

John J Mackay

List of Publications by Year in descending order

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98
papers

7,764
citations

61857

43
h-index

53109

85
g-index

100
all docs

100
docs citations

100
times ranked

6923
citing authors

#	ARTICLE	IF	CITATIONS
1	The Norway spruce genome sequence and conifer genome evolution. <i>Nature</i> , 2013, 497, 579-584.	13.7	1,303
2	RECENT ADVANCES IN UNDERSTANDING LIGNIN BIOSYNTHESIS. <i>Annual Review of Plant Biology</i> , 1998, 49, 585-609.	14.2	404
3	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
4	Abnormal Lignin in a Loblolly Pine Mutant. <i>Science</i> , 1997, 277, 235-239.	6.0	311
5	Unexpected variation in lignin. <i>Current Opinion in Plant Biology</i> , 1999, 2, 145-152.	3.5	213
6	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
7	Elucidation of new structures in lignins of CAD- and COMT-deficient plants by NMR. <i>Phytochemistry</i> , 2001, 57, 993-1003.	1.4	195
8	Inheritance, gene expression, and lignin characterization in a mutant pine deficient in cinnamyl alcohol dehydrogenase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 8255-8260.	3.3	194
9	Involvement of <i>Pinus taeda</i> MYB1 and MYB8 in phenylpropanoid metabolism and secondary cell wall biogenesis: a comparative in planta analysis. <i>Journal of Experimental Botany</i> , 2008, 59, 3925-3939.	2.4	183
10	<i>EgMYB1</i> , an R2R3 MYB transcription factor from eucalyptus negatively regulates secondary cell wall formation in <i>Arabidopsis</i> and poplar. <i>New Phytologist</i> , 2010, 188, 774-786.	3.5	180
11	Insights into Conifer Giga-Genomes. <i>Plant Physiology</i> , 2014, 166, 1724-1732.	2.3	164
12	Subgroup 4 R2R3-MYBs in conifer trees: gene family expansion and contribution to the isoprenoid- and flavonoid-oriented responses. <i>Journal of Experimental Botany</i> , 2010, 61, 3847-3864.	2.4	146
13	NMR analysis of lignins in CAD-deficient plants. Part 1. Incorporation of hydroxycinnamaldehydes and hydroxybenzaldehydes into lignins. <i>Organic and Biomolecular Chemistry</i> , 2003, 1, 268-281.	1.5	145
14	A White Spruce Gene Catalog for Conifer Genome Analyses. <i>Plant Physiology</i> , 2011, 157, 14-28.	2.3	143
15	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
16	Accuracy of genomic selection models in a large population of open-pollinated families in white spruce. <i>Heredity</i> , 2014, 113, 343-352.	1.2	127
17	Molecular characterization of <i>EgMYB1</i> , a putative transcriptional repressor of the lignin biosynthetic pathway. <i>Plant Science</i> , 2007, 173, 542-549.	1.7	123
18	Conifer R2R3-MYB transcription factors: sequence analyses and gene expression in wood-forming tissues of white spruce (<i>Picea glauca</i>). <i>BMC Plant Biology</i> , 2007, 7, 17.	1.6	121

