

Yousry A El-Kassaby

List of Publications by Year in descending order

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253
papers

6,444
citations

76326

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110387

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all docs

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docs citations

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times ranked

4753
citing authors

#	ARTICLE	IF	CITATIONS
1	Geographical and environmental gradients shape phenotypic trait variation and genetic structure in <i>Populus trichocarpa</i> . <i>New Phytologist</i> , 2014, 201, 1263-1276.	7.3	185
2	Quantitative Genetics and Genomics Converge to Accelerate Forest Tree Breeding. <i>Frontiers in Plant Science</i> , 2018, 9, 1693.	3.6	176
3	Genome resequencing reveals multiscale geographic structure and extensive linkage disequilibrium in the forest tree <i>Populus trichocarpa</i> . <i>New Phytologist</i> , 2012, 196, 713-725.	7.3	173
4	Genome-wide association implicates numerous genes underlying ecological trait variation in natural populations of <i>Populus trichocarpa</i> . <i>New Phytologist</i> , 2014, 203, 535-553.	7.3	171
5	Genome-wide association mapping for wood characteristics in <i>Populus trichocarpa</i> identifies an array of candidate single nucleotide polymorphisms. <i>New Phytologist</i> , 2013, 200, 710-726.	7.3	158
6	Single-copy, species-transferable microsatellite markers developed from loblolly pine ESTs. <i>Theoretical and Applied Genetics</i> , 2004, 109, 361-369.	3.6	136
7	The role of forest genetic resources in responding to biotic and abiotic factors in the context of anthropogenic climate change. <i>Forest Ecology and Management</i> , 2014, 333, 76-87.	3.2	125
8	The nature of inbreeding in a seed orchard of Douglas fir as shown by an efficient multilocus model. <i>Theoretical and Applied Genetics</i> , 1985, 71, 375-384.	3.6	109
9	Breeding without breeding. <i>Genetical Research</i> , 2009, 91, 111-120.	0.9	109
10	High-resolution genetic mapping of allelic variants associated with cell wall chemistry in <i>Populus</i> . <i>BMC Genomics</i> , 2015, 16, 24.	2.8	106
11	Association genetics, geography and ecophysiology link stomatal patterning in <i>Populus trichocarpa</i> with carbon gain and disease resistance trade-offs. <i>Molecular Ecology</i> , 2014, 23, 5771-5790.	3.9	103
12	<i>Populus trichocarpa</i> cell wall chemistry and ultrastructure trait variation, genetic control and genetic correlations. <i>New Phytologist</i> , 2013, 197, 777-790.	7.3	100
13	Inheritance of chloroplast and mitochondrial DNA in <i>Picea</i> and composition of hybrids from introgression zones. <i>Theoretical and Applied Genetics</i> , 1991, 82, 242-248.	3.6	97
14	A 34K SNP genotyping array for <i>Populus trichocarpa</i> : Design, application to the study of natural populations and transferability to other <i>Populus</i> species. <i>Molecular Ecology Resources</i> , 2013, 13, 306-323.	4.8	92
15	Assessment of the Genetic Diversity in Forest Tree Populations Using Molecular Markers. <i>Diversity</i> , 2014, 6, 283-295.	1.7	90
16	Chromosome-level genome assembly of a parent species of widely cultivated azaleas. <i>Nature Communications</i> , 2020, 11, 5269.	12.8	90
17	Bareroot versus container stocktypes: a performance comparison. <i>New Forests</i> , 2016, 47, 1-51.	1.7	87
18	Prediction accuracies for growth and wood attributes of interior spruce in space using genotyping-by-sequencing. <i>BMC Genomics</i> , 2015, 16, 370.	2.8	86

