

Yousry A El-Kassaby

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4735652/publications.pdf>

Version: 2024-02-01

253
papers

6,444
citations

76326

40
h-index

110387

64
g-index

260
all docs

260
docs citations

260
times ranked

4753
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptomic and proteomic analyses of far-red light effects in inducing shoot elongation in the presence or absence of paclobutrazol in Chinese pine. <i>Journal of Forestry Research</i> , 2022, 33, 1033-1043.	3.6	5
2	Phytohormone profiles and related gene expressions after endodormancy release in developing <i>Pinus tabulaeformis</i> male strobili. <i>Plant Science</i> , 2022, 316, 111167.	3.6	6
3	Predicting Potential Habitat of a Plant Species with Small Populations under Climate Change: <i>Ostrya rehderiana</i> . <i>Forests</i> , 2022, 13, 129.	2.1	10
4	Transposable Elements: Distribution, Polymorphism, and Climate Adaptation in <i>Populus</i> . <i>Frontiers in Plant Science</i> , 2022, 13, 814718.	3.6	3
5	Revealing the Genetic Structure and Differentiation in Endangered <i>Pinus bungeana</i> by Genome-Wide SNP Markers. <i>Forests</i> , 2022, 13, 326.	2.1	5
6	Improving lodgepole pine genomic evaluation using spatial correlation structure and SNP selection with single-step GBLUP. <i>Heredity</i> , 2022, 128, 209-224.	2.6	9
7	Genome Wide Association Study Identifies Candidate Genes Related to the Earlywood Tracheid Properties in <i>Picea crassifolia</i> Kom.. <i>Forests</i> , 2022, 13, 332.	2.1	2
8	Integrating genomic information and productivity and climate-adaptability traits into a regional white spruce breeding program. <i>PLoS ONE</i> , 2022, 17, e0264549.	2.5	7
9	LncRNA PMAT ¹ 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
10	S _{ub} P _{haser} : a robust allopolyploid subgenome phasing method based on subgenome ² -specific <i>k</i> -mers. <i>New Phytologist</i> , 2022, 235, 801-809.	7.3	33
11	The complete chloroplast genome of <i>Euonymus alatus</i> (Celastraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 707-708.	0.4	0
12	Closing the gap between phenotyping and genotyping: review of advanced, image-based phenotyping technologies in forestry. <i>Annals of Forest Science</i> , 2022, 79, .	2.0	15
13	Hydrothermal carbonization of waste ginkgo leaf residues for solid biofuel production: Hydrochar characterization and its pelletization. <i>Fuel</i> , 2022, 324, 124341.	6.4	19
14	Complete chloroplast genome of <i>Ilex dabieshanensis</i> : Genome structure, comparative analyses with three traditional <i>Ilex</i> tea species, and its phylogenetic relationships within the family Aquifoliaceae. <i>PLoS ONE</i> , 2022, 17, e0268679.	2.5	3
15	Identification and Comparative Analysis of Conserved and Species-Specific microRNAs in Four <i>Populus</i> Sections. <i>Forests</i> , 2022, 13, 873.	2.1	3
16	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
17	Involvement of PtCOL5-PtNF-YC4 in reproductive cone development and gibberellin signaling in Chinese pine. <i>Plant Science</i> , 2022, 323, 111383.	3.6	6
18	PagGRF11 Overexpression Promotes Stem Development and Dwarfing in <i>Populus</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 7858.	4.1	3