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19	Generation, annotation, analysis and database integration of 16,500 white spruce EST clusters. BMC Genomics, 2005, 6, 144.	1.2	119
20	Genotypic variation in wood density and growth traits of poplar hybrids at four clonal trials. Forest Ecology and Management, 2007, 238, 92-106.	1.4	119
21	Genes involved in the biosynthesis of lignin precursors in Arabidopsis thaliana. Plant Physiology and Biochemistry, 2003, 41, 677-687.	2.8	115
22	Genomic selection accuracies within and between environments and small breeding groups in white spruce. BMC Genomics, 2014, 15, 1048.	1.2	93
23	Towards decoding the conifer giga-genome. Plant Molecular Biology, 2012, 80, 555-569.	2.0	91
24	Identification of conserved core xylem gene sets: conifer cDNA microarray development, transcript profiling and computational analyses. New Phytologist, 2008, 180, 766-786.	3.5	87
25	Genetic control of wood properties in Picea glauca "an analysis of trends with cambial age. Canadian Journal of Forest Research, 2010, 40, 703-715.	0.8	82
26	Short-term effects of nitrogen availability on wood formation and fibre properties in hybrid poplar. Trees - Structure and Function, 2007, 21, 249-259.	0.9	80
27	Development of high-density SNP genotyping arrays for white spruce (Picea Tj ETQq1 1 0.784314 rgB 2013, 13, 324-336.	2.2	78
28	Expression profiling and functional analysis of Populus WRKY23 reveals a regulatory role in defense. New Phytologist, 2009, 184, 48-70.	3.5	77
29	Evaluation of the impact of single nucleotide polymorphisms and primer mismatches on quantitative PCR. BMC Biotechnology, 2009, 9, 75.	1.7	73
30	Conifer genomics and adaptation: at the crossroads of genetic diversity and genome function. New Phytologist, 2016, 209, 44-62.	3.5	73
31	Genetic analysis of cinnamyl alcohol dehydrogenase in loblolly pine: single gene inheritance, molecular characterization and evolution. Molecular Genetics and Genomics, 1995, 247, 537-545.	2.4	71
32	Automated SNP detection from a large collection of white spruce expressed sequences: contributing factors and approaches for the categorization of SNPs. BMC Genomics, 2006, 7, 174.	1.2	68
33	Genetic control of somatic embryogenesis initiation in loblolly pine and implications for breeding. Tree Genetics and Genomes, 2006, 2, 1-9.	0.6	66
34	Effects of Increased Nitrogen Supply on the Lignification of Poplar Wood. Journal of Agricultural and Food Chemistry, 2007, 55, 10306-10314.	2.4	64
35	Genetic Improvement of White Spruce Mechanical Wood Traits "Early Screening by Means of Acoustic Velocity. Forests, 2013, 4, 575-594.	0.9	63
36	Lignin Structure in a Mutant Pine Deficient in Cinnamyl Alcohol Dehydrogenase. Journal of Agricultural and Food Chemistry, 2000, 48, 2326-2331.	2.4	62

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37	Transcriptome profiling in conifers and the PiceaGenExpress database show patterns of diversification within gene families and interspecific conservation in vascular gene expression. <i>BMC Genomics</i> , 2012, 13, 434.	1.2	60
38	Large-scale screening of transcription factor-promoter interactions in spruce reveals a transcriptional network involved in vascular development. <i>Journal of Experimental Botany</i> , 2014, 65, 2319-2333.	2.4	59
39	High nitrogen fertilization and stem leaning have overlapping effects on wood formation in poplar but invoke largely distinct molecular pathways. <i>Tree Physiology</i> , 2010, 30, 1273-1289.	1.4	52
40	Expression of the Î²-glucosidase gene <i>Pgl1</i> underpins natural resistance of white spruce against spruce budworm. <i>Plant Journal</i> , 2015, 81, 68-80.	2.8	52
41	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
42	Gene Expression during Formation of Earlywood and Latewood in Loblolly Pine: Expression Profiles of 350 Genes. <i>Plant Biology</i> , 2004, 6, 654-663.	1.8	47
43	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
44	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
45	Heterologous Array Analysis in Pinaceae: Hybridization of <i>Pinus taeda</i> cDNA Arrays with cDNA from Needles and Embryogenic Cultures of <i>P. taeda</i> , <i>P. sylvestris</i> or <i>Picea abies</i> . <i>Comparative and Functional Genomics</i> , 2002, 3, 306-318.	2.0	45
46	Average effect of a mutation in lignin biosynthesis in loblolly pine. <i>Theoretical and Applied Genetics</i> , 1999, 99, 705-710.	1.8	43
47	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
48	Large-scale statistical analysis of secondary xylem ESTs in pine. <i>Plant Molecular Biology</i> , 2005, 57, 203-224.	2.0	42
49	Potential link between biotic defense activation and recalcitrance to induction of somatic embryogenesis in shoot primordia from adult trees of white spruce (<i>Picea glauca</i>). <i>BMC Plant Biology</i> , 2013, 13, 116.	1.6	42
50	Multiple Metabolic Innovations and Losses Are Associated with Major Transitions in Land Plant Evolution. <i>Current Biology</i> , 2020, 30, 1783-1800.e11.	1.8	42
51	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
52	Gene family structure, expression and functional analysis of HD-Zip III genes in angiosperm and gymnosperm forest trees. <i>BMC Plant Biology</i> , 2010, 10, 273.	1.6	39
53	Modified Lignin and Delignification with a CAD-Deficient Loblolly Pine. <i>Holzforschung</i> , 1999, 53, 403-410.	0.9	35
54	A robust neural networks approach for spatial and intensity-dependent normalization of cDNA microarray data. <i>Bioinformatics</i> , 2005, 21, 2674-2683.	1.8	35

