in forest trees. <i>Biological Research</i> , 2007, 40, .	3.4	110
27	Genomics of Fagaceae. <i>Tree Genetics and Genomes</i> , 2012, 8, 583-610.	1.6	109
28	Water-deficit-responsive proteins in maritime pine. <i>Plant Molecular Biology</i> , 1998, 38, 587-596.	3.9	108
29	Proteomics research on forest trees, the most recalcitrant and orphan plant species. <i>Phytochemistry</i> , 2011, 72, 1219-1242.	2.9	108
30	Decoding the oak genome: public release of sequence data, assembly, annotation and publication strategies. <i>Molecular Ecology Resources</i> , 2016, 16, 254-265.	4.8	108
31	Quantitative trait dissection analysis in <i>Eucalyptus</i> using RAPD markers: 1. Detection of QTL in interspecific hybrid progeny, stability of QTL expression across different ages. <i>Theoretical and Applied Genetics</i> , 1997, 95, 597-608.	3.6	105
32	Comparative mapping between <i>Quercus</i> and <i>Castanea</i> using simple-sequence repeats (SSRs). <i>Theoretical and Applied Genetics</i> , 2004, 108, 558-566.	3.6	105
33	Genomic mapping in <i>Pinus pinaster</i> (maritime pine) using RAPD and protein markers. <i>Heredity</i> , 1995, 74, 661-668.	2.6	101
34	Compression Wood-Responsive Proteins in Developing Xylem of Maritime Pine (<i>Pinus pinaster</i> Ait.) ^{1,2} . <i>Plant Physiology</i> , 2000, 123, 959-970.	4.8	101
35	Genomic analysis in maritime pine (<i>Pinus pinaster</i>). Comparison of two RAPD maps using selfed and open-pollinated seeds of the same individual. <i>Theoretical and Applied Genetics</i> , 1995, 90, 1028-1034.	3.6	100
36	The proteome of maritime pine wood forming tissue. <i>Proteomics</i> , 2005, 5, 3731-3751.	2.2	99

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37	Genomic selection in maritime pine. <i>Plant Science</i> , 2016, 242, 108-119.	3.6	99
38	Detection of quantitative trait loci controlling bud burst and height growth in <i>Quercus robur</i> L.. <i>Theoretical and Applied Genetics</i> , 2004, 109, 1648-1659.	3.6	93
39	Towards decoding the conifer giga-genome. <i>Plant Molecular Biology</i> , 2012, 80, 555-569.	3.9	91
40	Forest tree genomics: 10 achievements from the past 10 years and future prospects. <i>Annals of Forest Science</i> , 2016, 73, 77-103.	2.0	91
41	Identification of water-deficit responsive genes in maritime pine (<i>Pinus pinaster</i> Ait.) roots. <i>Plant Molecular Biology</i> , 2003, 51, 249-262.	3.9	90
42	High-resolution genetic maps of <i>Eucalyptus</i> improve <i>Eucalyptus grandis</i> genome assembly. <i>New Phytologist</i> , 2015, 206, 1283-1296.	7.3	90
43	Genetic dissection of height in maritime pine seedlings raised under accelerated growth conditions. <i>Theoretical and Applied Genetics</i> , 1996, 93-93, 849-858.	3.6	88
44	Advances in ecological genomics in forest trees and applications to genetic resources conservation and breeding. <i>Molecular Ecology</i> , 2017, 26, 706-717.	3.9	85
45	Proteomic analysis of differentially expressed proteins in hepatocellular carcinoma developed in patients with chronic viral hepatitis C. <i>Proteomics</i> , 2005, 5, 3778-3789.	2.2	83
46	Bioinformatic analysis of ESTs collected by Sanger and pyrosequencing methods for a keystone forest tree species: oak. <i>BMC Genomics</i> , 2010, 11, 650.	2.8	82
47	Transcriptional profiling of bud dormancy induction and release in oak by next-generation sequencing. <i>BMC Genomics</i> , 2013, 14, 236.	2.8	82
48	Performance of genomic prediction within and across generations in maritime pine. <i>BMC Genomics</i> , 2016, 17, 604.	2.8	82