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19	A comparison of genomic selection models across time in interior spruce (<i>Picea engelmannii</i> Å— <i>glauca</i>) using unordered SNP imputation methods. <i>Heredity</i> , 2015, 115, 547-555.	2.6	84
20	Impacts of Population Structure and Analytical Models in Genome-Wide Association Studies of Complex Traits in Forest Trees: A Case Study in <i>Eucalyptus globulus</i> . <i>PLoS ONE</i> , 2013, 8, e81267.	2.5	82
21	Breeding without Breeding: Is a Complete Pedigree Necessary for Efficient Breeding?. <i>PLoS ONE</i> , 2011, 6, e25737.	2.5	76
22	The developing xylem transcriptome and genome-wide analysis of alternative splicing in <i>Populus trichocarpa</i> (black cottonwood) populations. <i>BMC Genomics</i> , 2013, 14, 359.	2.8	76
23	Implementation of the Realized Genomic Relationship Matrix to Open-Pollinated White Spruce Family Testing for Disentangling Additive from Nonadditive Genetic Effects. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 743-753.	1.8	73
24	Impact of selection and breeding on the genetic diversity in Douglas-fir. <i>Biodiversity and Conservation</i> , 1996, 5, 795-813.	2.6	68
25	Classifying seedlots of <i>Picea sitchensis</i> and <i>P. glauca</i> in zones of introgression using restriction analysis of chloroplast DNA. <i>Theoretical and Applied Genetics</i> , 1988, 76, 841-845.	3.6	66
26	Cost of reproduction in Douglas-fir. <i>Canadian Journal of Botany</i> , 1992, 70, 1429-1432.	1.1	65
27	Enzyme variation in natural populations of Sitka spruce (<i>Piceasitchensis</i>). 1. Genetic variation patterns among trees from 10 IUFRO provenances. <i>Canadian Journal of Forest Research</i> , 1980, 10, 415-422.	1.7	62
28	Levels of genetic diversity at different stages of the domestication cycle of interior spruce in British Columbia. <i>Theoretical and Applied Genetics</i> , 1997, 94, 83-90.	3.6	61
29	Allozyme inheritance, heterozygosity and outcrossing rate among <i>Pinus monticola</i> near Ladysmith, British Columbia. <i>Heredity</i> , 1987, 58, 173-181.	2.6	59
30	Allozyme variation in <i>Piceamariana</i> from Newfoundland: genetic diversity, population structure, and analysis of differentiation. <i>Canadian Journal of Forest Research</i> , 1986, 16, 713-720.	1.7	55
31	Mining conifersâ€™ mega-genome using rapid and efficient multiplexed high-throughput genotyping-by-sequencing (GBS) SNP discovery platform. <i>Tree Genetics and Genomes</i> , 2013, 9, 1537-1544.	1.6	54
32	Sexual homomorphism in dioecious trees: extensive tests fail to detect sexual dimorphism in <i>Populus</i> . <i>Scientific Reports</i> , 2017, 7, 1831.	3.3	54
33	The effect of slope aspect on vegetation attributes in a mountainous dry valley, Southwest China. <i>Scientific Reports</i> , 2020, 10, 16465.	3.3	53
34	Using <i>Populus</i> as a lignocellulosic feedstock for bioethanol. <i>Biotechnology Journal</i> , 2015, 10, 510-524.	3.5	52
35	Genomic prediction accuracies in space and time for height and wood density of Douglas-fir using exome capture as the genotyping platform. <i>BMC Genomics</i> , 2017, 18, 930.	2.8	52
36	Mixed Mating in an Experimental Population of Western Red Cedar, <i>Thuja plicata</i> . <i>Journal of Heredity</i> , 1994, 85, 227-231.	2.4	50

