

Antoine Kremer

List of Publications by Year in descending order

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Version: 2024-02-01

159
papers

16,688
citations

13854

67
h-index

16636

123
g-index

173
all docs

173
docs citations

173
times ranked

13462
citing authors

#	ARTICLE	IF	CITATIONS
1	Climate change impacts, adaptive capacity, and vulnerability of European forest ecosystems. <i>Forest Ecology and Management</i> , 2010, 259, 698-709.	1.4	1,684
2	Potential for evolutionary responses to climate change – evidence from tree populations. <i>Global Change Biology</i> , 2013, 19, 1645-1661.	4.2	705
3	Forest tree genomics: growing resources and applications. <i>Nature Reviews Genetics</i> , 2011, 12, 111-122.	7.7	623
4	Identification of refugia and post-glacial colonisation routes of European white oaks based on chloroplast DNA and fossil pollen evidence. <i>Forest Ecology and Management</i> , 2002, 156, 49-74.	1.4	577
5	Long-distance gene flow and adaptation of forest trees to rapid climate change. <i>Ecology Letters</i> , 2012, 15, 378-392.	3.0	550
6	Chloroplast DNA variation in European white oaks. <i>Forest Ecology and Management</i> , 2002, 156, 5-26.	1.4	424
7	Hybridization as a mechanism of invasion in oaks. <i>New Phytologist</i> , 2004, 161, 151-164.	3.5	356
8	Leaf phenology sensitivity to temperature in European trees: Do within-species populations exhibit similar responses?. <i>Agricultural and Forest Meteorology</i> , 2009, 149, 735-744.	1.9	324
9	Oak genome reveals facets of long lifespan. <i>Nature Plants</i> , 2018, 4, 440-452.	4.7	303
10	Within-population genetic structure in <i>Quercus robur</i> L. and <i>Quercus petraea</i> (Matt.) Liebl. assessed with isozymes and microsatellites. <i>Molecular Ecology</i> , 1998, 7, 317-328.	2.0	299
11	Species relative abundance and direction of introgression in oaks. <i>Molecular Ecology</i> , 2009, 18, 2228-2242.	2.0	296
12	Pollen dispersal inferred from paternity analysis in a mixed oak stand of <i>Quercus robur</i> L. and <i>Q. petraea</i> (Matt.) Liebl.. <i>Molecular Ecology</i> , 1999, 8, 831-841.	2.0	286
13	Assessing the effects of climate change on the phenology of European temperate trees. <i>Agricultural and Forest Meteorology</i> , 2011, 151, 969-980.	1.9	286
14	The genetic differentiation at quantitative trait loci under local adaptation. <i>Molecular Ecology</i> , 2012, 21, 1548-1566.	2.0	278
15	Fine-scale genetic structure and gene dispersal inferences in 10 Neotropical tree species. <i>Molecular Ecology</i> , 2005, 15, 559-571.	2.0	277
16	Identification and characterization of (GA/CT) _n -microsatellite loci from <i>Quercus petraea</i> . <i>Plant Molecular Biology</i> , 1997, 33, 1093-1096.	2.0	261
17	Altitudinal differentiation in growth and phenology among populations of temperate-zone tree species growing in a common garden. <i>Canadian Journal of Forest Research</i> , 2009, 39, 1259-1269.	0.8	253
18	Responses of canopy duration to temperature changes in four temperate tree species: relative contributions of spring and autumn leaf phenology. <i>Oecologia</i> , 2009, 161, 187-198.	0.9	248

