

# Yousry A El-Kassaby

## List of Publications by Year in descending order

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253  
papers

6,444  
citations

87401

40  
h-index

124990

64  
g-index

260  
all docs

260  
docs citations

260  
times ranked

5239  
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.	1.7	5
2	Phytohormone profiles and related gene expressions after endodormancy release in developing <i>Pinus tabuliformis</i> male strobili. <i>Plant Science</i> , 2022, 316, 111167.	1.7	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.	0.9	10
4	Transposable Elements: Distribution, Polymorphism, and Climate Adaptation in <i>Populus</i> . <i>Frontiers in Plant Science</i> , 2022, 13, 814718.	1.7	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.	0.9	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.	1.2	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.	0.9	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.	1.1	7
9	LncRNA PMAT <sup>1</sup> PtoMYB46 module represses PtoMATE and PtoARF2 promoting Pb <sup>2+</sup> uptake and plant growth in poplar. <i>Journal of Hazardous Materials</i> , 2022, 433, 128769.	6.5	12
10	S <sub>ub</sub> P <sub>haser</sub> : a robust allopolyploid subgenome phasing method based on subgenome <sup>2</sup> -specific <i>k</i> -mers. <i>New Phytologist</i> , 2022, 235, 801-809.	3.5	33
11	The complete chloroplast genome of <i>Euonymus alatus</i> (Celastraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 707-708.	0.2	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, .	0.8	15
13	Hydrothermal carbonization of waste ginkgo leaf residues for solid biofuel production: Hydrochar characterization and its pelletization. <i>Fuel</i> , 2022, 324, 124341.	3.4	19
14	Complete chloroplast genome of <i>Ilex dabieshanensis</i> : Genome structure, comparative analyses with three traditional Ilex tea species, and its phylogenetic relationships within the family Aquifoliaceae. <i>PLoS ONE</i> , 2022, 17, e0268679.	1.1	3
15	Identification and Comparative Analysis of Conserved and Species-Specific microRNAs in Four <i>Populus</i> Sections. <i>Forests</i> , 2022, 13, 873.	0.9	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, .	2.0	13
17	Involvement of PtCOL5-PtNF-YC4 in reproductive cone development and gibberellin signaling in Chinese pine. <i>Plant Science</i> , 2022, 323, 111383.	1.7	6
18	PagGRF11 Overexpression Promotes Stem Development and Dwarfing in <i>Populus</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 7858.	1.8	3

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19	Transcriptome-wide isolation and expression of <i>NF-<math>\kappa</math>B</i> gene family in male cone development and hormonal treatment of <i>Pinus tabulaeformis</i> . <i>Physiologia Plantarum</i> , 2021, 171, 34-47.	2.6	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.	1.2	2
21	<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
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.	1.2	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.	1.8	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.	2.4	18
25	Monitoring genetic diversity across <i>Pinus tabulaeformis</i> seed orchard generations using SSR markers. <i>Canadian Journal of Forest Research</i> , 2021, 51, 1534-1540.	0.8	8
26	Genetic architecture of the metabolic pathway of salicylic acid biosynthesis in <i>Populus</i> . <i>Tree Physiology</i> , 2021, 41, 2198-2215.	1.4	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.	2.5	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.	3.5	13
29	Hybridization and introgression in sympatric and allopatric populations of four oak species. <i>BMC Plant Biology</i> , 2021, 21, 266.	1.6	8
30	A comprehensive annotation dataset of intact LTR retrotransposons of 300 plant genomes. <i>Scientific Data</i> , 2021, 8, 174.	2.4	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.	2.5	8
32	Haplotype-resolved genome assembly and allele-specific gene expression in cultivated ginger. <i>Horticulture Research</i> , 2021, 8, 188.	2.9	31
33	Evolutionary patterns of nucleotide substitution rates in plastid genomes of <i>Quercus</i> . <i>Ecology and Evolution</i> , 2021, 11, 13401-13414.	0.8	9
34	Chromosome-scale assembly and evolution of the tetraploid <i>Salvia splendens</i> (Lamiaceae) genome. <i>Horticulture Research</i> , 2021, 8, 177.	2.9	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.	1.6	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.	0.8	2