49	Genetic mapping in <i>Eucalyptus urophylla</i> and <i>Eucalyptus grandis</i> using RAPD markers. <i>Genome</i> , 1996, 39, 1051-1061.	2.0	81
50	Distribution of genomic regions differentiating oak species assessed by QTL detection. <i>Heredity</i> , 2004, 92, 20-30.	2.6	79
51	Comparative genome and QTL mapping between maritime and loblolly pines. <i>Molecular Breeding</i> , 2003, 12, 185-195.	2.1	78
52	Molecular Proxies for Climate Maladaptation in a Long-Lived Tree (<i>Pinus pinaster</i> Aiton.) <i>Trends in Ecology & Evolution</i> , 2014, 29, 101-109.	2.9	78
53	High-throughput DNA sequencing of ancient wood. <i>Molecular Ecology</i> , 2018, 27, 1138-1154.	3.9	73
54	Genetic control of pulp and timber properties in maritime pine (<i>Pinus pinaster</i> Ait.). <i>Annals of Forest Science</i> , 2002, 59, 563-575.	2.0	71

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55	Identification of QTLs affecting adaptive traits in <i>Castanea sativa</i> Mill. <i>Plant, Cell and Environment</i> , 2004, 27, 1088-1101.	5.7	71
56	Nucleotide variation in genes involved in wood formation in two pine species. <i>New Phytologist</i> , 2005, 167, 101-112.	7.3	71
57	A genetic map of Maritime pine based on AFLP, RAPD and protein markers. <i>Theoretical and Applied Genetics</i> , 2000, 100, 39-48.	3.6	67
58	Development and implementation of a highly-multiplexed SNP array for genetic mapping in maritime pine and comparative mapping with loblolly pine. <i>BMC Genomics</i> , 2011, 12, 368.	2.8	66
59	Automated SNP Detection in Expressed Sequence Tags: Statistical Considerations and Application to Maritime Pine Sequences. <i>Plant Molecular Biology</i> , 2004, 54, 461-470.	3.9	65
60	High-density linkage mapping in a pine tree reveals a genomic region associated with inbreeding depression and provides clues to the extent and distribution of meiotic recombination. <i>BMC Biology</i> , 2013, 11, 50.	3.8	63
61	The genetics of water-use efficiency and its relation to growth in maritime pine. <i>Journal of Experimental Botany</i> , 2014, 65, 4757-4768.	4.8	62
62	A high density genetic map of maritime pine based on AFLPs. <i>Annals of Forest Science</i> , 2002, 59, 627-636.	2.0	61
63	Comparison of genetic diversity estimates within and among populations of maritime pine using chloroplast simple-sequence repeat and amplified fragment length polymorphism data. <i>Molecular Ecology</i> , 2002, 11, 869-877.	3.9	61
64	High-density linkage mapping and distribution of segregation distortion regions in the oak genome. <i>DNA Research</i> , 2016, 23, 115-124.	3.4	61
65	Drought differentially affects expression of a PR10 protein, in needles of maritime pine (<i>Pinus pinaster</i>) Tj ETQq1_1_0.784314 rgBT /Ov	4.8	59
66	Identification and characterization of water-stress-responsive genes in hydroponically grown maritime pine (<i>Pinus pinaster</i>) seedlings. <i>Tree Physiology</i> , 2003, 23, 169-179.	3.1	58
67	Separation and characterization of needle and xylem maritime pine proteins. <i>Electrophoresis</i> , 1999, 20, 1098-1108.	2.4	57
68	Seasonal variation in transcript accumulation in wood-forming tissues of maritime pine (<i>Pinus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 222	3.2	57
69	Leaf proteome analysis of eight <i>Populus trichocarpa</i> genotypes: Genetic variation in drought response and in water-use efficiency involves photosynthesis-related proteins. <i>Proteomics</i> , 2009, 9, 4121-4142.	2.2	57