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19	Comparison of microsatellites and amplified fragment length polymorphism markers for parentage analysis. <i>Molecular Ecology</i> , 2000, 9, 1037-1048.	2.0	233
20	Genetic Variability at Neutral Markers, Quantitative Trait Loci and Trait in a Subdivided Population Under Selection. <i>Genetics</i> , 2003, 164, 1205-1219.	1.2	211
21	Geographic structure of chloroplast DNA polymorphisms in European oaks. <i>Theoretical and Applied Genetics</i> , 1993, 87, 122-128.	1.8	204
22	Quantifying phenological plasticity to temperature in two temperate tree species. <i>Functional Ecology</i> , 2010, 24, 1211-1218.	1.7	203
23	Genome Scanning for Interspecific Differentiation Between Two Closely Related Oak Species [<i>Quercus robur</i> L. and <i>Q. petraea</i> (Matt.) Liebl.]. <i>Genetics</i> , 2004, 168, 1615-1626.	1.2	201
24	famoz: a software for parentage analysis using dominant, codominant and uniparentally inherited markers. <i>Molecular Ecology Notes</i> , 2003, 3, 479-481.	1.7	198
25	Genomic landscape of the global oak phylogeny. <i>New Phytologist</i> , 2020, 226, 1198-1212.	3.5	186
26	Finite island model for organelle and nuclear genes in plants. <i>Heredity</i> , 1993, 71, 630-641.	1.2	183
27	Reviewing the Science and Implementation of Climate Change Adaptation Measures in European Forestry. <i>Forests</i> , 2011, 2, 961-982.	0.9	169
28	Leaf morphological differentiation between <i>Quercus robur</i> and <i>Quercus petraea</i> is stable across western European mixed oak stands. <i>Annals of Forest Science</i> , 2002, 59, 777-787.	0.8	161
29	Colonization with long-distance seed dispersal and genetic structure of maternally inherited genes in forest trees: a simulation study. <i>Genetical Research</i> , 1997, 69, 117-125.	0.3	160
30	To what extent is altitudinal variation of functional traits driven by genetic adaptation in European oak and beech?. <i>Tree Physiology</i> , 2011, 31, 1164-1174.	1.4	157
31	Molecular technologies for biodiversity evaluation: Opportunities and challenges. <i>Nature Biotechnology</i> , 1997, 15, 625-628.	9.4	147
32	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.	1.2	144
33	Cumulative effects of founding events during colonisation on genetic diversity and differentiation in an island and stepping-stone model. <i>Journal of Evolutionary Biology</i> , 1998, 11, 495.	0.8	142
34	Signatures of local adaptation in candidate genes of oaks (<i>Quercus</i> spp.) with respect to present and future climatic conditions. <i>Molecular Ecology</i> , 2016, 25, 5907-5924.	2.0	141
35	Multiple nuclear genes stabilize the phylogenetic backbone of the genus <i>Quercus</i> . <i>Systematics and Biodiversity</i> , 2014, 12, 405-423.	0.5	134
36	Sampling within the genome for measuring within-population diversity: trade-offs between markers. <i>Molecular Ecology</i> , 2002, 11, 1145-1156.	2.0	129