#	ARTICLE	IF	CITATIONS
19	Transcriptome-wide isolation and expression of <i>NF-Y</i> gene family in male cone development and hormonal treatment of <i>Pinus tabuliformis</i> . <i>Physiologia Plantarum</i> , 2021, 171, 34-47.	5.2	13
20	Transcriptome-wide analysis of introgression-resistant regions reveals genetic divergence genes under positive selection in <i>Populus trichocarpa</i> . <i>Heredity</i> , 2021, 126, 442-462.	2.6	2
21	<i>Quercus</i> species divergence is driven by natural selection on evolutionarily less integrated traits. <i>Heredity</i> , 2021, 126, 366-382.	2.6	5
22	Deriving internal crown geometric features of Douglas-fir from airborne laser scanning in a realized-gain trial. <i>Forestry</i> , 2021, 94, 442-454.	2.3	6
23	Metabolome and Transcriptome Analyses Reveal the Regulatory Mechanisms of Photosynthesis in Developing <i>Ginkgo biloba</i> Leaves. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2601.	4.1	7
24	Synonymous mutation in <i>Growth Regulating Factor 15</i> of miR396a target sites enhances photosynthetic efficiency and heat tolerance in poplar. <i>Journal of Experimental Botany</i> , 2021, 72, 4502-4519.	4.8	18
25	Monitoring genetic diversity across <i>Pinus tabuliformis</i> seed orchard generations using SSR markers. <i>Canadian Journal of Forest Research</i> , 2021, 51, 1534-1540.	1.7	8
26	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
27	Amino acid metabolism reprogramming in response to changing growth environment in <i>Ginkgo biloba</i> leaves. <i>LWT - Food Science and Technology</i> , 2021, 144, 111276.	5.2	6
28	Integration of genome wide association studies and co-expression networks reveal roles of <i>PtoWRKY42</i> and <i>PtoUGT76C1</i> in <i>trans</i> -zeatin metabolism and cytokinin sensitivity in poplar. <i>New Phytologist</i> , 2021, 231, 1462-1477.	7.3	13
29	Hybridization and introgression in sympatric and allopatric populations of four oak species. <i>BMC Plant Biology</i> , 2021, 21, 266.	3.6	8
30	A comprehensive annotation dataset of intact LTR retrotransposons of 300 plant genomes. <i>Scientific Data</i> , 2021, 8, 174.	5.3	14
31	Spatial prediction and delineation of <i>Ginkgo biloba</i> production areas under current and future climatic conditions. <i>Industrial Crops and Products</i> , 2021, 166, 113444.	5.2	8
32	Haplotype-resolved genome assembly and allele-specific gene expression in cultivated ginger. <i>Horticulture Research</i> , 2021, 8, 188.	6.3	31
33	Evolutionary patterns of nucleotide substitution rates in plastid genomes of <i>Quercus</i> . <i>Ecology and Evolution</i> , 2021, 11, 13401-13414.	1.9	9
34	Chromosome-scale assembly and evolution of the tetraploid <i>Salvia splendens</i> (Lamiaceae) genome. <i>Horticulture Research</i> , 2021, 8, 177.	6.3	27
35	Soil Bacteria to Regulate <i>Phoebe bournei</i> Seedling Growth and Sustainable Soil Utilization under NPK Fertilization. <i>Plants</i> , 2021, 10, 1868.	3.5	1
36	Eliciting increased flavonoids content in <i>Ginkgo biloba</i> leaves through exogenous salicylic acid and methyl jasmonate treatments. <i>Canadian Journal of Forest Research</i> , 2021, 51, 1339-1346.	1.7	2

#	ARTICLE	IF	CITATIONS
37	Integrative analysis of the metabolome and transcriptome reveals seed germination mechanism in <i>Punica granatum</i> L.. <i>Journal of Integrative Agriculture</i> , 2021, 20, 132-146.	3.5	17
38	Variation in <i>Platycladus orientalis</i> (Cupressaceae) Reproductive Output and Its Effect on Seed Orchard Crops™ Genetic Diversity. <i>Forests</i> , 2021, 12, 1429.	2.1	2
39	Phenotypic variation of floral organs in flowering crabapples and its taxonomic significance. <i>BMC Plant Biology</i> , 2021, 21, 503.	3.6	1
40	Centromere-Specific Retrotransposons and Very-Long-Chain Fatty Acid Biosynthesis in the Genome of Yellowhorn (<i>Xanthoceras sorbifolium</i> , Sapindaceae), an Oil-Producing Tree With Significant Drought Resistance. <i>Frontiers in Plant Science</i> , 2021, 12, 766389.	3.6	6
41	Genetic diversity of Norway spruce ecotypes assessed by GBS-derived SNPs. <i>Scientific Reports</i> , 2021, 11, 23119.	3.3	12
42	Characterization of the complete chloroplast genome of <i>Quercus acrodonta</i> (Fagaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3320-3321.	0.4	0
43	Characterization of <i>Pinus densiflora</i> var <i>zhangwuensis</i> . S.J.Zhang, C.X.Li & X.Y.Yuan complete chloroplast genome. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3515-3516.	0.4	1
44	Fertilization Regulates Accumulation and Allocation of Biomass and Nutrients in <i>Phoebe bournei</i> Seedlings. <i>Agriculture (Switzerland)</i> , 2021, 11, 1187.	3.1	6
45	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
46	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
47	Chromosome-level genome assembly of a parent species of widely cultivated azaleas. <i>Nature Communications</i> , 2020, 11, 5269.	12.8	90
48	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
49	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
50	Formula Fertilization Promotes <i>Phoebe bournei</i> Robust Seedling Cultivation. <i>Forests</i> , 2020, 11, 781.	2.1	15
51	Gender, reproductive output covariation and their role on gene diversity of <i>Pinus koraiensis</i> seed orchard crops. <i>BMC Plant Biology</i> , 2020, 20, 418.	3.6	6
52	Temporospatial Flavonoids Metabolism Variation in <i>Ginkgo biloba</i> Leaves. <i>Frontiers in Genetics</i> , 2020, 11, 589326.	2.3	18
53	Multiple Ecological Drivers Determining Vegetation Attributes across Scales in a Mountainous Dry Valley, Southwest China. <i>Forests</i> , 2020, 11, 1140.	2.1	5
54	Ecological drivers of plant life-history traits: Assessment of seed mass and germination variation using climate cues and nitrogen resources in conifers. <i>Ecological Indicators</i> , 2020, 117, 106517.	6.3	6