70	Variation in chloroplast single-sequence repeats in Portuguese maritime pine (<i>Pinus pinaster</i> Ait.). <i>Theoretical and Applied Genetics</i> , 2001, 102, 97-103.	3.6	54
71	Geographical diversity and genetic relationships among <i>Cedrus</i> species estimated by AFLP. <i>Tree Genetics and Genomes</i> , 2007, 3, 275-285.	1.6	54
72	Comparative mapping in the Fagaceae and beyond with EST-SSRs. <i>BMC Plant Biology</i> , 2012, 12, 153.	3.6	54

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73	Combining proteomic and genetic studies in plants. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2002, 782, 137-149.	2.3	53
74	High-density SNP assay development for genetic analysis in maritime pine (<i>Pinus pinaster</i>). <i>Molecular Ecology Resources</i> , 2016, 16, 574-587.	4.8	53
75	Title is missing!. <i>Molecular Breeding</i> , 2000, 6, 451-458.	2.1	52
76	In Vitro vs In Silico Detected SNPs for the Development of a Genotyping Array: What Can We Learn from a Non-Model Species?. <i>PLoS ONE</i> , 2010, 5, e11034.	2.5	52
77	Association mapping for growth, straightness and wood chemistry traits in the <i>Pinus pinaster</i> Aquitaine breeding population. <i>Tree Genetics and Genomes</i> , 2012, 8, 113-126.	1.6	51
78	Hardwood Tree Genomics: Unlocking Woody Plant Biology. <i>Frontiers in Plant Science</i> , 2018, 9, 1799.	3.6	50
79	Developing SSCP markers in two <i>Pinus</i> species. <i>Molecular Breeding</i> , 1999, 5, 21-31.	2.1	49
80	Mapping candidate genes in <i>Eucalyptus</i> with emphasis on lignification genes. <i>Molecular Breeding</i> , 2000, 6, 441-449.	2.1	49
81	Genetic resources in maritime pine (<i>Pinus pinaster</i> Aiton): molecular and quantitative measures of genetic variation and differentiation among maternal lineages. <i>Forest Ecology and Management</i> , 2004, 197, 103-115.	3.2	49
82	Molecular and phenotypic profiling from the base to the crown in maritime pine wood-forming tissue. <i>New Phytologist</i> , 2008, 178, 283-301.	7.3	49
83	The oak gene expression atlas: insights into Fagaceae genome evolution and the discovery of genes regulated during bud dormancy release. <i>BMC Genomics</i> , 2015, 16, 112.	2.8	49
84	Wood Formation in Trees. <i>Plant Physiology</i> , 2001, 127, 1513-1523.	4.8	48
85	Comprehensive genetic dissection of wood properties in a widely-grown tropical tree: <i>Eucalyptus</i> . <i>BMC Genomics</i> , 2011, 12, 301.	2.8	48
86	QTLs and candidate genes for wood properties in maritime pine (<i>Pinus pinaster</i> Ait.). <i>Tree Genetics and Genomes</i> , 2006, 2, 10-24.	1.6	47
87	Secretome of the Free-living Mycelium from the Ectomycorrhizal Basidiomycete <i>Laccaria bicolor</i> . <i>Journal of Proteome Research</i> , 2012, 11, 157-171.	3.7	47
88	Massive postglacial gene flow between European white oaks uncovered genes underlying species barriers. <i>New Phytologist</i> , 2020, 226, 1183-1197.	7.3	46
89	Soil water stress affects both cuticular wax content and cuticle-related gene expression in young saplings of maritime pine (<i>Pinus pinaster</i> Ait.). <i>BMC Plant Biology</i> , 2013, 13, 95.	3.6	43
90	Single-nucleotide polymorphism discovery and validation in high-density SNP array for genetic analysis in European white oaks. <i>Molecular Ecology Resources</i> , 2015, 15, 1446-1459.	4.8	43

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91	Recombination rate differences for pollen parents and seed parents in <i>Pinus pinaster</i> . <i>Heredity</i> , 1996, 77, 341-350.	2.6	42