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55	Modular organization of the white spruce (<i>Picea glauca</i>) transcriptome reveals functional organization and evolutionary signatures. <i>New Phytologist</i> , 2015, 207, 172-187.	3.5	35
56	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
57	Sequence analysis and functional characterization of the promoter of the <i>Picea glauca</i> Cinnamyl Alcohol Dehydrogenase gene in transgenic white spruce plants. <i>Plant Cell Reports</i> , 2009, 28, 787-800.	2.8	34
58	Opposite action of R2R3-MYBs from different subgroups on key genes of the shikimate and monolignol pathways in spruce. <i>Journal of Experimental Botany</i> , 2014, 65, 495-508.	2.4	34
59	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
60	CNVs into the wild: screening the genomes of conifer trees (<i>Picea</i> spp.) reveals fewer gene copy number variations in hybrids and links to adaptation. <i>BMC Genomics</i> , 2017, 18, 97.	1.2	32
61	Diverse developmental mutants revealed in an activation-tagged population of poplar This article is one of a selection of papers published on the Special Issue of Poplar Research in Canada.. <i>Canadian Journal of Botany</i> , 2007, 85, 1071-1081.	1.2	31
62	Gene copy number variations involved in balsam poplar (<i>Populus balsamifera</i> L.) adaptive variations. <i>Molecular Ecology</i> , 2019, 28, 1476-1490.	2.0	31
63	The influence of cambial age on breeding for wood properties in <i>Picea glauca</i> . <i>Tree Genetics and Genomes</i> , 2011, 7, 641-653.	0.6	30
64	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
65	Dissection of expression quantitative trait locus and allele specificity using a haploid/diploid plant system – insights into compensatory evolution of transcriptional regulation within populations. <i>New Phytologist</i> , 2016, 211, 159-171.	3.5	28
66	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
67	A Conifer UDP-Sugar Dependent Glycosyltransferase Contributes to Acetophenone Metabolism and Defense against Insects. <i>Plant Physiology</i> , 2017, 175, 641-651.	2.3	24
68	ForestTreeDB: a database dedicated to the mining of tree transcriptomes. <i>Nucleic Acids Research</i> , 2007, 35, D888-D894.	6.5	22
69	Characterization of NAD-dependent mannitol dehydrogenase from celery as affected by ions, chelators, reducing agents and metabolites. <i>Plant Science</i> , 1998, 131, 43-51.	1.7	21
70	PYROLYSIS MASS SPECTRAL CHARACTERIZATION OF WOOD FROM CAD-DEFICIENT PINE. <i>Journal of Wood Chemistry and Technology</i> , 2001, 21, 19-29.	0.9	21
71	Biochar and plant growth promoting rhizobacteria effects on switchgrass (<i>Panicum virgatum</i> cv.) Tj ETQq1 1 0.784314 rgBT /Overlook and Bioenergy, 2016, 95, 167-173.	2.9	21
72	PULPING AND BLEACHING OF CAD-DEFICIENT WOOD. <i>Journal of Wood Chemistry and Technology</i> , 2001, 21, 1-17.	0.9	20