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37	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.	1.8	125
38	MATING SYSTEM AND ASYMMETRIC HYBRIDIZATION IN A MIXED STAND OF EUROPEAN OAKS. <i>Evolution; International Journal of Organic Evolution</i> , 1996, 50, 900-908.	1.1	120
39	Genetic diversity within and among <i>Pinus pinaster</i> populations: comparison between AFLP and microsatellite markers. <i>Heredity</i> , 2001, 86, 469-479.	1.2	117
40	Adaptive introgression as a driver of local adaptation to climate in European white oaks. <i>New Phytologist</i> , 2020, 226, 1171-1182.	3.5	117
41	Transcriptome analysis of bud burst in sessile oak (<i>Quercus petraea</i>). <i>New Phytologist</i> , 2006, 170, 723-738.	3.5	116
42	Extensive recent secondary contacts between four European white oak species. <i>New Phytologist</i> , 2017, 214, 865-878.	3.5	113
43	Oaks: an evolutionary success story. <i>New Phytologist</i> , 2020, 226, 987-1011.	3.5	112
44	Genomics of Fagaceae. <i>Tree Genetics and Genomes</i> , 2012, 8, 583-610.	0.6	109
45	Water-deficit-responsive proteins in maritime pine. <i>Plant Molecular Biology</i> , 1998, 38, 587-596.	2.0	108
46	Decoding the oak genome: public release of sequence data, assembly, annotation and publication strategies. <i>Molecular Ecology Resources</i> , 2016, 16, 254-265.	2.2	108
47	Genetic divergence in forest trees: understanding the consequences of climate change. <i>Functional Ecology</i> , 2014, 28, 22-36.	1.7	105
48	Imprints of Natural Selection Along Environmental Gradients in Phenology-Related Genes of <i>Quercus petraea</i> . <i>Genetics</i> , 2013, 195, 495-512.	1.2	104
49	Is there a correlation between chloroplastic and nuclear divergence, or what are the roles of history and selection on genetic diversity in European oaks?. <i>Forest Ecology and Management</i> , 2002, 156, 75-87.	1.4	101
50	Quantitative trait loci controlling water use efficiency and related traits in <i>Quercus robur</i> L.. <i>Tree Genetics and Genomes</i> , 2008, 4, 263-278.	0.6	96
51	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.	1.8	93
52	Impact of selective logging on genetic composition and demographic structure of four tropical tree species. <i>Biological Conservation</i> , 2006, 131, 386-401.	1.9	93
53	Shared alleles in sympatric oaks: recurrent gene flow is a more parsimonious explanation than ancestral polymorphism. <i>Molecular Ecology</i> , 2006, 15, 2007-2012.	2.0	93
54	Comparison of Quantitative Trait Loci for Adaptive Traits Between Oak and Chestnut Based on an Expressed Sequence Tag Consensus Map. <i>Genetics</i> , 2006, 172, 533-546.	1.2	93

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55	High Rates of Gene Flow by Pollen and Seed in Oak Populations across Europe. PLoS ONE, 2014, 9, e85130.	1.1	92
56	Adaptive and plastic responses of <i>Quercus petraea</i> populations to climate across Europe. Global Change Biology, 2017, 23, 2831-2847.	4.2	92
57	Assessing inter- and intraspecific variability of xylem vulnerability to embolism in oaks. Forest Ecology and Management, 2018, 424, 53-61.	1.4	84
58	Bioinformatic analysis of ESTs collected by Sanger and pyrosequencing methods for a keystone forest tree species: oak. BMC Genomics, 2010, 11, 650.	1.2	82
59	Transcriptional profiling of bud dormancy induction and release in oak by next-generation sequencing. BMC Genomics, 2013, 14, 236.	1.2	82
60	Geographical structure of gene diversity in <i>Quercus petraea</i> (Matt.) Liebl. I. Monolocus patterns of variation. Heredity, 1995, 75, 506-517.	1.2	81
61	Interspecific gene flow in a multispecies oak hybrid zone in the Sierra Tarahumara of Mexico. Annals of Botany, 2010, 105, 389-399.	1.4	81
62	Intraspecific genetic structure in a mixed population of <i>Quercus petraea</i> (Matt.) Liebl and <i>Q. robur</i> L.. Heredity, 1994, 73, 130-141.	1.2	79
63	Chloroplast DNA variation of <i>Quercus rubra</i> L. in North America and comparison with other Fagaceae. Molecular Ecology, 2005, 14, 513-524.	2.0	77
64	Mating System and Asymmetric Hybridization in a Mixed Stand of European Oaks. Evolution; International Journal of Organic Evolution, 1996, 50, 900.	1.1	76
65	Chilling and heat requirements for leaf unfolding in European beech and sessile oak populations at the southern limit of their distribution range. International Journal of Biometeorology, 2014, 58, 1853-1864.	1.3	75
66	Increasing spring temperatures favor oak seed production in temperate areas. Scientific Reports, 2017, 7, 8555.	1.6	73
67	High-throughput <i>sc</i> DNA sequencing of ancient wood. Molecular Ecology, 2018, 27, 1138-1154.	2.0	73
68	A framework for modeling adaptive forest management and decision making under climate change. Ecology and Society, 2017, 22, .	1.0	72
69	Chloroplast DNA variation of oaks in France and the influence of forest fragmentation on genetic diversity. Forest Ecology and Management, 2002, 156, 115-129.	1.4	70
70	Population differentiation of sessile oak at the altitudinal front of migration in the French Pyrenees. Molecular Ecology, 2010, 19, 2626-2639.	2.0	68
71	Development and implementation of a highly-multiplexed SNP array for genetic mapping in maritime pine and comparative mapping with loblolly pine. BMC Genomics, 2011, 12, 368.	1.2	66
72	Checking the geographical origin of oak wood: molecular and statistical tools. Molecular Ecology, 2003, 12, 1629-1636.	2.0	63