92	PROTICdb: A web-based application to store, track, query, and compare plant proteome data. <i>Proteomics</i> , 2005, 5, 2069-2081.	2.2	42
93	Plasticity of maritime pine (<i>Pinus pinaster</i>) wood-forming tissues during a growing season. <i>New Phytologist</i> , 2008, 179, 1180-1194.	7.3	42
94	A micromethod for high throughput RNA extraction in forest trees. <i>Biological Research</i> , 2007, 40, 291-7.	3.4	42
95	Genome-wide distribution of genetic diversity and linkage disequilibrium in a mass-selected population of maritime pine. <i>BMC Genomics</i> , 2014, 15, 171.	2.8	41
96	Microsatellite markers for <i>Pinus pinaster</i> Ait.. <i>Annals of Forest Science</i> , 2001, 58, 203-206.	2.0	39
97	Genetic variation and drought response in two <i>Populus</i> — <i>euramericana</i> genotypes through 2-DE proteomic analysis of leaves from field and glasshouse cultivated plants. <i>Phytochemistry</i> , 2009, 70, 988-1002.	2.9	39
98	Epigenetics in Forest Trees. <i>Advances in Botanical Research</i> , 2018, 88, 387-453.	1.1	37
99	Microsatellite primers for <i>Sorbus torminalis</i> and related species. <i>Molecular Ecology Notes</i> , 2001, 1, 297-299.	1.7	36
100	Role of waterlogging-responsive genes in shaping interspecific differentiation between two sympatric oak species. <i>Tree Physiology</i> , 2012, 32, 119-134.	3.1	36
101	Implication of the suberin pathway in adaptation to waterlogging and hypertrophied lenticels formation in pedunculate oak (<i>Quercus robur</i> L.). <i>Tree Physiology</i> , 2016, 36, tpw056.	3.1	36
102	Linkage and Association Mapping for Two Major Traits Used in the Maritime Pine Breeding Program: Height Growth and Stem Straightness. <i>PLoS ONE</i> , 2016, 11, e0165323.	2.5	36
103	A unigene set for European beech (<i>Fagus sylvatica</i> L.) and its use to decipher the molecular mechanisms involved in dormancy regulation. <i>Molecular Ecology Resources</i> , 2015, 15, 1192-1204.	4.8	35
104	Heat induced changes in protein expression profiles of Norway spruce (<i>Picea abies</i>) ecotypes from different elevations. <i>Proteomics</i> , 2008, 8, 4287-4302.	2.2	34
105	Pollen contamination in a maritime pine polycross seed orchard and certification of improved seeds using chloroplast microsatellites. <i>Canadian Journal of Forest Research</i> , 2001, 31, 1816-1825.	1.7	33
106	Analysis of BAC end sequences in oak, a keystone forest tree species, providing insight into the composition of its genome. <i>BMC Genomics</i> , 2011, 12, 292.	2.8	33
107	Plasticity of primary and secondary growth dynamics in Eucalyptushybrids: a quantitative genetics and QTL mapping perspective. <i>BMC Plant Biology</i> , 2013, 13, 120.	3.6	33
108	Paternity recovery in two maritime pine polycross mating designs and consequences for breeding. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	1.6	33

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109	Two genes encoding distinct cytosolic glutamine synthetases are closely linked in the pine genome. <i>FEBS Letters</i> , 2000, 477, 237-243.	2.8	32
110	Hunting down fungal secretomes using liquidâ€phase IEF prior to high resolution 2â€DE. <i>Electrophoresis</i> , 2009, 30, 4118-4136.	2.4	31
111	Characterisation and natural variation of a dehydrin gene in <i>Quercus petraea</i> (Matt.) Liebl.. <i>Plant Biology</i> , 2011, 13, 881-887.	3.8	30
