

Jean Bousquet

List of Publications by Year in descending order

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132
papers

8,225
citations

50170

46
h-index

54797

84
g-index

138
all docs

138
docs citations

138
times ranked

7924
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic influence on components of wood density variation in white spruce. <i>Forestry</i> , 2022, 95, 153-165.	1.2	8
2	Breeding for adaptation to climate change: genomic selection for drought response in a white spruce multi-site polycross test. <i>Evolutionary Applications</i> , 2022, 15, 383-402.	1.5	14
3	Multi-trait selection for improved solid wood physical and flexural properties in white spruce. <i>Forestry</i> , 2022, 95, 492-503.	1.2	1
4	Metadata analysis indicates biased estimation of genetic parameters and gains using conventional pedigree information instead of genomic-based approaches in tree breeding. <i>Scientific Reports</i> , 2022, 12, 3933.	1.6	6
5	Spruce gigabase genomes: structurally similar yet distinctive with differentially expanding gene families and rapidly evolving genes. <i>Plant Journal</i> , 2022, 111, 1469-1485.	2.8	17
6	Connecting tree-ring phenotypes, genetic associations and transcriptomics to decipher the genomic architecture of drought adaptation in a widespread conifer. <i>Molecular Ecology</i> , 2021, 30, 3898-3917.	2.0	35
7	SNP-based analysis reveals unexpected features of genetic diversity, parental contributions and pollen contamination in a white spruce breeding program. <i>Scientific Reports</i> , 2021, 11, 4990.	1.6	11
8	Combining QTL Mapping and Transcriptomics to Decipher the Genetic Architecture of Phenolic Compounds Metabolism in the Conifer White Spruce. <i>Frontiers in Plant Science</i> , 2021, 12, 675108.	1.7	7
9	Spruce Population Genomics. <i>Population Genomics</i> , 2021, , 1.	0.2	2
10	Multi-trait genomic selection for weevil resistance, growth, and wood quality in Norway spruce. <i>Evolutionary Applications</i> , 2020, 13, 76-94.	1.5	78
11	Complete Chloroplast Genome Sequence of a Black Spruce (<i>Picea mariana</i>) from Eastern Canada. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	4
12	Genomic selection for resistance to spruce budworm in white spruce and relationships with growth and wood quality traits. <i>Evolutionary Applications</i> , 2020, 13, 2704-2722.	1.5	19
13	Complete Mitochondrial Genome of a Gymnosperm, Sitka Spruce (<i>Picea sitchensis</i>), Indicates a Complex Physical Structure. <i>Genome Biology and Evolution</i> , 2020, 12, 1174-1179.	1.1	49
14	Adaptive genetic variation to drought in a widely distributed conifer suggests a potential for increasing forest resilience in a drying climate. <i>New Phytologist</i> , 2020, 227, 427-439.	3.5	66
15	Genomic prediction for hastening and improving efficiency of forward selection in conifer polycross mating designs: an example from white spruce. <i>Heredity</i> , 2020, 124, 562-578.	1.2	38
16	Complete Chloroplast Genome Sequence of an Engelmann Spruce (<i>Picea engelmannii</i> , Genotype) Tj ETQq0,0,0 rgBT /Overlock 1	0,3	4
17	White spruce wood quality for lumber products: priority traits and their enhancement through tree improvement. <i>Forestry</i> , 2019, , .	1.2	10
18	The large repertoire of conifer NLR resistance genes includes drought responsive and highly diversified RNLs. <i>Scientific Reports</i> , 2019, 9, 11614.	1.6	49