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37	Single-Step BLUP with Varying Genotyping Effort in Open-Pollinated <i>Picea glauca</i> . <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 935-942.	1.8	50
38	Genetic Diversity, Differentiation, and Inbreeding in Pacific Yew from British Columbia. <i>Journal of Heredity</i> , 1994, 85, 112-117.	2.4	49
39	Population Density and Mating Pattern in Western Larch. <i>Journal of Heredity</i> , 1996, 87, 438-443.	2.4	49
40	Landscape genomics predicts climate change-related genetic offset for the widespread <i>Platycladus orientalis</i> (Cupressaceae). <i>Evolutionary Applications</i> , 2020, 13, 665-676.	3.1	47
41	Levels of outcrossing and contamination in two <i>Pinus sylvestris</i> L. seed orchards in Northern Sweden. <i>Scandinavian Journal of Forest Research</i> , 1989, 4, 41-49.	1.4	46
42	Population structure and migration pattern of a conifer pathogen, <i>Grosmannia clavigera</i> , as influenced by its symbiont, the mountain pine beetle. <i>Molecular Ecology</i> , 2012, 21, 71-86.	3.9	46
43	Practical application of genomic selection in a doubled-haploid winter wheat breeding program. <i>Molecular Breeding</i> , 2017, 37, 117.	2.1	45
44	Light intensity affects the growth and flavonol biosynthesis of Ginkgo (<i>Ginkgo biloba</i> L.). <i>New Forests</i> , 2014, 45, 765-776.	1.7	43
45	Reproductive phenology, parental balance, and supplemental mass pollination in a sitka-spruce seed-orchard. <i>Forest Ecology and Management</i> , 1990, 31, 45-54.	3.2	42
46	Ecological genomics of variation in bud-break phenology and mechanisms of response to climate warming in <i>Populus trichocarpa</i> . <i>New Phytologist</i> , 2018, 220, 300-316.	7.3	40
47	Metabolome and transcriptome analyses reveal flavonoids biosynthesis differences in <i>Ginkgo biloba</i> associated with environmental conditions. <i>Industrial Crops and Products</i> , 2020, 158, 112963.	5.2	40
48	Interpretation of seed-germination parameters. <i>New Forests</i> , 1993, 7, 123-132.	1.7	39
49	De Novo Transcriptome Assembly and Characterization for the Widespread and Stress-Tolerant Conifer <i>Platycladus orientalis</i> . <i>PLoS ONE</i> , 2016, 11, e0148985.	2.5	39
50	Network analysis reveals the relationship among wood properties, gene expression levels and genotypes of natural <i>Populus trichocarpa</i> accessions. <i>New Phytologist</i> , 2013, 200, 727-742.	7.3	37
51	Geographic pattern of genetic variation in photosynthetic capacity and growth in two hardwood species from British Columbia. <i>Oecologia</i> , 2000, 123, 168-174.	2.0	36
52	Development of high transferability cpSSR markers for individual identification and genetic investigation in Cupressaceae species. <i>Ecology and Evolution</i> , 2018, 8, 4967-4977.	1.9	36
53	Estimation of relationship coefficients among progeny derived from wind-pollinated orchard seeds. <i>Theoretical and Applied Genetics</i> , 1994, 88, 267-272.	3.6	34
54	Estimating selfing rates from reconstructed pedigrees using multilocus genotype data. <i>Molecular Ecology</i> , 2012, 21, 100-116.	3.9	34