#	ARTICLE	IF	CITATIONS
55	Linkage disequilibrium vs. pedigree: Genomic selection prediction accuracy in conifer species. PLoS ONE, 2020, 15, e0232201.	2.5	28
56	Changes in DNA Methylation in Response to 6-Benzylaminopurine Affect Allele-Specific Gene Expression in Populus Tomentosa. International Journal of Molecular Sciences, 2020, 21, 2117.	4.1	3
57	In Situ Genetic Evaluation of European Larch Across Climatic Regions Using Marker-Based Pedigree Reconstruction. Frontiers in Genetics, 2020, 11, 28.	2.3	15
58	Modeling realized gains in Douglas-fir (<i>Pseudotsuga menziesii</i>) using laser scanning data from unmanned aircraft systems (UAS). Forest Ecology and Management, 2020, 473, 118284.	3.2	12
59	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
60	Transcriptome-wide identification and profiling of miRNAs in a stress-tolerant conifer <i>Sabina chinensis</i> . Journal of Biosciences, 2020, 45, 1.	1.1	2
61	Genomic Diversity Evaluation of <i>Populus trichocarpa</i> Germplasm for Rare Variant Genetic Association Studies. Frontiers in Genetics, 2020, 10, 1384.	2.3	11
62	A Binary-Based Matrix Model for <i>Malus Corolla</i> Symmetry and Its Variational Significance. Frontiers in Plant Science, 2020, 11, 416.	3.6	4
63	Improved genetic distance-based spatial deployment can effectively minimize inbreeding in seed orchard. Forest Ecosystems, 2020, 7, .	3.1	9
64	Marker-assisted selection in <i>C. oleifera</i> hybrid population. Silvae Genetica, 2020, 69, 63-72.	0.8	5
65	Techniques for Small Non-Coding RNA Analysis in Seeds of Forest Tree Species. Methods in Molecular Biology, 2020, 2093, 217-225.	0.9	0
66	Prospects: The Spruce Genome, a Model for Understanding Gymnosperm Evolution and Supporting Tree Improvement Efforts. Compendium of Plant Genomes, 2020, , 215-218.	0.5	0
67	Genomic Selection in Canadian Spruces. Compendium of Plant Genomes, 2020, , 115-127.	0.5	3
68	Species association in <i>Xanthoceras sorbifolium</i> Bunge communities and selection for agroforestry establishment. Agroforestry Systems, 2019, 93, 1531-1543.	2.0	6
69	Current Advances in Seed Orchard Layouts: Two Case Studies in Conifers. Forests, 2019, 10, 93.	2.1	8
70	Local Adaptation and Response of <i>Platycladus orientalis</i> (L.) Franco Populations to Climate Change. Forests, 2019, 10, 622.	2.1	15
71	SNP variable selection by generalized graph domination. PLoS ONE, 2019, 14, e0203242.	2.5	7
72	Conservation of genetic diversity hotspots of the high-valued relic yellowhorn (<i>Xanthoceras</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 62	1.9	0

#	ARTICLE	IF	CITATIONS
73	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
74	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
75	Novel Insights into Plant Genome Evolution and Adaptation as Revealed through Transposable Elements and Non-Coding RNAs in Conifers. <i>Genes</i> , 2019, 10, 228.	2.4	7
76	Genome-Wide Variant Identification and High-Density Genetic Map Construction Using RADseq for <i>Platycladus orientalis</i> (Cupressaceae). <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3663-3672.	1.8	5
77	Phenotypic plasticity of natural <i>Populus trichocarpa</i> populations in response to temporally environmental change in a common garden. <i>BMC Evolutionary Biology</i> , 2019, 19, 231.	3.2	18
78	Genomic selection of juvenile height across a single-generational gap in Douglas-fir. <i>Heredity</i> , 2019, 122, 848-863.	2.6	26
79	Concept for gene conservation strategy for the endangered Chinese yellowhorn, <i>Xanthoceras sorbifolium</i> , based on simulation of pairwise kinship coefficients. <i>Forest Ecology and Management</i> , 2019, 432, 976-982.	3.2	6
80	Genetic Variation Related to High Elevation Adaptation Revealed by Common Garden Experiments in <i>Pinus yunnanensis</i> . <i>Frontiers in Genetics</i> , 2019, 10, 1405.	2.3	17
81	Multienvironment genomic variance decomposition analysis of open-pollinated Interior spruce (<i>Picea</i>) Tj ETQq1 1 0,784314 rgBT /Ove	2.1	80
82	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
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	Pollination dynamics in a <i>Platycladus orientalis</i> seed orchard as revealed by partial pedigree reconstruction. <i>Canadian Journal of Forest Research</i> , 2018, 48, 952-957.	1.7	7
85	Quantitative Genetics and Genomics Converge to Accelerate Forest Tree Breeding. <i>Frontiers in Plant Science</i> , 2018, 9, 1693.	3.6	176
86	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
87	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
88	Temporal quantification of mating system parameters in a coastal Douglas-fir seed orchard under manipulated pollination environment. <i>Scientific Reports</i> , 2018, 8, 11593.	3.3	13
89	Evapotranspiration and favorable growing degree-days are key to tree height growth and ecosystem functioning: Meta-analyses of Pacific Northwest historical data. <i>Scientific Reports</i> , 2018, 8, 8228.	3.3	15
90	Machine learning use in predicting interior spruce wood density utilizing progeny test information. <i>Neural Computing and Applications</i> , 2017, 28, 505-519.	5.6	13