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73	Multilocus and Multitrait Measures of Differentiation for Gene Markers and Phenotypic Traits. <i>Genetics</i> , 1997, 145, 1229-1241.	1.2	63
74	Long-distance pollen flow and tolerance to selfing in a neotropical tree species. <i>Molecular Ecology</i> , 2004, 13, 1055-1064.	2.0	62
75	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.	2.0	61
76	High-density linkage mapping and distribution of segregation distortion regions in the oak genome. <i>DNA Research</i> , 2016, 23, 115-124.	1.5	61
77	Spatial and temporal distribution of chloroplast DNA polymorphism in a tropical tree species. <i>Molecular Ecology</i> , 2000, 9, 1089-1098.	2.0	59
78	Fine-scale spatial genetic structure of eight tropical tree species as analysed by RAPDs. <i>Heredity</i> , 2001, 87, 497-507.	1.2	58
79	Separation and characterization of needle and xylem maritime pine proteins. <i>Electrophoresis</i> , 1999, 20, 1098-1108.	1.3	57
80	Range margin populations show high climate adaptation lags in European trees. <i>Global Change Biology</i> , 2020, 26, 484-495.	4.2	56
81	Heritability and genetic architecture of reproduction-related traits in a temperate oak species. <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	0.6	55
82	Comparative mapping in the Fagaceae and beyond with EST-SSRs. <i>BMC Plant Biology</i> , 2012, 12, 153.	1.6	54
83	Genetic Diversity Increases Insect Herbivory on Oak Saplings. <i>PLoS ONE</i> , 2012, 7, e44247.	1.1	54
84	Peut-on efficacement sélectionner la densité du bois chez le pin maritime (<i>Pinus pinaster</i> Ait.) au stade juvénile?. <i>Annals of Forest Science</i> , 2008, 65, 106-106.	0.8	52
85	Hardwood Tree Genomics: Unlocking Woody Plant Biology. <i>Frontiers in Plant Science</i> , 2018, 9, 1799.	1.7	50
86	Developing SSCP markers in two <i>Pinus</i> species. <i>Molecular Breeding</i> , 1999, 5, 21-31.	1.0	49
87	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.	1.4	49
88	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.	1.2	49
89	Quantitative trait loci of tolerance to waterlogging in a European oak (<i>Quercus robur</i> L.): physiological relevance and temporal effect patterns. <i>Plant, Cell and Environment</i> , 2007, 30, 422-434.	2.8	47
90	Strength and variability of postmating reproductive isolating barriers between four European white oak species. <i>Tree Genetics and Genomes</i> , 2013, 9, 841-853.	0.6	46