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55	A transcriptomics investigation into pine reproductive organ development. <i>New Phytologist</i> , 2016, 209, 1278-1289.	7.3	34
56	Landscape of fluid sets of hairpin-derived 21-/24-nt-long small RNAs at seed set uncovers special epigenetic features in <i>Picea glauca</i> . <i>Genome Biology and Evolution</i> , 2017, 9, evw283.	2.5	34
57	ASSOCIATIONS BETWEEN ALLOZYME GENOTYPES AND QUANTITATIVE TRAITS IN DOUGLAS-FIR [<i>PSEUDOTSUGA MENZIESII</i> (MIRB.) FRANCO]. <i>Genetics</i> , 1982, 101, 103-115.	2.9	33
58	<i>SubP</i> : a robust allopolyploid subgenome phasing method based on subgenome-specific <i>mers</i> . <i>New Phytologist</i> , 2022, 235, 801-809.	7.3	33
59	Genetic evaluation of alternative silvicultural systems in coastal montane forests: western hemlock and amabilis fir. <i>Theoretical and Applied Genetics</i> , 2003, 107, 598-610.	3.6	32
60	Improving accuracy of breeding values by incorporating genomic information in spatial-competition mixed models. <i>Molecular Breeding</i> , 2017, 37, 1.	2.1	32
61	In situ wood quality assessment in Douglas-fir. <i>Tree Genetics and Genomes</i> , 2011, 7, 553-561.	1.6	31
62	Evolutionary Quantitative Genomics of <i>Populus trichocarpa</i> . <i>PLoS ONE</i> , 2015, 10, e0142864.	2.5	31
63	Haplotype-resolved genome assembly and allele-specific gene expression in cultivated ginger. <i>Horticulture Research</i> , 2021, 8, 188.	6.3	31
64	Association Analysis Identifies <i>Melampsora columbiana</i> Poplar Leaf Rust Resistance SNPs. <i>PLoS ONE</i> , 2013, 8, e78423.	2.5	31
65	Budburst phenology of sitka spruce and its relationship to white pine weevil attack. <i>Forest Ecology and Management</i> , 2000, 127, 19-29.	3.2	30
66	Pedigree and mating system analyses in a western larch (<i>Larix occidentalis</i> Nutt.) experimental population. <i>Annals of Forest Science</i> , 2008, 65, 705-705.	2.0	30
67	Multienvironment genomic variance decomposition analysis of open-pollinated Interior spruce (<i>Picea</i>) Tj ETQq1 1 0.784314 rgBT /Ove	2.1	30
68	Estimation of clonal contribution to cone and seed crops in a Sitka spruce seed orchard. <i>Annales Des Sciences ForestiÃ`res</i> , 1993, 50, 461-467.	1.2	30
69	Population Structure of Mountain Pine Beetle Symbiont <i>Leptographium longiclavatum</i> and the Implication on the Multipartite Beetle-Fungi Relationships. <i>PLoS ONE</i> , 2014, 9, e105455.	2.5	30
70	Optimization of combined genetic gain and diversity for collection and deployment of seed orchard crops. <i>Tree Genetics and Genomes</i> , 2009, 5, 583-593.	1.6	28
71	Linkage disequilibrium vs. pedigree: Genomic selection prediction accuracy in conifer species. <i>PLoS ONE</i> , 2020, 15, e0232201.	2.5	28
72	Pollination dynamics in a Douglas-fir seed orchard as revealed by pedigree reconstruction. <i>Annals of Forest Science</i> , 2010, 67, 808-808.	2.0	27

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73	Breeding without breeding: selection using the genomic best linear unbiased predictor method (GBLUP). <i>New Forests</i> , 2012, 43, 631-637.	1.7	27
74	Chromosome-scale assembly and evolution of the tetraploid <i>Salvia splendens</i> (Lamiaceae) genome. <i>Horticulture Research</i> , 2021, 8, 177.	6.3	27
75	Genomic selection of juvenile height across a single-generational gap in Douglas-fir. <i>Heredity</i> , 2019, 122, 848-863.	2.6	26
76	Genetic variation in low elevation Douglas-fir of British Columbia and its relevance to gene conservation. <i>Biodiversity and Conservation</i> , 1996, 5, 779-794.	2.6	25
77	Comparative Nucleotide Diversity Across North American and European <i>Populus</i> Species. <i>Journal of Molecular Evolution</i> , 2012, 74, 257-272.	1.8	25
78	A role for <i>SPEECHLESS</i> in the integration of leaf stomatal patterning with the growth vs disease trade-off in poplar. <i>New Phytologist</i> , 2019, 223, 1888-1903.	7.3	25
79	Linkage disequilibrium dissection of the epigenetic quantitative trait loci (epiQTLs) underlying growth and wood properties in <i>Populus</i> . <i>New Phytologist</i> , 2020, 225, 1218-1233.	7.3	25
80	Impact of pollination environment manipulation on the apparent outcrossing rate in a Douglas-fir seed orchard. <i>Heredity</i> , 1991, 66, 55-59.	2.6	24
81	Considerations of correlated fertility between genders on genetic diversity: the <i>Pinus densiflora</i> seed orchard as a model. <i>Theoretical and Applied Genetics</i> , 2002, 105, 1183-1189.	3.6	24
82	Estimates of genetic parameters and breeding values from western larch open-pollinated families using marker-based relationship. <i>Tree Genetics and Genomes</i> , 2014, 10, 241-249.	1.6	24
83	Genomic-based multiple-trait evaluation in <i>Eucalyptus grandis</i> using dominant DArT markers. <i>Plant Science</i> , 2018, 271, 27-33.	3.6	23
84	Genetic variation of allozyme and quantitative traits in a selected Douglas-fir [<i>Pseudotsuga menziesii</i> var. <i>menziesii</i> (Mirb.) Franco] population. <i>Forest Ecology and Management</i> , 1982, 4, 115-126.	3.2	22
85	Effective number of pollen parents in clonal seed orchards. <i>Theoretical and Applied Genetics</i> , 1991, 82, 313-320.	3.6	22
86	Inbreeding and conservation genetics in whitebark pine. <i>Conservation Genetics</i> , 2003, 4, 581-593.	1.5	22
87	Development and characterization of microsatellite loci in western larch (<i>Larix occidentalis</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 4.8	4.8	22
88	Female Reproductive Success Variation in a <i>Pseudotsuga menziesii</i> Seed Orchard as Revealed by Pedigree Reconstruction from a Bulk Seed Collection. <i>Journal of Heredity</i> , 2010, 101, 164-168.	2.4	22
89	Localization of gene expression, tissue specificity of <i>Populus xylosyltransferase</i> genes by isolation and functional characterization of their promoters. <i>Plant Cell, Tissue and Organ Culture</i> , 2018, 134, 503-508.	2.3	22
90	Genetic interpretation of malate dehydrogenase isozymes in some conifer species. <i>Journal of Heredity</i> , 1981, 72, 451-452.	2.4	20