#	ARTICLE	IF	CITATIONS
91	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
92	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
93	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
94	Signaling pathway in development of <i>Camellia oleifera</i> nurse seedling grafting union. <i>Trees - Structure and Function</i> , 2017, 31, 1543-1558.	1.9	3
95	Solubilization of aluminum-bound phosphorus by root cell walls: evidence from Chinese fir, <i>Cunninghamia lanceolata</i> . <i>Canadian Journal of Forest Research</i> , 2017, 47, 419-423.	1.7	5
96	Tree size predicts vascular epiphytic richness of traditional cultivated tea plantations in Southwestern China. <i>Global Ecology and Conservation</i> , 2017, 10, 147-153.	2.1	9
97	Improving accuracy of breeding values by incorporating genomic information in spatial-competition mixed models. <i>Molecular Breeding</i> , 2017, 37, 1.	2.1	32
98	Practical application of genomic selection in a doubled-haploid winter wheat breeding program. <i>Molecular Breeding</i> , 2017, 37, 117.	2.1	45
99	Transcriptome comparative analysis of two <i>Camellia</i> species reveals lipid metabolism during mature seed natural drying. <i>Trees - Structure and Function</i> , 2017, 31, 1827-1848.	1.9	8
100	Impact of temperature shifts on the joint evolution of seed dormancy and size. <i>Ecology and Evolution</i> , 2017, 7, 26-37.	1.9	14
101	Distribution and in situ conservation of a relic Chinese oil woody species <i>Xanthoceras sorbifolium</i> (yellowhorn). <i>Canadian Journal of Forest Research</i> , 2017, 47, 1450-1456.	1.7	20
102	The gibberellin GID1-DELLA signalling module exists in evolutionarily ancient conifers. <i>Scientific Reports</i> , 2017, 7, 16637.	3.3	13
103	Integrating fecundity variation and genetic relatedness in estimating the gene diversity of seed crops: <i>Pinus koraiensis</i> seed orchard as an example. <i>Canadian Journal of Forest Research</i> , 2017, 47, 366-370.	1.7	20
104	Fruit shape and reproductive self and cross compatibility for the performance of fruit set in an andromonoecious species: <i>Xanthoceras sorbifolium</i> Bunge. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	1.6	8
105	Roles of the Environment in Plant Life-History Trade-offs. , 2017, , .		6
106	Global Analysis of Small RNA Dynamics during Seed Development of <i>Picea glauca</i> and <i>Arabidopsis thaliana</i> Populations Reveals Insights on their Evolutionary Trajectories. <i>Frontiers in Plant Science</i> , 2017, 8, 1719.	3.6	8
107	Dynamic Gene-Resource Landscape Management of Norway Spruce: Combining Utilization and Conservation. <i>Frontiers in Plant Science</i> , 2017, 8, 1810.	3.6	7
108	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. <i>BMC Genomics</i> , 2017, 18, 546.	2.8	20