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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.	1.7	17
38	Variation in <i>Platycladus orientalis</i> (Cupressaceae) Reproductive Output and Its Effect on Seed Orchard Crops™ <i>Genetic Diversity. Forests</i> , 2021, 12, 1429.	0.9	2
39	Phenotypic variation of floral organs in flowering crabapples and its taxonomic significance. <i>BMC Plant Biology</i> , 2021, 21, 503.	1.6	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.	1.7	6
41	Genetic diversity of Norway spruce ecotypes assessed by GBS-derived SNPs. <i>Scientific Reports</i> , 2021, 11, 23119.	1.6	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.	0.2	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.	0.2	1
44	Fertilization Regulates Accumulation and Allocation of Biomass and Nutrients in <i>Phoebe bournei</i> Seedlings. <i>Agriculture (Switzerland)</i> , 2021, 11, 1187.	1.4	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.	1.5	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.	3.5	25
47	Chromosome-level genome assembly of a parent species of widely cultivated azaleas. <i>Nature Communications</i> , 2020, 11, 5269.	5.8	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.	2.5	40
49	The effect of slope aspect on vegetation attributes in a mountainous dry valley, Southwest China. <i>Scientific Reports</i> , 2020, 10, 16465.	1.6	53
50	Formula Fertilization Promotes <i>Phoebe bournei</i> Robust Seedling Cultivation. <i>Forests</i> , 2020, 11, 781.	0.9	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.	1.6	6
52	Temporospatial Flavonoids Metabolism Variation in <i>Ginkgo biloba</i> Leaves. <i>Frontiers in Genetics</i> , 2020, 11, 589326.	1.1	18
53	Multiple Ecological Drivers Determining Vegetation Attributes across Scales in a Mountainous Dry Valley, Southwest China. <i>Forests</i> , 2020, 11, 1140.	0.9	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.	2.6	6

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55	Linkage disequilibrium vs. pedigree: Genomic selection prediction accuracy in conifer species. PLoS ONE, 2020, 15, e0232201.	1.1	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.	1.8	3
57	In Situ Genetic Evaluation of European Larch Across Climatic Regions Using Marker-Based Pedigree Reconstruction. Frontiers in Genetics, 2020, 11, 28.	1.1	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.	1.4	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.	0.9	15
60	Transcriptome-wide identification and profiling of miRNAs in a stress-tolerant conifer <i>Sabina chinensis</i> . Journal of Biosciences, 2020, 45, 1.	0.5	2
61	Genomic Diversity Evaluation of <i>Populus trichocarpa</i> Germplasm for Rare Variant Genetic Association Studies. Frontiers in Genetics, 2020, 10, 1384.	1.1	11
62	A Binary-Based Matrix Model for <i>Malus</i> Corolla Symmetry and Its Variational Significance. Frontiers in Plant Science, 2020, 11, 416.	1.7	4
63	Improved genetic distance-based spatial deployment can effectively minimize inbreeding in seed orchard. Forest Ecosystems, 2020, 7, .	1.3	9
64	Marker-assisted selection in <i>C. oleifera</i> hybrid population. Silvae Genetica, 2020, 69, 63-72.	0.4	5
65	Techniques for Small Non-Coding RNA Analysis in Seeds of Forest Tree Species. Methods in Molecular Biology, 2020, 2093, 217-225.	0.4	0
66	Prospects: The Spruce Genome, a Model for Understanding Gymnosperm Evolution and Supporting Tree Improvement Efforts. Compendium of Plant Genomes, 2020, , 215-218.	0.3	0
67	Genomic Selection in Canadian Spruces. Compendium of Plant Genomes, 2020, , 115-127.	0.3	3
68	Species association in <i>Xanthoceras sorbifolium</i> Bunge communities and selection for agroforestry establishment. Agroforestry Systems, 2019, 93, 1531-1543.	0.9	6
69	Current Advances in Seed Orchard Layouts: Two Case Studies in Conifers. Forests, 2019, 10, 93.	0.9	8
70	Local Adaptation and Response of <i>Platycladus orientalis</i> (L.) Franco Populations to Climate Change. Forests, 2019, 10, 622.	0.9	15
71	SNP variable selection by generalized graph domination. PLoS ONE, 2019, 14, e0203242.	1.1	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	0.8	0