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91	Supplemental mass pollination success rate in a mature Douglas-fir seed orchard. Canadian Journal of Forest Research, 1993, 23, 1096-1099.	1.7	20
92	Timing of seed germination correlated with temperature-based environmental conditions during seed development in conifers. Seed Science Research, 2015, 25, 29-45.	1.7	20
93	Distribution and in situ conservation of a relic Chinese oil woody species <i>Xanthoceras sorbifolium</i> (yellowhorn). Canadian Journal of Forest Research, 2017, 47, 1450-1456.	1.7	20
94	Integrating fecundity variation and genetic relatedness in estimating the gene diversity of seed crops: <i>Pinus koraiensis</i> seed orchard as an example. Canadian Journal of Forest Research, 2017, 47, 366-370.	1.7	20
95	High throughput sequencing of small RNAs reveals dynamic microRNAs expression of lipid metabolism during <i>Camellia oleifera</i> and <i>C. meiocarpa</i> seed natural drying. BMC Genomics, 2017, 18, 546.	2.8	20
96	Predicting Douglas-fir wood density by artificial neural networks (ANN) based on progeny testing information. Holzforschung, 2013, 67, 771-777.	1.9	19
97	Colonization History, Host Distribution, Anthropogenic Influence and Landscape Features Shape Populations of White Pine Blister Rust, an Invasive Alien Tree Pathogen. PLoS ONE, 2015, 10, e0127916.	2.5	19
98	Hydrothermal carbonization of waste ginkgo leaf residues for solid biofuel production: Hydrochar characterization and its pelletization. Fuel, 2022, 324, 124341.	6.4	19
99	Congruence between parental reproductive investment and success determined by DNA-based pedigree reconstruction in conifer seed orchards. Canadian Journal of Forest Research, 2011, 41, 380-389.	1.7	18
100	Comparison of genetic parameters from marker-based relationship, sibship, and combined models in Scots pine multi-site open-pollinated tests. Tree Genetics and Genomes, 2013, 9, 1227-1235.	1.6	18
101	Phenotypic plasticity of natural <i>Populus trichocarpa</i> populations in response to temporally environmental change in a common garden. BMC Evolutionary Biology, 2019, 19, 231.	3.2	18
102	Temporospatial Flavonoids Metabolism Variation in <i>Ginkgo biloba</i> Leaves. Frontiers in Genetics, 2020, 11, 589326.	2.3	18
103	Synonymous mutation in <i>Growth Regulating Factor 15</i> of miR396a target sites enhances photosynthetic efficiency and heat tolerance in poplar. Journal of Experimental Botany, 2021, 72, 4502-4519.	4.8	18
104	Inheritance of Null Alleles for Microsatellites in the White Pine Weevil (<i>Pissodes strobi</i> [Peck]) Tj ETQq0 0 0 rgBT /Overlock 1QJf 50 222		17
105	Extensive Functional Pleiotropy of REVOLUTA Substantiated through Forward Genetics. Plant Physiology, 2014, 164, 548-554.	4.8	17
106	Changes in hormone flux and signaling in white spruce (<i>Picea glauca</i>) seeds during the transition from dormancy to germination in response to temperature cues. BMC Plant Biology, 2015, 15, 292.	3.6	17
107	Genetic Variation Related to High Elevation Adaptation Revealed by Common Garden Experiments in <i>Pinus yunnanensis</i> . Frontiers in Genetics, 2019, 10, 1405.	2.3	17
108	Integrative analysis of the metabolome and transcriptome reveals seed germination mechanism in <i>Punica granatum</i> L.. Journal of Integrative Agriculture, 2021, 20, 132-146.	3.5	17