#	ARTICLE	IF	CITATIONS
109	Predicting Future Seed Sourcing of <i>Platycladus orientalis</i> (L.) for Future Climates Using Climate Niche Models. <i>Forests</i> , 2017, 8, 471.	2.1	15
110	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
111	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
112	Simple Genetic Distance-Optimized Field Deployments for Clonal Seed Orchards Based on Microsatellite Markers: As a Case of Chinese Pine Seed Orchard. <i>PLoS ONE</i> , 2016, 11, e0157646.	2.5	5
113	Contributions of dynamic environmental signals during life-cycle transitions to early life-history traits in lodgepole pine (<i>Pinus contorta</i> Dougl.). <i>Biogeosciences</i> , 2016, 13, 2945-2958.	3.3	9
114	Global transcriptome analysis of <i>Sabina chinensis</i> (Cupressaceae), a valuable reforestation conifer. <i>Molecular Breeding</i> , 2016, 36, 1.	2.1	6
115	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
116	A transcriptomics investigation into pine reproductive organ development. <i>New Phytologist</i> , 2016, 209, 1278-1289.	7.3	34
117	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.	1.6	6
118	Optimum neighborhood seed orchard design. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	1.6	10
119	Bareroot versus container stocktypes: a performance comparison. <i>New Forests</i> , 2016, 47, 1-51.	1.7	87
120	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
121	Pollination dynamics variation in a Douglas-fir seed orchard as revealed by microsatellite analysis. <i>Silva Fennica</i> , 2016, 50, .	1.3	12
122	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. <i>BMC Plant Biology</i> , 2015, 15, 292.	3.6	17
123	Colonization History, Host Distribution, Anthropogenic Influence and Landscape Features Shape Populations of White Pine Blister Rust, an Invasive Alien Tree Pathogen. <i>PLoS ONE</i> , 2015, 10, e0127916.	2.5	19
124	Evolutionary Quantitative Genomics of <i>Populus trichocarpa</i> . <i>PLoS ONE</i> , 2015, 10, e0142864.	2.5	31
125	Using <i>Populus</i> as a lignocellulosic feedstock for bioethanol. <i>Biotechnology Journal</i> , 2015, 10, 510-524.	3.5	52
126	Forest genomics research and development in Canada: Priorities for developing an economic framework. <i>Forestry Chronicle</i> , 2015, 91, 60-70.	0.6	15

#	ARTICLE	IF	CITATIONS
127	Expansion of the minimum-inbreeding seed orchard design to operational scale. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	1.6	10
128	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
129	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
130	Timing of seed germination correlated with temperature-based environmental conditions during seed development in conifers. <i>Seed Science Research</i> , 2015, 25, 29-45.	1.7	20
131	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
132	Congruence between theory and practice: reduced contamination rate following phenotypic pre-selection within the Breeding without Breeding framework. <i>Scandinavian Journal of Forest Research</i> , 2014, 29, 552-554.	1.4	3
133	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
134	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
135	Extensive Functional Pleiotropy of REVOLUTA Substantiated through Forward Genetics. <i>Plant Physiology</i> , 2014, 164, 548-554.	4.8	17
136	Assessment of the Genetic Diversity in Forest Tree Populations Using Molecular Markers. <i>Diversity</i> , 2014, 6, 283-295.	1.7	90
137	Jackknife resampling for precision measurement of direct gene flow estimates. <i>Scandinavian Journal of Forest Research</i> , 2014, 29, 707-712.	1.4	0
138	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
139	Genetics of wood quality attributes in Western Larch. <i>Annals of Forest Science</i> , 2014, 71, 415-424.	2.0	12
140	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
141	Randomized, replicated, staggered clonal-row (R2SCR) seed orchard design. <i>Tree Genetics and Genomes</i> , 2014, 10, 555-563.	1.6	12
142	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
143	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
144	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

#	ARTICLE	IF	CITATIONS
145	Modern Advances in Tree Breeding. <i>Forestry Sciences</i> , 2014, , 441-459.	0.4	4
146	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
147	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
148	Genome-wide association mapping for wood characteristics in <i>Populus</i> identifies an array of candidate single nucleotide polymorphisms. <i>New Phytologist</i> , 2013, 200, 710-726.	7.3	158
149	Comparison of genetic parameters from marker-based relationship, sibship, and combined models in Scots pine multi-site open-pollinated tests. <i>Tree Genetics and Genomes</i> , 2013, 9, 1227-1235.	1.6	18
150	Mining conifers' 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
151	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
152	<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
153	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
154	Predicting Douglas-fir wood density by artificial neural networks (ANN) based on progeny testing information. <i>Holzforschung</i> , 2013, 67, 771-777.	1.9	19
155	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
156	The role of moist-chilling and thermo-priming on the germination characteristics of white spruce (<i>Picea glauca</i>) seed. <i>Seed Science and Technology</i> , 2013, 41, 321-335.	1.4	7
157	Association Analysis Identifies <i>Melampsora</i> — <i>columbiana</i> Poplar Leaf Rust Resistance SNPs. <i>PLoS ONE</i> , 2013, 8, e78423.	2.5	31
158	Genetic analysis and clonal stability of two yellow cypress clonal populations in British Columbia. <i>Silvae Genetica</i> , 2013, 62, 173-186.	0.8	4
159	Optimization of genetic gain and diversity in seed orchard crops considering variation in seed germination. <i>Scandinavian Journal of Forest Research</i> , 2012, 27, 787-793.	1.4	4
160	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
161	Breeding without breeding: selection using the genomic best linear unbiased predictor method (GBLUP). <i>New Forests</i> , 2012, 43, 631-637.	1.7	27
162	Breeding without Breeding. <i>Tree Genetics and Genomes</i> , 2012, 8, 873-877.	1.6	11