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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.	3.5	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.	1.2	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.	1.0	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.	0.8	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.	1.2	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.	1.4	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.	1.1	17
81	Multienvironment genomic variance decomposition analysis of open-pollinated Interior spruce ( <i>Picea</i> ) Tj ETQq1 1 0.784314 rgBT /Ove	1.0	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.	0.8	36
83	Genomic-based multiple-trait evaluation in <i>Eucalyptus grandis</i> using dominant DArT markers. <i>Plant Science</i> , 2018, 271, 27-33.	1.7	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.	0.8	7
85	Quantitative Genetics and Genomics Converge to Accelerate Forest Tree Breeding. <i>Frontiers in Plant Science</i> , 2018, 9, 1693.	1.7	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.	1.2	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.	3.5	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.	1.6	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.	1.6	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.	3.2	13

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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.	2.8	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.	0.8	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.	1.6	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.	0.9	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.	0.8	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.	1.0	9
97	Improving accuracy of breeding values by incorporating genomic information in spatial-competition mixed models. <i>Molecular Breeding</i> , 2017, 37, 1.	1.0	32
98	Practical application of genomic selection in a doubled-haploid winter wheat breeding program. <i>Molecular Breeding</i> , 2017, 37, 117.	1.0	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.	0.9	8
100	Impact of temperature shifts on the joint evolution of seed dormancy and size. <i>Ecology and Evolution</i> , 2017, 7, 26-37.	0.8	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.	0.8	20
102	The gibberellin <i>GID1-DELLA</i> signalling module exists in evolutionarily ancient conifers. <i>Scientific Reports</i> , 2017, 7, 16637.	1.6	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.	0.8	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.	0.6	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.	1.7	8
107	Dynamic Gene-Resource Landscape Management of Norway Spruce: Combining Utilization and Conservation. <i>Frontiers in Plant Science</i> , 2017, 8, 1810.	1.7	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.	1.2	20

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109	Predicting Future Seed Sourcing of <i>Platycladus orientalis</i> (L.) for Future Climates Using Climate Niche Models. <i>Forests</i> , 2017, 8, 471.	0.9	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.	1.2	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.	1.1	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.	1.1	5
113	Contributions of dynamic environmental signals during life-cycle transitions to early life-history traits in lodgepole pine (&lt;i>Pinus contorta&lt;/i> Dougl.). <i>Biogeosciences</i> , 2016, 13, 2945-2958.	1.3	9
114	Global transcriptome analysis of <i>Sabina chinensis</i> (Cupressaceae), a valuable reforestation conifer. <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	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.	0.8	73
116	A transcriptomics investigation into pine reproductive organ development. <i>New Phytologist</i> , 2016, 209, 1278-1289.	3.5	34
117	Species-specific alleles at a $\beta$ -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
118	Optimum neighborhood seed orchard design. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	10
119	Bareroot versus container stocktypes: a performance comparison. <i>New Forests</i> , 2016, 47, 1-51.	0.7	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.	1.1	39
121	Pollination dynamics variation in a Douglas-fir seed orchard as revealed by microsatellite analysis. <i>Silva Fennica</i> , 2016, 50, .	0.5	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.	1.6	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.	1.1	19
124	Evolutionary Quantitative Genomics of <i>Populus trichocarpa</i> . <i>PLoS ONE</i> , 2015, 10, e0142864.	1.1	31
125	Using <i>Populus</i> as a lignocellulosic feedstock for bioethanol. <i>Biotechnology Journal</i> , 2015, 10, 510-524.	1.8	52
126	Forest genomics research and development in Canada: Priorities for developing an economic framework. <i>Forestry Chronicle</i> , 2015, 91, 60-70.	0.5	15

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127	Expansion of the minimum-inbreeding seed orchard design to operational scale. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	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.	1.2	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.	1.2	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.	0.8	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.	1.2	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.	0.5	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.	2.0	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.	0.8	11
135	Extensive Functional Pleiotropy of REVOLUTA Substantiated through Forward Genetics. <i>Plant Physiology</i> , 2014, 164, 548-554.	2.3	17
136	Assessment of the Genetic Diversity in Forest Tree Populations Using Molecular Markers. <i>Diversity</i> , 2014, 6, 283-295.	0.7	90
137	Jackknife resampling for precision measurement of direct gene flow estimates. <i>Scandinavian Journal of Forest Research</i> , 2014, 29, 707-712.	0.5	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.	1.4	125
139	Genetics of wood quality attributes in Western Larch. <i>Annals of Forest Science</i> , 2014, 71, 415-424.	0.8	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.	0.6	24
141	Randomized, replicated, staggered clonal-row (R2SCR) seed orchard design. <i>Tree Genetics and Genomes</i> , 2014, 10, 555-563.	0.6	12
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