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91	Massive postglacial gene flow between European white oaks uncovered genes underlying species barriers. <i>New Phytologist</i> , 2020, 226, 1183-1197.	3.5	46
92	Common garden comparisons confirm inherited differences in sensitivity to climate change between forest tree species. <i>PeerJ</i> , 2019, 7, e6213.	0.9	43
93	Geographical structure of gene diversity in <i>Quercus petraea</i> (Matt.) Liebl. III. Patterns of variation identified by geostatistical analyses. <i>Heredity</i> , 1998, 80, 464-473.	1.2	39
94	Assortative mating and gene flow generate clinal phenological variation in trees. <i>BMC Evolutionary Biology</i> , 2012, 12, 79.	3.2	39
95	Predictions of age-age correlations of total height based on serial correlations between height increments in Maritime pine (<i>Pinus pinaster</i> Ait.). <i>Theoretical and Applied Genetics</i> , 1992, 85-85, 152-158.	1.8	38
96	Genetic differentiation in functional traits among European sessile oak populations. <i>Tree Physiology</i> , 2019, 39, 1736-1749.	1.4	38
97	Role of waterlogging-responsive genes in shaping interspecific differentiation between two sympatric oak species. <i>Tree Physiology</i> , 2012, 32, 119-134.	1.4	36
98	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.	2.2	35
99	What are the consequences of growth selection on wood density in the French maritime pine breeding programme?. <i>Tree Genetics and Genomes</i> , 2009, 5, 11-25.	0.6	34
100	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.	1.2	33
101	Fine-scale species distribution changes in a mixed oak stand over two successive generations. <i>New Phytologist</i> , 2017, 215, 126-139.	3.5	33
102	Genome-wide analyses of introgression between two sympatric Asian oak species. <i>Nature Ecology and Evolution</i> , 2022, 6, 924-935.	3.4	32
103	Characterisation and natural variation of a dehydrin gene in <i>Quercus petraea</i> (Matt.) Liebl.. <i>Plant Biology</i> , 2011, 13, 881-887.	1.8	30
104	<i>Q_{ST} <math>\hat{A}</math></i> & <i>F_{ST} <math>\hat{A}</math></i> As a signature of canalization. <i>Molecular Ecology</i> , 2012, 21, 5646-5655.	2.0	30
105	Provenance hybridization in a diallel mating scheme of maritime pine (<i>Pinus pinaster</i>). I. Means and variance components. <i>Canadian Journal of Forest Research</i> , 2000, 30, 1-9.	0.8	29
106	Historical and contemporary dynamics of adaptive differentiation in European oaks. , 2010, , 101-122.		29
107	Impacts of local adaptation of forest trees on associations with herbivorous insects: implications for adaptive forest management. <i>Evolutionary Applications</i> , 2015, 8, 972-987.	1.5	29
108	Inheritance of Isozymes in Pedunculate Oak (<i>Quercus robur</i> L.). <i>Journal of Heredity</i> , 1996, 87, 364-370.	1.0	27