#	ARTICLE	IF	CITATIONS
163	Comparative Nucleotide Diversity Across North American and European Populus Species. Journal of Molecular Evolution, 2012, 74, 257-272.	1.8	25
164	Population structure and migration pattern of a conifer pathogen, <i>Grosmannia clavigera</i> , as influenced by its symbiont, the mountain pine beetle. Molecular Ecology, 2012, 21, 71-86.	3.9	46
165	Estimating selfing rates from reconstructed pedigrees using multilocus genotype data. Molecular Ecology, 2012, 21, 100-116.	3.9	34
166	Evaluating Interior Spruce Seed Deployment with GIS-Based Modeling Using British Columbia's Prince George Seed Planning Zone as a Model. Silvae Genetica, 2012, 61, 271-279.	0.8	1
167	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
168	Breeding without Breeding: Is a Complete Pedigree Necessary for Efficient Breeding?. PLoS ONE, 2011, 6, e25737.	2.5	76
169	Two-dimensional penalized splines via Gibbs sampling to account for spatial variability in forest genetic trials with small amount of information available. Silvae Genetica, 2011, 60, 25-35.	0.8	11
170	In situ wood quality assessment in Douglas-fir. Tree Genetics and Genomes, 2011, 7, 553-561.	1.6	31
171	Breeding without breeding: minimum fingerprinting effort with respect to the effective population size. Tree Genetics and Genomes, 2011, 7, 1069-1078.	1.6	12
172	Challenges Facing the Forest Industry in Relation to Seed Dormancy and Seed Quality. Methods in Molecular Biology, 2011, 773, 3-15.	0.9	2
173	Pollination dynamics in a Douglas-fir seed orchard as revealed by pedigree reconstruction. Annals of Forest Science, 2010, 67, 808-808.	2.0	27
174	Genealogical Relationship among Members of Selection and Production Populations of Yellow Cedar (<i>Callitropsis nootkatensis</i> [D. Don] Oerst.) in the Absence of Parental Information. Journal of Heredity, 2010, 101, 154-163.	2.4	10
175	Female Reproductive Success Variation in a <i>Pseudotsuga menziesii</i> Seed Orchard as Revealed by Pedigree Reconstruction from a Bulk Seed Collection. Journal of Heredity, 2010, 101, 164-168.	2.4	22
176	Clonal Variation in Acorn Production and its Effect on the Effective Population Size in a <i>Quercus acutissima</i> Seed Orchard. Silvae Genetica, 2010, 59, 170-175.	0.8	3
177	Breeding without breeding. Genetical Research, 2009, 91, 111-120.	0.9	109
178	Optimization of combined genetic gain and diversity for collection and deployment of seed orchard crops. Tree Genetics and Genomes, 2009, 5, 583-593.	1.6	28
179	Genetic resistance of spruce to gall-forming adelgids (Hemiptera: Adelgidae). Canadian Journal of Forest Research, 2009, 39, 2536-2541.	1.7	4
180	Development and characterization of microsatellite loci in western larch (<i>Larix occidentalis</i>)	4.8	22

#	ARTICLE	IF	CITATIONS
181	Understanding lodgepole pine seed germination for improved utilization. <i>Seed Science and Technology</i> , 2009, 37, 316-328.	1.4	1
182	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
183	Clonal-row versus random seed orchard designs: interior spruce mating system evaluation. <i>Canadian Journal of Forest Research</i> , 2007, 37, 690-696.	1.7	16
184	Advanced generation seed orchards™ turnover as affected by breeding advance, time to sexual maturity and costs, with special reference to <i>Pinus sylvestris</i> in Sweden. <i>Scandinavian Journal of Forest Research</i> , 2007, 22, 88-98.	1.4	5
185	The impact of differential success of somatic embryogenesis on the outcome of clonal forestry programs. I. Initial comparison under multitrait selection. <i>Canadian Journal of Forest Research</i> , 2006, 36, 1376-1384.	1.7	5
186	Is linear deployment of clones optimal under different clonal outcrossing contributions in seed orchards?. <i>Tree Genetics and Genomes</i> , 2006, 2, 25-29.	1.6	3
187	Fertility Variation and Genetic Diversity in a Clonal Seed Orchard of <i>Cryptomeria japonica</i> . <i>Silvae Genetica</i> , 2005, 54, 104-107.	0.8	9
188	Population genetics of <i>Gaultheria shallon</i> in British Columbia and the implications for management using biocontrol. <i>Canadian Journal of Botany</i> , 2005, 83, 501-509.	1.1	3
189	Effects of serial propagation, donor age, and genotype on <i>Chamaecyparis nootkatensis</i> physiology and growth traits. <i>Canadian Journal of Forest Research</i> , 2005, 35, 623-632.	1.7	8
190	Genetic diversity and population structure of <i>Valdensinia heterodoxa</i> , a potential biocontrol agent for salal in coastal British Columbia. <i>Canadian Journal of Plant Pathology</i> , 2005, 27, 559-571.	1.4	4
191	Genetic gain and diversity under different thinning scenarios in a breeding seed orchard of <i>Quercus accutissima</i> . <i>Forest Ecology and Management</i> , 2005, 212, 405-410.	3.2	7
192	Lodgepole Pine and White Spruce Germination: Effects of Stratification and Simulated Aging. <i>Silvae Genetica</i> , 2005, 54, 138-144.	0.8	6
193	Single-copy, species-transferable microsatellite markers developed from loblolly pine ESTs. <i>Theoretical and Applied Genetics</i> , 2004, 109, 361-369.	3.6	136
194	Inbreeding and conservation genetics in whitebark pine. <i>Conservation Genetics</i> , 2003, 4, 581-593.	1.5	22
195	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
196	Experimental analysis of the mating system of the white pine weevil, <i>Pissodes strobi</i> (Peck) (Coleoptera: Tj ETQq0 0,0 rgBT /Overlock 10	1.0	1
197	Inheritance of Null Alleles for Microsatellites in the White Pine Weevil (<i>Pissodes strobi</i> [Peck]) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.7	17
198	Field assessment of Douglas-fir somatic and zygotic seedlings with respect to gas exchange, water relations, and frost hardiness. <i>Canadian Journal of Forest Research</i> , 2002, 32, 1822-1828.	1.7	11