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19	Analysis of genetic diversity of lychee (<i>Litchi chinensis</i> Sonn.) and wild forest relatives in the Sapindaceae from Vietnam using microsatellites. <i>Genetic Resources and Crop Evolution</i> , 2019, 66, 1653-1669.	0.8	3
20	Complete Chloroplast Genome Sequence of a White Spruce (<i>Picea glauca</i> , Genotype WS77111) from Eastern Canada. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	7
21	ntEdit: scalable genome sequence polishing. <i>Bioinformatics</i> , 2019, 35, 4430-4432.	1.8	67
22	Thermal acclimation of photosynthesis and respiration of southern and northern white spruce seed sources tested along a regional climatic gradient indicates limited potential to cope with temperature warming. <i>Annals of Botany</i> , 2018, 121, 443-457.	1.4	44
23	Expansion of the dehydrin gene family in the Pinaceae is associated with considerable structural diversity and drought-responsive expression. <i>Tree Physiology</i> , 2018, 38, 442-456.	1.4	30
24	A catalog of annotated high-confidence SNPs from exome capture and sequencing reveals highly polymorphic genes in Norway spruce (<i>Picea abies</i>). <i>BMC Genomics</i> , 2018, 19, 942.	1.2	22
25	Association genetics of acetophenone defence against spruce budworm in mature white spruce. <i>BMC Plant Biology</i> , 2018, 18, 231.	1.6	18
26	A high-resolution reference genetic map positioning 8.8K genes for the conifer white spruce: structural genomics implications and correspondence with physical distance. <i>Plant Journal</i> , 2017, 90, 189-203.	2.8	47
27	Factors affecting the accuracy of genomic selection for growth and wood quality traits in an advanced-breeding population of black spruce (<i>Picea mariana</i>). <i>BMC Genomics</i> , 2017, 18, 335.	1.2	92
28	Gene copy number variations in adaptive evolution: The genomic distribution of gene copy number variations revealed by genetic mapping and their adaptive role in an undomesticated species, white spruce (<i>Picea glauca</i>). <i>Molecular Ecology</i> , 2017, 26, 5989-6001.	2.0	25
29	Asymmetry matters: A genomic assessment of directional biases in gene flow between hybridizing spruces. <i>Ecology and Evolution</i> , 2017, 7, 3883-3893.	0.8	14
30	Development of a Traceability System Based on a SNP Array for Large-Scale Production of High-Value White Spruce (<i>Picea glauca</i>). <i>Frontiers in Plant Science</i> , 2017, 8, 1264.	1.7	14
31	Ecophysiology and Growth of White Spruce Seedlings from Various Seed Sources along a Climatic Gradient Support the Need for Assisted Migration. <i>Frontiers in Plant Science</i> , 2017, 8, 2214.	1.7	35
32	Genetic Adaptation vs. Ecophysiological Plasticity of Photosynthetic-Related Traits in Young <i>Picea glauca</i> Trees along a Regional Climatic Gradient. <i>Frontiers in Plant Science</i> , 2016, 7, 48.	1.7	48
33	Morpho-Physiological Variation of White Spruce Seedlings from Various Seed Sources and Implications for Deployment under Climate Change. <i>Frontiers in Plant Science</i> , 2016, 7, 1450.	1.7	9
34	Development of highly reliable in silico SNP resource and genotyping assay from exome capture and sequencing: an example from black spruce (<i>Picea mariana</i>). <i>Molecular Ecology Resources</i> , 2016, 16, 588-598.	2.2	32
35	Joint inferences from cytoplasmic <i>scp</i> DNA and fossil data provide evidence for glacial vicariance and contrasted post-glacial dynamics in tamarack, a transcontinental conifer. <i>Journal of Biogeography</i> , 2016, 43, 1227-1241.	1.4	10
36	Genetic architecture of wood properties based on association analysis and co-expression networks in white spruce. <i>New Phytologist</i> , 2016, 210, 240-255.	3.5	43