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109	Augmentation de la capacité photosynthétique avec l'altitude: mesures des changements gazeux et pressions partielles de CO ₂ ambiante et constante. <i>Annals of Forest Science</i> , 2009, 66, 505-505.	0.8	27
110	Community genetics in the time of next-generation molecular technologies. <i>Molecular Ecology</i> , 2013, 22, 3198-3207.	2.0	25
111	Quantitative trait loci mapping for vegetative propagation in pedunculate oak. <i>Annals of Forest Science</i> , 2005, 62, 369-374.	0.8	24
112	Linkage mapping of osmotic stress induced genes of oak. <i>Tree Genetics and Genomes</i> , 2005, 1, 31-40.	0.6	24
113	Insights into drought adaptation of two European oak species revealed by nucleotide diversity of candidate genes. <i>Tree Genetics and Genomes</i> , 2013, 9, 1179-1192.	0.6	24
114	Genome-wide evolutionary response of European oaks during the Anthropocene. <i>Evolution Letters</i> , 2022, 6, 4-20.	1.6	24
115	Oak symbolism in the light of genomics. <i>New Phytologist</i> , 2020, 226, 1012-1017.	3.5	23
116	Standardized genetic diversity-life history correlates for improved genetic resource management of Neotropical trees. <i>Diversity and Distributions</i> , 2018, 24, 730-741.	1.9	21
117	Fagaceae Trees. , 2007, , 161-187.		20
118	Development of Target Sequence Capture and Estimation of Genomic Relatedness in a Mixed Oak Stand. <i>Frontiers in Plant Science</i> , 2018, 9, 996.	1.7	18
119	How does contemporary selection shape oak phenotypes?. <i>Evolutionary Applications</i> , 2020, 13, 2772-2790.	1.5	18
120	Inferring phenotypic plasticity and population responses to climate across tree species ranges using forest inventory data. <i>Global Ecology and Biogeography</i> , 2019, 28, 1259-1271.	2.7	17
121	Reproductive biology of <i>Corymbia citriodora</i> subsp. <i>variegata</i> and effective pollination across its native range in Queensland, Australia. <i>Southern Forests</i> , 2009, 71, 125-132.	0.2	16
122	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.	0.6	16
123	Low genetic differentiation between two morphologically and ecologically distinct giant-leaved Mexican oaks. <i>Plant Systematics and Evolution</i> , 2019, 305, 89-101.	0.3	16
124	Microevolution of European temperate oaks in response to environmental changes. <i>Comptes Rendus - Biologies</i> , 2016, 339, 263-7.	0.1	15
125	Back to America: tracking the origin of European introduced populations of <i>Quercus rubra</i> L.. <i>Genome</i> , 2017, 60, 778-790.	0.9	15
126	Wood density variability in successive breeding populations of maritime pine. <i>Canadian Journal of Forest Research</i> , 2008, 38, 2148-2158.	0.8	14

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127	Maturation of maritime pine (<i>Pinus pinaster</i> Ait.) seedlings after exposure to a period of continuous light. <i>Tree Physiology</i> , 1993, 12, 363-378.	1.4	13
128	Growth and phenology of 1-year-old maritime pine (<i>Pinus pinaster</i>) seedlings under continuous light: implications for early selection. <i>Canadian Journal of Forest Research</i> , 1993, 23, 1325-1336.	0.8	12
129	Provenance hybridization in a diallel mating scheme of maritime pine (<i>Pinus pinaster</i>). I. Means and variance components. <i>Canadian Journal of Forest Research</i> , 2000, 30, 1-9.	0.8	12
130	Relationship between first-season free growth components and later field height growth in maritime pine (<i>Pinus pinaster</i>). <i>Canadian Journal of Forest Research</i> , 1989, 19, 690-699.	0.8	11
131	Provenance hybridization in a diallel mating scheme of maritime pine (<i>Pinus pinaster</i>). II. Heterosis. <i>Canadian Journal of Forest Research</i> , 2000, 30, 10-16.	0.8	11
132	Germination and phenology of 1-year-old maritime pine (<i>Pinus pinaster</i> Ait.) seedlings under continuous light. <i>Trees - Structure and Function</i> , 1992, 7, 48.	0.9	9
133	Characterization of <i>Pinus pinaster</i> seedling growth in different photoperiods and thermoperiods in a phytotron as a basis for early selection. <i>Scandinavian Journal of Forest Research</i> , 1995, 10, 129-139.	0.5	9
134	In situ estimation of genetic variation of functional and ecological traits in <i>Quercus petraea</i> and <i>Q. robur</i> . <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	0.6	9
135	Provenance variation and seed sourcing for sessile oak (<i>Quercus petraea</i> (Matt.) Liebl.) in France. <i>Annals of Forest Science</i> , 2022, 79, .	0.8	9
136	The relation between first-season bud morphology and second-season shoot morphology of jack pine seedlings. <i>Canadian Journal of Forest Research</i> , 1982, 12, 893-904.	0.8	8
137	Forest ecosystem genomics and adaptation: EVOLTREE conference report. <i>Tree Genetics and Genomes</i> , 2011, 7, 869-875.	0.6	7
138	A sample view of the pedunculate oak (<i>Quercus robur</i>) genome from the sequencing of hypomethylated and random genomic libraries. <i>Tree Genetics and Genomes</i> , 2011, 7, 1277-1285.	0.6	7
139	Organisation spatiale de la diversité génétique et flux polliniques dans une chênaie mixte. <i>Genetics Selection Evolution</i> , 1998, 30, 1.	1.2	6
140	Species-specific alleles at a β -tubulin gene show significant associations with leaf morphological variation within <i>Quercus petraea</i> and <i>Q. robur</i> populations. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	6
141	X-ray computed tomography to decipher the genetic architecture of tree branching traits: oak as a case study. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	6
142	Distribution of relative growth rates and variation of cytohistological zonation in apical meristems of seedlings of two contrasting open-pollinated jack pine (<i>Pinus banksiana</i>) families. <i>Canadian Journal of Forest Research</i> , 1984, 14, 297-310.	0.8	5
143	The beta-binomial model for estimating heritabilities of binary traits. <i>Theoretical and Applied Genetics</i> , 1995, 91, 544-552.	1.8	5
144	Dynamics and conservation of genetic diversity in forest ecosystems. <i>Forest Ecology and Management</i> , 2004, 197, 1-2.	1.4	5