#	ARTICLE	IF	CITATIONS
199	Sexual Reproduction in the White Pine Weevil (<i>Pissodes strobi</i> [Peck] [Coleoptera: Curculionidae]): Implications for Population Genetic Diversity. , 2002, 93, 165-169.		4
200	Growth, morphology, and cold hardiness of <i>Chamaecyparis nootkatensis</i> seedlings originating from an abbreviated reproductive cycle. Canadian Journal of Forest Research, 2002, 32, 52-58.	1.7	3
201	Considerations of correlated fertility between genders on genetic diversity: the <i>Pinus densiflora</i> seed orchard as a model. Theoretical and Applied Genetics, 2002, 105, 1183-1189.	3.6	24
202	Title is missing!. New Forests, 2002, 24, 97-112.	1.7	13
203	Germination ecology in mountain hemlock (<i>Tsuga mertensiana</i> (Bong.) Carr.). Forest Ecology and Management, 2001, 144, 183-188.	3.2	11
204	Patterns of genetic variation in mountain hemlock (<i>Tsuga mertensiana</i> (Bong.) Carr.) with respect to height growth and frost hardiness. Forest Ecology and Management, 2001, 154, 23-33.	3.2	9
205	Characterization of microsatellite loci in white pine weevil (<i>Pissodes strobi</i>). Molecular Ecology Notes, 2001, 1, 248-249.	1.7	10
206	Application of Somatic Embryogenesis to Tree Improvement in Conifers. Progress in Biotechnology, 2001, , 305-312.	0.2	4
207	Randomly amplified polymorphic DNA reveals fine-scale genetic structure in <i>Pissodes strobi</i> (Coleoptera: Curculionidae). Canadian Entomologist, 2001, 133, 229-238.	0.8	8
208	Geographic pattern of genetic variation in photosynthetic capacity and growth in two hardwood species from British Columbia. Oecologia, 2000, 123, 168-174.	2.0	36
209	Population Genetic Structure of <i>Pissodes strobi</i> (Coleoptera: Curculionidae) in British Columbia, Canada. Annals of the Entomological Society of America, 2000, 93, 807-818.	2.5	9
210	Budburst phenology of sitka spruce and its relationship to white pine weevil attack. Forest Ecology and Management, 2000, 127, 19-29.	3.2	30
211	Genetic variation in mountain hemlock (<i>Tsuga mertensiana</i> Bong.): quantitative and adaptive attributes. Forest Ecology and Management, 1999, 123, 205-215.	3.2	8
212	Genetic control of germination and the effects of accelerated aging in mountain hemlock seeds and its relevance to gene conservation. Forest Ecology and Management, 1998, 112, 203-211.	3.2	10
213	Levels of genetic diversity at different stages of the domestication cycle of interior spruce in British Columbia. Theoretical and Applied Genetics, 1997, 94, 83-90.	3.6	61
214	Genetic variation in low elevation Douglas-fir of British Columbia and its relevance to gene conservation. Biodiversity and Conservation, 1996, 5, 779-794.	2.6	25
215	Impact of selection and breeding on the genetic diversity in Douglas-fir. Biodiversity and Conservation, 1996, 5, 795-813.	2.6	68
216	Population Density and Mating Pattern in Western Larch. Journal of Heredity, 1996, 87, 438-443.	2.4	49