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37	Organellar Genomes of White Spruce (<i>Picea glauca</i>): Assembly and Annotation. <i>Genome Biology and Evolution</i> , 2016, 8, 29-41.	1.1	46
38	Tracking the progression of speciation: variable patterns of introgression across the genome provide insights on the species delimitation between progenitor and derivative spruces (<i>Picea mariana</i> and <i>P. canadensis</i>). <i>Evolution</i> , 2016, 70, 1000-1010.	0.0	0
39	Improved white spruce (<i>Picea glauca</i>) genome assemblies and annotation of large gene families of conifer terpenoid and phenolic defense metabolism. <i>Plant Journal</i> , 2015, 83, 189-212.	2.8	200
40	Integrating phylogeography and paleoecology to investigate the origin and dynamics of hybrid zones: insights from two widespread North American firs. <i>Molecular Ecology</i> , 2015, 24, 2856-2870.	2.0	30
41	Less Pollen-Mediated Gene Flow for More Signatures of Glacial Lineages: Congruent Evidence from Balsam Fir cpDNA and mtDNA for Multiple Refugia in Eastern and Central North America. <i>PLoS ONE</i> , 2015, 10, e0122815.	1.1	14
42	Variations in foliar monoterpenes across the range of jack pine reveal three widespread chemotypes: implications to host expansion of invasive mountain pine beetle. <i>Frontiers in Plant Science</i> , 2015, 6, 342.	1.7	44
43	Inferring and outlining past population declines with linked microsatellites: a case study in two spruce species. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	4
44	Family Variation in the Morphology and Physiology of White Spruce (<i>Picea glauca</i>) Seedlings in Response to Elevated CO ₂ and Temperature. <i>Journal of Sustainable Forestry</i> , 2015, 34, 169-198.	0.6	7
45	Fine-scale geographic variation in photosynthetic-related traits of <i>Picea glauca</i> seedlings indicates local adaptation to climate. <i>Tree Physiology</i> , 2015, 35, 864-878.	1.4	16
46	From genotypes to phenotypes: expression levels of genes encompassing adaptive SNPs in black spruce. <i>Plant Cell Reports</i> , 2015, 34, 2111-2125.	2.8	5
47	Genetic Adaptation to Climate in White Spruce Involves Small to Moderate Allele Frequency Shifts in Functionally Diverse Genes. <i>Genome Biology and Evolution</i> , 2015, 7, 3269-3285.	1.1	47
48	A <i>Picea abies</i> Linkage Map Based on SNP Markers Identifies QTLs for Four Aspects of Resistance to <i>Heterobasidion parviporum</i> Infection. <i>PLoS ONE</i> , 2014, 9, e101049.	1.1	52
49	The bud break process and its variation among local populations of boreal black spruce. <i>Frontiers in Plant Science</i> , 2014, 5, 574.	1.7	40
50	Genomic selection accuracies within and between environments and small breeding groups in white spruce. <i>BMC Genomics</i> , 2014, 15, 1048.	1.2	93
51	The phylogeography of Eurasian <i>Fraxinus</i> species reveals ancient transcontinental reticulation. <i>Molecular Phylogenetics and Evolution</i> , 2014, 77, 223-237.	1.2	15
52	Insights into Conifer Gigabase Genomes. <i>Plant Physiology</i> , 2014, 166, 1724-1732.	2.3	164
53	Relationship between genome and epigenome - challenges and requirements for future research. <i>BMC Genomics</i> , 2014, 15, 487.	1.2	24
54	Rates of spontaneous hybridization and hybrid recruitment in co-existing exotic and native mature larch populations. <i>Tree Genetics and Genomes</i> , 2014, 10, 965-975.	0.6	12