112	<i>Q</i> & <i>F</i> As a signature of canalization. <i>Molecular Ecology</i> , 2012, 21, 5646-5655.	3.9	30
113	Genetic determinism of β -carene in maritime pine using RAPD markers. <i>Genome</i> , 1996, 39, 1123-1127.	2.0	29
114	Proteomic plasticity of two <i>Eucalyptus</i> genotypes under contrasted water regimes in the field. <i>Plant, Cell and Environment</i> , 2012, 35, 790-805.	5.7	29
115	Transcriptional changes in two types of pre-mycorrhizal roots and in ectomycorrhizas of oak microcuttings inoculated with <i>Piloderma croceum</i> . <i>Planta</i> , 2006, 225, 331-340.	3.2	28
116	Genetic parameters of growth, straightness and wood chemistry traits in <i>Pinus pinaster</i> . <i>Annals of Forest Science</i> , 2011, 68, 873-884.	2.0	28
117	Evidence of intense chromosomal shuffling during conifer evolution. <i>Genome Biology and Evolution</i> , 2015, 7, evv185.	2.5	26
118	Origin identification of maritime pine stands in France using chloroplast simple-sequence repeats. <i>Annals of Forest Science</i> , 2002, 59, 53-62.	2.0	25
119	Transcriptional analysis of differentially expressed genes in response to stem inclination in young seedlings of pine. <i>Plant Biology</i> , 2012, 14, 923-933.	3.8	25
120	What can nuclear microsatellites tell us about maritime pine genetic resources conservation and provenance certification strategies?. <i>Annals of Forest Science</i> , 2002, 59, 699-708.	2.0	24
121	Quantitative trait loci mapping for vegetative propagation in pedunculate oak. <i>Annals of Forest Science</i> , 2005, 62, 369-374.	2.0	24
122	A linkage disequilibrium perspective on the genetic mosaic of speciation in two hybridizing Mediterranean white oaks. <i>Heredity</i> , 2015, 114, 373-386.	2.6	24
123	Genome-wide evolutionary response of European oaks during the Anthropocene. <i>Evolution Letters</i> , 2022, 6, 4-20.	3.3	24
124	Improved AFLP analysis of tree species. <i>Canadian Journal of Forest Research</i> , 2000, 30, 1608-1616.	1.7	23
125	(Not) Keeping the stem straight: a proteomic analysis of maritime pine seedlings undergoing phototropism and gravitropism. <i>BMC Plant Biology</i> , 2010, 10, 217.	3.6	23
126	Oak symbolism in the light of genomics. <i>New Phytologist</i> , 2020, 226, 1012-1017.	7.3	23

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127	Differential accumulation of soluble proteins in roots of metallicolous and nonmetallicolous populations of <i>Agrostis capillaris</i> L. exposed to Cu. <i>Proteomics</i> , 2014, 14, 1746-1758.	2.2	22
128	Oak genotype and phenolic compounds differently affect the performance of two insect herbivores with contrasting diet breadth. <i>Tree Physiology</i> , 2019, 39, 615-627.	3.1	22
129	Analysis of Protein Expression along the Normal to Tension Wood Gradient in <i>Eucalyptus gunnii</i> . <i>Holzforschung</i> , 2003, 57, 353-358.	1.9	21
130	Isolation and characterization of nuclear microsatellite loci in <i>Pinus pinaster</i> Ait. <i>Molecular Ecology Notes</i> , 2005, 5, 57-59.	1.7	21
131	Polygenic adaptation and negative selection across traits, years and environments in a long-lived plant species (<i>Pinus pinaster</i> Ait., Pinaceae). <i>Molecular Ecology</i> , 2022, 31, 2089-2105.	3.9	21
132	Genotype x environment interaction for root traits in maize, as analysed with factorial regression models. <i>Euphytica</i> , 1995, 81, 85-92.	1.2	20
133	<i>Fagaceae Trees.</i> , 2007, , 161-187.		20