#	ARTICLE	IF	CITATIONS
217	Variation in the mating system of Sitka spruce (<i>Picea sitchensis</i>): evidence for partial assortative mating. <i>American Journal of Botany</i> , 1994, 81, 1410-1415.	1.7	14
218	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
219	Genetic Diversity, Differentiation, and Inbreeding in Pacific Yew from British Columbia. <i>Journal of Heredity</i> , 1994, 85, 112-117.	2.4	49
220	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
221	Variation in the Mating System of Sitka Spruce (<i>Picea sitchensis</i>): Evidence for Partial Assortative Mating. <i>American Journal of Botany</i> , 1994, 81, 1410.	1.7	4
222	Interpretation of seed-germination parameters. <i>New Forests</i> , 1993, 7, 123-132.	1.7	39
223	Supplemental mass pollination success rate in a mature Douglas-fir seed orchard. <i>Canadian Journal of Forest Research</i> , 1993, 23, 1096-1099.	1.7	20
224	Genetic Control of Isoenzymes in Sitka Spruce. <i>Journal of Heredity</i> , 1993, 84, 206-211.	2.4	6
225	Estimation of clonal contribution to cone and seed crops in a Sitka spruce seed orchard. <i>Annales Des Sciences Forestières</i> , 1993, 50, 461-467.	1.2	30
226	Cost of reproduction in Douglas-fir. <i>Canadian Journal of Botany</i> , 1992, 70, 1429-1432.	1.1	65
227	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
228	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
229	Effective number of pollen parents in clonal seed orchards. <i>Theoretical and Applied Genetics</i> , 1991, 82, 313-320.	3.6	22
230	Reproductive-cycle plasticity in yellow-cedar (<i>Chamaecyparis nootkatensis</i>). <i>Canadian Journal of Forest Research</i> , 1991, 21, 1360-1364.	1.7	10
231	Inherent differences in response of Douglas fir families to nitrogen and phosphorus supply levels. <i>Water, Air, and Soil Pollution</i> , 1990, 54, 657-663.	2.4	0
232	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
233	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
234	Variation in growth rate within and among full-sib families of Douglas-fir (<i>Pseudotsuga</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf,50 62 Td (1.1	7

#	ARTICLE	IF	CITATIONS
235	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
236	Effect of flowering phenology, date of cone collection, cone-storage treatment and seed pretreatment on yield and germination of seeds from a Douglas-Fir seed orchard. <i>Forest Ecology and Management</i> , 1988, 25, 17-29.	3.2	8
237	Trend surface analysis of a Douglas-fir provenance "progeny transfer test. <i>Canadian Journal of Forest Research</i> , 1988, 18, 515-520.	1.7	9
238	Multivariate variation within and between open-pollinated families of Douglas-fir (<i>Pseudotsuga</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.1	4
239	Effect of family size and number on the accuracy and precision of the estimates of genetic parameters in the IUFRO Douglas-fir provenance-progeny trial. <i>Forest Ecology and Management</i> , 1987, 18, 35-48.	3.2	3
240	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
241	Allozyme variation in <i>Picea mariana</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
242	Elemental profiles for Douglas-fir seeds: evidence of genetic control. <i>Canadian Journal of Forest Research</i> , 1986, 16, 650-654.	1.7	7
243	Evaluation of interclonal elemental-profile variation in Sitka spruce seed. <i>Biochemical Genetics</i> , 1986, 24, 729-741.	1.7	0
244	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
245	Assessing sample size and variable number in multivariate data, with specific reference to cone morphology variation in a population of <i>Picea sitchensis</i> . <i>Canadian Journal of Botany</i> , 1985, 63, 232-241.	1.1	15
246	Characterization of seeds from 10 IUFRO Sitka spruce provenances using trace element profiles as determined by X-ray energy-dispersive spectrometry. <i>Canadian Journal of Forest Research</i> , 1983, 13, 929-937.	1.7	2
247	A numerical analysis of karyotypes in the genus <i>Pseudotsuga</i> . <i>Canadian Journal of Botany</i> , 1983, 61, 536-544.	1.1	13
248	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
249	ASSOCIATIONS BETWEEN ALLOZYME GENOTYPES AND QUANTITATIVE TRAITS IN DOUGLAS-FIR [PSEUDOTSUGA MENZIESII (MIRB.) FRANCO]. <i>Genetics</i> , 1982, 101, 103-115.	2.9	33
250	Genetic interpretation of malate dehydrogenase isozymes in some conifer species. <i>Journal of Heredity</i> , 1981, 72, 451-452.	2.4	20
251	Enzyme variation in natural populations of Sitka spruce (<i>Picea sitchensis</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
252	Estimates of pollen contamination and selfing in a coastal Douglas-fir seed orchard. <i>Scandinavian Journal of Forest Research</i> , 0, , 1-10.	1.4	6

#	ARTICLE	IF	CITATIONS
253	Genomics-Based Systems and Multi-disciplinary Approaches to Unlock Complex Gene Networks Underlying Wood Formation. Current Forestry Reports, 0, , 1.	7.4	0