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55	Evolution of gene structure in the conifer <i>Picea glauca</i> : a comparative analysis of the impact of intron size. <i>BMC Plant Biology</i> , 2014, 14, 95.	1.6	46
56	Evolution of an Ancient Microsatellite Hotspot in the Conifer Mitochondrial Genome and Comparison with Other Plants. <i>Journal of Molecular Evolution</i> , 2013, 76, 146-157.	0.8	16
57	The genomic architecture and association genetics of adaptive characters using a candidate SNP approach in boreal black spruce. <i>BMC Genomics</i> , 2013, 14, 368.	1.2	41
58	The Norway spruce genome sequence and conifer genome evolution. <i>Nature</i> , 2013, 497, 579-584.	13.7	1,303
59	Assembling the 20 Gb white spruce (<i>Picea glauca</i>) genome from whole-genome shotgun sequencing data. <i>Bioinformatics</i> , 2013, 29, 1492-1497.	1.8	356
60	The Landscape of Nucleotide Polymorphism among 13,500 Genes of the Conifer <i>Picea glauca</i> , Relationships with Functions, and Comparison with <i>Medicago truncatula</i> . <i>Genome Biology and Evolution</i> , 2013, 5, 1910-1925.	1.1	33
61	Development of high-density SNP genotyping arrays for white spruce (<i>Picea</i>) Tj ETQq1 1 0.784314 rgB 2013, 13, 324-336.	2.2	78
62	The Phylogeny and Biogeographic History of Ashes (<i>Fraxinus</i> , Oleaceae) Highlight the Roles of Migration and Vicariance in the Diversification of Temperate Trees. <i>PLoS ONE</i> , 2013, 8, e80431.	1.1	52
63	When exotic poplars and native <i>Populus balsamifera</i> L. meet on the Canadian Prairies: Spontaneous hybridization and establishment of interspecific hybrids. <i>Forest Ecology and Management</i> , 2012, 285, 142-152.	1.4	21
64	Phylogeny, diversification rates and species boundaries of Mesoamerican firs (<i>Abies</i> , Pinaceae) in a genus-wide context. <i>Molecular Phylogenetics and Evolution</i> , 2012, 62, 263-274.	1.2	65
65	A spruce gene map infers ancient plant genome reshuffling and subsequent slow evolution in the gymnosperm lineage leading to extant conifers. <i>BMC Biology</i> , 2012, 10, 84.	1.7	97
66	Understanding the complexity of IgE-related phenotypes from childhood to young adulthood: A Mechanisms of the Development of Allergy (MeDALL) Seminar. <i>Journal of Allergy and Clinical Immunology</i> , 2012, 129, 943-954.e4.	1.5	68
67	Large-scale asymmetric introgression of cytoplasmic DNA reveals Holocene range displacement in a North American boreal pine complex. <i>Ecology and Evolution</i> , 2012, 2, 1853-1866.	0.8	28
68	Disentangling the Roles of History and Local Selection in Shaping Clinal Variation of Allele Frequencies and Gene Expression in Norway Spruce (<i>Picea abies</i>). <i>Genetics</i> , 2012, 191, 865-881.	1.2	195
69	Scanning SNPs from a large set of expressed genes to assess the impact of artificial selection on the undomesticated genetic diversity of white spruce. <i>Evolutionary Applications</i> , 2012, 5, 641-656.	1.5	23
70	Parallel and lineage-specific molecular adaptation to climate in boreal black spruce. <i>Molecular Ecology</i> , 2012, 21, 4270-4286.	2.0	61
71	Deciduous Trees and the Application of Universal DNA Barcodes: A Case Study on the Circumpolar <i>Fraxinus</i> . <i>PLoS ONE</i> , 2012, 7, e34089.	1.1	40
72	Chloroplast DNA polymorphisms in eastern hemlock: range-wide genogeographic analyses and implications for gene conservation. <i>Canadian Journal of Forest Research</i> , 2011, 41, 1047-1059.	0.8	12