134	Interaction between environmental factors affects the accumulation of root proteins in hydroponically grown <i>Eucalyptus globulus</i> (Labill.). <i>Plant Physiology and Biochemistry</i> , 2011, 49, 69-76.	5.8	20
135	Genetic architecture of carbon isotope composition and growth in <i>Eucalyptus</i> across multiple environments. <i>New Phytologist</i> , 2015, 206, 1437-1449.	7.3	20
136	The genetics of exapted resistance to two exotic pathogens in pedunculate oak. <i>New Phytologist</i> , 2020, 226, 1088-1103.	7.3	20
137	Micro-evolutionary patterns of juvenile wood density in a pine species. <i>Plant Ecology</i> , 2012, 213, 1781-1792.	1.6	19
138	Osmotic adjustment in <i>Pinus pinaster</i> cuttings in response to a soil drying cycle. <i>Annals of Forest Science</i> , 2002, 59, 795-799.	2.0	18
139	Development of Target Sequence Capture and Estimation of Genomic Relatedness in a Mixed Oak Stand. <i>Frontiers in Plant Science</i> , 2018, 9, 996.	3.6	18
140	A candidate gene for lignin composition in <i>Eucalyptus</i> : cinnamoyl-CoA reductase (CCR). <i>Tree Genetics and Genomes</i> , 2012, 8, 353-364.	1.6	17
141	Contribution of two-dimensional electrophoresis of proteins to maritime pine genetics. <i>Annales Des Sciences Forestières</i> , 1997, 54, 225-236.	1.2	17
142	Understanding the genetic bases of adaptation to soil water deficit in trees through the examination of water use efficiency and cavitation resistance: maritime pine as a case study. <i>The Journal of Plant Hydraulics</i> , 0, 3, e008.	1.0	17
143	A Chromosome-Level Genome Assembly of the European Beech (<i>Fagus sylvatica</i>) Reveals Anomalies for Organelle DNA Integration, Repeat Content and Distribution of SNPs. <i>Frontiers in Genetics</i> , 2021, 12, 691058.	2.3	17
144	Genetic mapping of EST-derived simple sequence repeats (EST-SSRs) to identify QTL for leaf morphological characters in a <i>Quercus robur</i> full-sib family. <i>Tree Genetics and Genomes</i> , 2013, 9, 1361-1367.	1.6	16

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145	Forward selection in a maritime pine polycross progeny trial using pedigree reconstruction. <i>Annals of Forest Science</i> , 2017, 74, 1.	2.0	16
146	Marker trait association for autumn cold acclimation and growth rhythm in <i>Pinus sylvestris</i> . <i>Scandinavian Journal of Forest Research</i> , 2003, 18, 29-38.	1.4	15
147	Analysis of the distribution of marker classes in a genetic linkage map: a case study in Norway spruce (<i>Picea abies</i> karst). <i>Tree Genetics and Genomes</i> , 2005, 1, 93-102.	1.6	15
148	Copper stress-induced changes in leaf soluble proteome of Cu-sensitive and tolerant <i>Agrostis capillaris</i> L. populations. <i>Proteomics</i> , 2016, 16, 1386-1397.	2.2	15
149	Linked selection shapes the landscape of genomic variation in three oak species. <i>New Phytologist</i> , 2022, 233, 555-568.	7.3	14
150	Genetic basis of growth, spring phenology, and susceptibility to biotic stressors in maritime pine. <i>Evolutionary Applications</i> , 2021, 14, 2750-2772.	3.1	14
151	A proteomic analysis of Spanish broom (<i>Spartium junceum</i> L.) root growing on a slope condition. <i>Plant Science</i> , 2006, 170, 926-935.	3.6	13
152	<i>Pines</i> , 2007, , 29-92.		13
153	ACC Oxidase and ACC Synthase Expression Profiles after Leaning of Young <i>Radiata</i> (<i>P. radiata</i> D. Don) and Maritime Pine (<i>P. pinaster</i> Ait.) Seedlings. <i>Journal of Plant Growth Regulation</i> , 2012, 31, 382-391.	5.1	13
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