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145	Genomics of forest and ecosystem health in the Fagaceae: meeting report. <i>Tree Genetics and Genomes</i> , 2010, 6, 815-820.	0.6	5
146	<i>Quercus</i> species divergence is driven by natural selection on evolutionarily less integrated traits. <i>Heredity</i> , 2021, 126, 366-382.	1.2	5
147	Provenance hybridization in a diallel mating scheme of maritime pine (<i>Pinus pinaster</i>). II. Heterosis. <i>Canadian Journal of Forest Research</i> , 2000, 30, 10-16.	0.8	5
148	Metapop: An individual-based model for simulating the evolution of tree populations in spatially and temporally heterogeneous landscapes. <i>Molecular Ecology Resources</i> , 2019, 19, 296-305.	2.2	4
149	Population differentiation for adaptive traits and their underlying loci in forest trees: theoretical predictions and experimental results. <i>Forestry Sciences</i> , 2000, , 59-74.	0.4	4
150	Detection of genes involved in bud phenology in sessile oak (<i>Quercus petraea</i> Matt. Liebl) combining digital expression analysis and Q-PCR. <i>BMC Proceedings</i> , 2011, 5, .	1.8	3
151	Genomic Resources Notes Accepted 1 August 2015 - 31 September 2015. <i>Molecular Ecology Resources</i> , 2016, 16, 377-377.	2.2	3
152	Countergradient variation of reproductive effort in a widely distributed temperate oak. <i>Functional Ecology</i> , 2021, 35, 1745-1755.	1.7	3
153	Effect of the purposive choice of families on the estimates of the juvenile-mature correlation derived from retrospective tests. <i>Canadian Journal of Forest Research</i> , 1994, 24, 756-761.	0.8	2
154	La gestion de la variabilité génétique dans le programme d'amélioration du Pin maritime (<i>Pinus pinaster</i>). <i>Tj ETQ</i> , 2000, 0, 0 rgBT	0.0	0
155	Missing heritability and missing Fst of candidate genes: why does gene variation differ from trait variation in trees?. <i>BMC Proceedings</i> , 2011, 5, .	1.8	2
156	Long-term and large-scale <i>Quercus petraea</i> population survey conducted in provenance tests installed in France. <i>Annals of Forest Science</i> , 2022, 79, .	0.8	2
157	Secondary leader growth as a selection criterion in <i>Pinus pinaster</i> . <i>Scandinavian Journal of Forest Research</i> , 1994, 9, 233-244.	0.5	1
158	WALLENBERG PRICE 2006. <i>Annals of Forest Science</i> , 2006, 63, 809-811.	0.8	1
159	Migrer, une condition d'existence du vivant. <i>Lignes</i> , 2019, n° 58, 187-193.	0.0	0