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73	Association Genetics of Wood Physical Traits in the Conifer White Spruce and Relationships With Gene Expression. <i>Genetics</i> , 2011, 188, 197-214.	1.2	131
74	Scanning the genome for gene SNPs related to climate adaptation and estimating selection at the molecular level in boreal black spruce. <i>Molecular Ecology</i> , 2011, 20, 1702-1716.	2.0	135
75	Discordant mtDNA and cpDNA phylogenies indicate geographic speciation and reticulation as driving factors for the diversification of the genus <i>Picea</i> . <i>Tree Genetics and Genomes</i> , 2011, 7, 469-484.	0.6	83
76	Range-wide chloroplast and mitochondrial DNA imprints reveal multiple lineages and complex biogeographic history for Douglas-fir. <i>Tree Genetics and Genomes</i> , 2011, 7, 1025-1040.	0.6	26
77	Gene mapping in white spruce (<i>P. glauca</i>): QTL and association studies integrating population and expression data. <i>BMC Proceedings</i> , 2011, 5, .	1.8	2
78	QTL mapping in white spruce: gene maps and genomic regions underlying adaptive traits across pedigrees, years and environments. <i>BMC Genomics</i> , 2011, 12, 145.	1.2	110
79	A White Spruce Gene Catalog for Conifer Genome Analyses. <i>Plant Physiology</i> , 2011, 157, 14-28.	2.3	143
80	Molecular Evolution of Regulatory Genes in Spruces from Different Species and Continents: Heterogeneous Patterns of Linkage Disequilibrium and Selection but Correlated Recent Demographic Changes. <i>Journal of Molecular Evolution</i> , 2010, 70, 371-386.	0.8	40
81	TreeSNPs: a laboratory information management system (LIMS) dedicated to SNP discovery in trees. <i>Tree Genetics and Genomes</i> , 2010, 6, 435-438.	0.6	10
82	From glacial refugia to modern populations: new assemblages of organelle genomes generated by differential cytoplasmic gene flow in transcontinental black spruce. <i>Molecular Ecology</i> , 2010, 19, 5265-5280.	2.0	48
83	Phylogeographic structure of jack pine (<i>Pinus banksiana</i> ; Pinaceae) supports the existence of a coastal glacial refugium in northeastern North America. <i>American Journal of Botany</i> , 2010, 97, 1903-1912.	0.8	43
84	Complex patterns of hybridization between exotic and native North American poplar species. <i>American Journal of Botany</i> , 2010, 97, 1688-1697.	0.8	41
85	A metapopulation model for the introgression from genetically modified plants into their wild relatives. <i>Evolutionary Applications</i> , 2009, 2, 160-171.	1.5	22
86	Inferring the past from the present phylogeographic structure of North American forest trees: seeing the forest for the genes. <i>Canadian Journal of Forest Research</i> , 2009, 39, 286-307.	0.8	120
87	Glacial vicariance in the Pacific Northwest: evidence from a lodgepole pine mitochondrial DNA minisatellite for multiple genetically distinct and widely separated refugia. <i>Molecular Ecology</i> , 2008, 17, 2463-2475.	2.0	92
88	Ancestry and divergence of subtropical montane forest isolates: molecular biogeography of the genus <i>Abies</i> (Pinaceae) in southern Mexico and Guatemala. <i>Molecular Ecology</i> , 2008, 17, 2476-2490.	2.0	89
89	Scanning the genome for gene single nucleotide polymorphisms involved in adaptive population differentiation in white spruce. <i>Molecular Ecology</i> , 2008, 17, 3599-3613.	2.0	230
90	Enhancing genetic mapping of complex genomes through the design of highly-multiplexed SNP arrays: application to the large and unsequenced genomes of white spruce and black spruce. <i>BMC Genomics</i> , 2008, 9, 21.	1.2	116