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109	Clonal-row versus random seed orchard designs: interior spruce mating system evaluation. Canadian Journal of Forest Research, 2007, 37, 690-696.	1.7	16
110	Assessing sample size and variable number in multivariate data, with specific reference to cone morphology variation in a population of <i>Picea sitchensis</i> . Canadian Journal of Botany, 1985, 63, 232-241.	1.1	15
111	Forest genomics research and development in Canada: Priorities for developing an economic framework. Forestry Chronicle, 2015, 91, 60-70.	0.6	15
112	Predicting Future Seed Sourcing of <i>Platycladus orientalis</i> (L.) for Future Climates Using Climate Niche Models. Forests, 2017, 8, 471.	2.1	15
113	Evapotranspiration and favorable growing degree-days are key to tree height growth and ecosystem functioning: Meta-analyses of Pacific Northwest historical data. Scientific Reports, 2018, 8, 8228.	3.3	15
114	Local Adaptation and Response of <i>Platycladus orientalis</i> (L.) Franco Populations to Climate Change. Forests, 2019, 10, 622.	2.1	15
115	Formula Fertilization Promotes <i>Phoebe bournei</i> Robust Seedling Cultivation. Forests, 2020, 11, 781.	2.1	15
116	In Situ Genetic Evaluation of European Larch Across Climatic Regions Using Marker-Based Pedigree Reconstruction. Frontiers in Genetics, 2020, 11, 28.	2.3	15
117	Characterizing variations in growth characteristics between Douglas-fir with different genetic gain levels using airborne laser scanning. Trees - Structure and Function, 2020, 34, 649-664.	1.9	15
118	Closing the gap between phenotyping and genotyping: review of advanced, image-based phenotyping technologies in forestry. Annals of Forest Science, 2022, 79, .	2.0	15
119	Variation in the mating system of Sitka spruce (<i>Picea sitchensis</i>): evidence for partial assortative mating. American Journal of Botany, 1994, 81, 1410-1415.	1.7	14
120	Impact of temperature shifts on the joint evolution of seed dormancy and size. Ecology and Evolution, 2017, 7, 26-37.	1.9	14
121	A comprehensive annotation dataset of intact LTR retrotransposons of 300 plant genomes. Scientific Data, 2021, 8, 174.	5.3	14
122	A numerical analysis of karyotypes in the genus <i>Pseudotsuga</i> . Canadian Journal of Botany, 1983, 61, 536-544.	1.1	13
123	Title is missing!. New Forests, 2002, 24, 97-112.	1.7	13
124	Machine learning use in predicting interior spruce wood density utilizing progeny test information. Neural Computing and Applications, 2017, 28, 505-519.	5.6	13
125	The gibberellin GID1-DELLA signalling module exists in evolutionarily ancient conifers. Scientific Reports, 2017, 7, 16637.	3.3	13
126	Temporal quantification of mating system parameters in a coastal Douglas-fir seed orchard under manipulated pollination environment. Scientific Reports, 2018, 8, 11593.	3.3	13