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73	SABATH methyltransferases from white spruce (<i>Picea glauca</i>): gene cloning, functional characterization and structural analysis. <i>Tree Physiology</i> , 2009, 29, 947-957.	1.4	20
74	Are long-lived trees poised for evolutionary change? Single locus effects in the evolution of gene expression networks in spruce. <i>Molecular Ecology</i> , 2013, 22, 2369-2379.	2.0	20
75	Reference transcriptomes and comparative analyses of six species in the threatened rosewood genus <i>Dalbergia</i> . <i>Scientific Reports</i> , 2020, 10, 17749.	1.6	20
76	Evolution of the biosynthesis of two hydroxyacetophenones in plants. <i>Plant, Cell and Environment</i> , 2018, 41, 620-629.	2.8	19
77	Functional genomics of PycR, a LysR family transcriptional regulator essential for maintenance of <i>Pseudomonas aeruginosa</i> in the rat lung. <i>Microbiology (United Kingdom)</i> , 2008, 154, 2106-2118.	0.7	18
78	Association genetics of acetophenone defence against spruce budworm in mature white spruce. <i>BMC Plant Biology</i> , 2018, 18, 231.	1.6	18
79	Spruce giga-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
80	PULPING AND BLEACHING OF PARTIALLY CAD-DEFICIENT WOOD. <i>Journal of Wood Chemistry and Technology</i> , 2002, 22, 235-248.	0.9	16
81	Can wood properties be predicted from the morphological traits of a tree? A canonical correlation study of plantation-grown white spruce. <i>Canadian Journal of Forest Research</i> , 2012, 42, 1518-1529.	0.8	16
82	Insect herbivory (<i>Choristoneura fumiferana</i> , Tortricidea) underlies tree population structure (<i>Picea</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.6	15
83	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
84	Age trends in genotypic variation of wood density and its intra-ring components in young poplar hybrid crosses. <i>Annals of Forest Science</i> , 2006, 63, 673-685.	0.8	14
85	What do ecological regions tell us about wood quality? A case study in eastern Canadian white spruce. <i>Canadian Journal of Forest Research</i> , 2014, 44, 1383-1393.	0.8	13
86	Differential gene expression patterns in white spruce newly formed tissue on board the International Space Station. <i>Advances in Space Research</i> , 2013, 52, 760-772.	1.2	12
87	Genetic control and evolutionary potential of a constitutive resistance mechanism against the spruce budworm (<i>Choristoneura fumiferana</i>) in white spruce (<i>Picea glauca</i>). <i>Heredity</i> , 2018, 121, 142-154.	1.2	12
88	Hydroxyacetophenone defenses in white spruce against spruce budworm. <i>Evolutionary Applications</i> , 2020, 13, 62-75.	1.5	12
89	Report on the Forest Trees Workshop at the Plant and Animal Genome Conference. <i>Comparative and Functional Genomics</i> , 2003, 4, 229-238.	2.0	10
90	Carbon dynamics in a biochar-amended loamy soil under switchgrass. <i>Canadian Journal of Soil Science</i> , 2015, 95, 1-13.	0.5	10

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91	Forest Tree Genomics: Review of Progress. <i>Advances in Botanical Research</i> , 2015, 74, 39-92.	0.5	9
92	Physiological responses of rosewoods <i>Dalbergia cochinchinensis</i> and <i>D. oliveri</i> under drought and heat stresses. <i>Ecology and Evolution</i> , 2020, 10, 10872-10885.	0.8	8
93	<i>In vivo</i> function of <i>Pg¹glu-1</i> in the release of acetophenones in white spruce. <i>PeerJ</i> , 2017, 5, e3535.	0.9	7
94	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
95	Functional Analysis of the <i>PgCesA3</i> White Spruce Cellulose Synthase Gene Promoter in Secondary Xylem. <i>Frontiers in Plant Science</i> , 2019, 10, 626.	1.7	5
96	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
97	Identification of nitrogen responsive genes in poplar roots grown under two contrasting nitrogen levels. <i>Plant Root</i> , 2014, 8, 42-54.	0.3	2
98	Competing MYB networks as switches in primary and secondary metabolism in spruce. <i>BMC Proceedings</i> , 2011, 5, .	1.8	1