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91	Spruce. , 2007, , 93-114.		5
92	Glacial vicariance in Eurasia: mitochondrial DNA evidence from Scots pine for a complex heritage involving genetically distinct refugia at mid-northern latitudes and in Asia Minor. <i>BMC Evolutionary Biology</i> , 2007, 7, 233.	3.2	118
93	Ectomycorrhizal fungal communities of nursery-inoculated seedlings outplanted on clear-cut sites in northern Alberta. <i>Canadian Journal of Forest Research</i> , 2006, 36, 1684-1694.	0.8	30
94	Decoupled mitochondrial and chloroplast DNA population structure reveals Holocene collapse and population isolation in a threatened Mexican-endemic conifer. <i>Molecular Ecology</i> , 2006, 15, 2787-2800.	2.0	83
95	Contrasting microsatellite variation between subalpine and western larch, two closely related species with different distribution patterns. <i>Molecular Ecology</i> , 2006, 15, 3907-3918.	2.0	33
96	Comparative genome mapping among <i>Picea glauca</i> , <i>P. mariana</i> — <i>P. rubens</i> and <i>P. abies</i> , and correspondence with other Pinaceae. <i>Theoretical and Applied Genetics</i> , 2006, 113, 1371-1393.	1.8	81
97	Simple sequence repeat (SSR) markers in the ectomycorrhizal fungus <i>Laccaria bicolor</i> for environmental monitoring of introduced strains and molecular ecology applications. <i>Mycological Research</i> , 2006, 110, 51-59.	2.5	25
98	Automated SNP detection from a large collection of white spruce expressed sequences: contributing factors and approaches for the categorization of SNPs. <i>BMC Genomics</i> , 2006, 7, 174.	1.2	68
99	A mitochondrial DNA minisatellite reveals the postglacial history of jack pine (<i>Pinus banksiana</i>), a broad-range North American conifer. <i>Molecular Ecology</i> , 2005, 14, 3497-3512.	2.0	121
100	Generation, annotation, analysis and database integration of 16,500 white spruce EST clusters. <i>BMC Genomics</i> , 2005, 6, 144.	1.2	119
101	A composite linkage map from two crosses for the species complex <i>Picea mariana</i> — <i>Picea rubens</i> and analysis of synteny with other Pinaceae. <i>Theoretical and Applied Genetics</i> , 2005, 111, 1466-1488.	1.8	33
102	Species-diagnostic markers in <i>Larix</i> spp. based on RAPDs and nuclear, cpDNA, and mtDNA gene sequences, and their phylogenetic implications. <i>Tree Genetics and Genomes</i> , 2005, 1, 50-63.	0.6	35
103	Large-scale statistical analysis of secondary xylem ESTs in pine. <i>Plant Molecular Biology</i> , 2005, 57, 203-224.	2.0	42
104	Trans-specific shared polymorphisms at orthologous nuclear gene loci among distant species in the conifer <i>Picea</i> (Pinaceae): implications for the long-term maintenance of genetic diversity in trees. <i>American Journal of Botany</i> , 2005, 92, 63-73.	0.8	113
105	Mitochondrial Genome Recombination in the Zone of Contact Between Two Hybridizing Conifers. <i>Genetics</i> , 2005, 171, 1951-1962.	1.2	69
106	The impact of climate change on growth of local white spruce populations in Québec, Canada. <i>Forest Ecology and Management</i> , 2005, 205, 169-182.	1.4	113
107	The Evolutionary Implications of <i>knox-I</i> Gene Duplications in Conifers: Correlated Evidence from Phylogeny, Gene Mapping, and Analysis of Functional Divergence. <i>Molecular Biology and Evolution</i> , 2004, 21, 2232-2245.	3.5	69
108	Variation in mitochondrial DNA reveals multiple distant glacial refugia in black spruce (<i>Picea</i>)	2.0	144