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127	Transcriptome-wide isolation and expression of <i>NF-κB</i> gene family in male cone development and hormonal treatment of <i>Pinus tabulaeformis</i> . <i>Physiologia Plantarum</i> , 2021, 171, 34-47.	5.2	13
128	Genetic architecture of the metabolic pathway of salicylic acid biosynthesis in <i>Populus</i> . <i>Tree Physiology</i> , 2021, 41, 2198-2215.	3.1	13
129	Integration of genome wide association studies and co-expression networks reveal roles of <i>PtoWRKY42</i> and <i>PtoUGT76C1</i> in <i>trans-zeatin</i> metabolism and cytokinin sensitivity in poplar. <i>New Phytologist</i> , 2021, 231, 1462-1477.	7.3	13
130	Lilac (<i>Syringa oblata</i>) genome provides insights into its evolution and molecular mechanism of petal color change. <i>Communications Biology</i> , 2022, 5, .	4.4	13
131	Breeding without breeding: minimum fingerprinting effort with respect to the effective population size. <i>Tree Genetics and Genomes</i> , 2011, 7, 1069-1078.	1.6	12
132	Genetics of wood quality attributes in Western Larch. <i>Annals of Forest Science</i> , 2014, 71, 415-424.	2.0	12
133	Randomized, replicated, staggered clonal-row (R2SCR) seed orchard design. <i>Tree Genetics and Genomes</i> , 2014, 10, 555-563.	1.6	12
134	Regulatory crosstalk between microRNAs and hormone signalling cascades controls the variation on seed dormancy phenotype at <i>Arabidopsis thaliana</i> seed set. <i>Plant Cell Reports</i> , 2017, 36, 705-717.	5.6	12
135	In-depth transcriptome characterization uncovers distinct gene family expansions for <i>Cupressus gigantea</i> important to this long-lived species' adaptability to environmental cues. <i>BMC Genomics</i> , 2019, 20, 213.	2.8	12
136	Modeling realized gains in Douglas-fir (<i>Pseudotsuga menziesii</i>) using laser scanning data from unmanned aircraft systems (UAS). <i>Forest Ecology and Management</i> , 2020, 473, 118284.	3.2	12
137	Pollination dynamics variation in a Douglas-fir seed orchard as revealed by microsatellite analysis. <i>Silva Fennica</i> , 2016, 50, .	1.3	12
138	Genetic diversity of Norway spruce ecotypes assessed by GBS-derived SNPs. <i>Scientific Reports</i> , 2021, 11, 23119.	3.3	12
139	LncRNA PMAT-PtoMYB46 module represses PtoMATE and PtoARF2 promoting Pb ²⁺ uptake and plant growth in poplar. <i>Journal of Hazardous Materials</i> , 2022, 433, 128769.	12.4	12
140	Germination ecology in mountain hemlock (<i>Tsuga mertensiana</i> (Bong.) Carr.). <i>Forest Ecology and Management</i> , 2001, 144, 183-188.	3.2	11
141	Field assessment of Douglas-fir somatic and zygotic seedlings with respect to gas exchange, water relations, and frost hardness. <i>Canadian Journal of Forest Research</i> , 2002, 32, 1822-1828.	1.7	11
142	Two-dimensional penalized splines via Gibbs sampling to account for spatial variability in forest genetic trials with small amount of information available. <i>Silvae Genetica</i> , 2011, 60, 25-35.	0.8	11
143	Breeding without Breeding. <i>Tree Genetics and Genomes</i> , 2012, 8, 873-877.	1.6	11
144	Determination of paternal and maternal parentage in lodgepole pine seed: full versus partial pedigree reconstruction. <i>Canadian Journal of Forest Research</i> , 2014, 44, 1122-1127.	1.7	11

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145	Genomic Diversity Evaluation of <i>Populus trichocarpa</i> Germplasm for Rare Variant Genetic Association Studies. <i>Frontiers in Genetics</i> , 2020, 10, 1384.	2.3	11
146	Reproductive-cycle plasticity in yellow-cedar (<i>Chamaecyparis nootkatensis</i>). <i>Canadian Journal of Forest Research</i> , 1991, 21, 1360-1364.	1.7	10
147	Genetic control of germination and the effects of accelerated aging in mountain hemlock seeds and its relevance to gene conservation. <i>Forest Ecology and Management</i> , 1998, 112, 203-211.	3.2	10
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