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109	Efficient screening for expressed sequence tag polymorphisms (ESTPs) by DNA pool sequencing and denaturing gradient gel electrophoresis (DGGE) in spruces. <i>Molecular Breeding</i> , 2004, 13, 263-279.	1.0	25
110	Multivariate patterns of adaptive genetic variation and seed source transfer in <i>Picea mariana</i> . <i>Canadian Journal of Forest Research</i> , 2004, 34, 531-545.	0.8	66
111	Molecular phylogeny of <i>Alnus</i> (Betulaceae), inferred from nuclear ribosomal DNA ITS sequences. <i>Plant and Soil</i> , 2003, 254, 207-217.	1.8	45
112	Diverging patterns of mitochondrial and nuclear DNA diversity in subarctic black spruce: imprint of a founder effect associated with postglacial colonization. <i>Molecular Ecology</i> , 2003, 12, 891-901.	2.0	77
113	Molecular genetic diversity of the French-American grapevine hybrids cultivated in North America. <i>Genome</i> , 2003, 46, 1037-1048.	0.9	41
114	New evidence from mitochondrial DNA of a progenitor-derivative species relationship between black spruce and red spruce (Pinaceae). <i>American Journal of Botany</i> , 2003, 90, 1801-1806.	0.8	30
115	Molecular phylogeny of <i>Alnus</i> (Betulaceae), inferred from nuclear ribosomal DNA ITS sequences. , 2003, , 207-217.		2
116	Genetic diversity and mating system of post-fire and post-harvest black spruce: an investigation using codominant sequence-tagged-site (STS) markers. <i>Canadian Journal of Forest Research</i> , 2001, 31, 32-40.	0.8	40
117	Life span and biomass allocation of stunted black spruce clones in the subarctic environment. <i>Journal of Ecology</i> , 2000, 88, 584-593.	1.9	48
118	Direct evidence for biased gene diversity estimates from dominant random amplified polymorphic DNA (RAPD) fingerprints. <i>Molecular Ecology</i> , 1999, 8, 477-483.	2.0	92
119	Sequence-tagged-site (STS) markers of arbitrary genes: the amount and nature of variation revealed in Norway spruce. <i>Heredity</i> , 1999, 83, 239-248.	1.2	20
120	Sequence-Tagged-Site (STS) Markers of Arbitrary Genes: Development, Characterization and Analysis of Linkage in Black Spruce. <i>Genetics</i> , 1998, 149, 1089-1098.	1.2	51
121	Phylogeny and Phylogeography of the Circumpolar Genus <i>Fraxinus</i> (OLEACEAE) Based on Internal Transcribed Spacer Sequences of Nuclear Ribosomal DNA. <i>Molecular Phylogenetics and Evolution</i> , 1997, 7, 241-251.	1.2	58
122	Occurrence of somaclonal variation among somatic embryo-derived white spruces (<i>Picea</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 22	0.8	29
123	The evolution of the actinorhizal symbiosis through phylogenetic analysis of host plants. <i>Acta Botanica Gallica</i> , 1996, 143, 635-650.	0.9	7
124	Genetic Diversity and Phylogenetic Relationships between Birches and Alders Using ITS, 18S rRNA, and rbcL Gene Sequences. <i>Molecular Phylogenetics and Evolution</i> , 1993, 2, 112-118.	1.2	60
125	The rbcL gene sequence from chestnut indicates a slow rate of evolution in the Fagaceae. <i>Genome</i> , 1993, 36, 668-671.	0.9	62
126	Genetic diversity in Canadian Hardwoods: Implications for conservation. <i>Forestry Chronicle</i> , 1992, 68, 709-719.	0.5	12

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127	Relationships between balsam fir vulnerability to spruce budworm and ecological site conditions of fir stands in central Quebec. Canadian Journal of Forest Research, 1991, 21, 1752-1759.	0.8	31
128	The Genetics of Actinorhizal Betulaceae. , 1990, , 239-261.		9
129	Restriction fragment polymorphisms in the rDNA region among seven species of <i>Alnus</i> and <i>Betula papyrifera</i> . Plant and Soil, 1989, 118, 231-240.	1.8	15
130	ALLOZYME VARIATION WITHIN AND AMONG MATURE POPULATIONS OF SPECKLED ALDER (<i>ALNUS RUGOSA</i>) AND RELATIONSHIPS WITH GREEN ALDER (<i>A. CRISPA</i>). American Journal of Botany, 1988, 75, 1678-1686.	0.8	22
131	Isozyme Variation among 40 <i>Frankia</i> Strains. Applied and Environmental Microbiology, 1987, 53, 1596-1603.	1.4	48
132	Les g�nomes du pin gris et du pin tordu, t�moins des bouleversements climatiques pass�s. Le Naturaliste Canadien, 0, 138, 32-44.	0.2	1