

# Alexander Myburg

## List of Publications by Year in descending order

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129  
papers

5,543  
citations

76196

40  
h-index

95083

68  
g-index

131  
all docs

131  
docs citations

131  
times ranked

6521  
citing authors

#	ARTICLE	IF	CITATIONS
1	A genome-wide SNP genotyping resource for tropical pine tree species. <i>Molecular Ecology Resources</i> , 2022, 22, 695-710.	2.2	10
2	Genome-Wide Association Study identifies SNP markers and putative candidate genes for terpene traits important for <i>Leptocybe invasa</i> resistance in <i>Eucalyptus grandis</i> . <i>G3: Genes, Genomes, Genetics</i> , 2022, .	0.8	2
3	Genetic diversity and population structure analysis reveals the unique genetic composition of South African selected macadamia accessions. <i>Tree Genetics and Genomes</i> , 2022, 18, 1.	0.6	1
4	Genomic consequences of artificial selection during early domestication of a wood fibre crop. <i>New Phytologist</i> , 2022, 235, 1944-1956.	3.5	1
5	Insect egg-induced physiological changes and transcriptional reprogramming leading to gall formation. <i>Plant, Cell and Environment</i> , 2021, 44, 535-547.	2.8	9
6	Genomic evidence of introgression and adaptation in a model subtropical tree species, <i>Eucalyptus grandis</i> . <i>Molecular Ecology</i> , 2021, 30, 625-638.	2.0	12
7	Construction of a DArT-seq marker-based genetic linkage map and identification of QTLs for yield in tea ( <i>Camellia sinensis</i> (L.) O. Kuntze). <i>Tree Genetics and Genomes</i> , 2021, 17, 1.	0.6	3
8	Genomic Breeding for Diameter Growth and Tolerance to <i>Leptocybe</i> Gall Wasp and <i>Botryosphaeria/Teratosphaeria</i> Fungal Disease Complex in <i>Eucalyptus grandis</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 638969.	1.7	8
9	Genetic containment in vegetatively propagated forest trees: CRISPR disruption of <i>LEAFY</i> function in <i>Eucalyptus</i> gives sterile indeterminate inflorescences and normal juvenile development. <i>Plant Biotechnology Journal</i> , 2021, 19, 1743-1755.	4.1	23
10	qtIXplorer: an online systems genetics browser in the <i>Eucalyptus</i> Genome Integrative Explorer (EucGenIE). <i>BMC Bioinformatics</i> , 2021, 22, 595.	1.2	2
11	Expected benefits of genomic selection for growth and wood quality traits in <i>Eucalyptus grandis</i> . <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	0.6	22
12	A Genome-Wide Association Study for Resistance to the Insect Pest <i>Leptocybe invasa</i> in <i>Eucalyptus grandis</i> Reveals Genomic Regions and Positional Candidate Defense Genes. <i>Plant and Cell Physiology</i> , 2020, 61, 1285-1296.	1.5	19
13	Plant Biosystems Design Research Roadmap 1.0. <i>Biodesign Research</i> , 2020, 2020, .	0.8	16
14	Certification for gene-edited forests. <i>Science</i> , 2019, 365, 767-768.	6.0	12
15	Dual RNA-Seq Analysis of the Pine- <i>Fusarium circinatum</i> Interaction in Resistant ( <i>Pinus tecunumanii</i> ) and Susceptible ( <i>Pinus patula</i> ) Hosts. <i>Microorganisms</i> , 2019, 7, 315.	1.6	18
16	Analysis of Orthologous SECONDARY WALL-ASSOCIATED NAC DOMAIN1 (SND1) Promotor Activity in Herbaceous and Woody Angiosperms. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4623.	1.8	2
17	A systems genetics analysis in <i>Eucalyptus</i> reveals coordination of metabolic pathways associated with xylan modification in wood-forming tissues. <i>New Phytologist</i> , 2019, 223, 1952-1972.	3.5	10
18	Systems and Synthetic Biology of Forest Trees: A Bioengineering Paradigm for Woody Biomass Feedstocks. <i>Frontiers in Plant Science</i> , 2019, 10, 775.	1.7	17

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19	Identification and functional evaluation of accessible chromatin associated with wood formation in <i>Eucalyptus grandis</i> . <i>New Phytologist</i> , 2019, 223, 1937-1951.	3.5	10
20	Xylan in the Middle: Understanding Xylan Biosynthesis and Its Metabolic Dependencies Toward Improving Wood Fiber for Industrial Processing. <i>Frontiers in Plant Science</i> , 2019, 10, 176.	1.7	52
21	Organellar carbon metabolism is coordinated with distinct developmental phases of secondary xylem. <i>New Phytologist</i> , 2019, 222, 1832-1845.	3.5	11
22	The plastid and mitochondrial genomes of <i>Eucalyptus grandis</i> . <i>BMC Genomics</i> , 2019, 20, 132.	1.2	35
23	A Standardized Synthetic <i>Eucalyptus</i> Transcription Factor and Promoter Panel for Re-engineering Secondary Cell Wall Regulation in Biomass and Bioenergy Crops. <i>ACS Synthetic Biology</i> , 2019, 8, 463-465.	1.9	15
24	Terpenes associated with resistance against the gall wasp, <i>Leptocybe invasa</i> , in <i>Eucalyptus grandis</i> . <i>Plant, Cell and Environment</i> , 2018, 41, 1840-1851.	2.8	17
25	Genomewide analysis of the lateral organ boundaries domain gene family in <i>Eucalyptus grandis</i> reveals members that differentially impact secondary growth. <i>Plant Biotechnology Journal</i> , 2018, 16, 124-136.	4.1	44
26	Carbohydrate active enzyme domains from extreme thermophiles: components of a modular toolbox for lignocellulose degradation. <i>Extremophiles</i> , 2018, 22, 1-12.	0.9	14
27	Hardwood Tree Genomics: Unlocking Woody Plant Biology. <i>Frontiers in Plant Science</i> , 2018, 9, 1799.	1.7	50
28	Temporal analysis of Arabidopsis genes activated by <i>Eucalyptus grandis</i> NAC transcription factors associated with xylem fibre and vessel development. <i>Scientific Reports</i> , 2018, 8, 10983.	1.6	16
29	Defence transcriptome assembly and pathogenesis related gene family analysis in <i>Pinus tecunumanii</i> (low elevation). <i>BMC Genomics</i> , 2018, 19, 632.	1.2	32
30	Network-based integration of systems genetics data reveals pathways associated with lignocellulosic biomass accumulation and processing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1195-1200.	3.3	55
31	Integrated analysis and transcript abundance modelling of H3K4me3 and H3K27me3 in developing secondary xylem. <i>Scientific Reports</i> , 2017, 7, 3370.	1.6	32
32	Evidence for salicylic acid signalling and histological changes in the defence response of <i>Eucalyptus grandis</i> to <i>Chrysoporthe austroafricana</i> . <i>Scientific Reports</i> , 2017, 7, 45402.	1.6	9
33	In planta expression of hyperthermophilic enzymes as a strategy for accelerated lignocellulosic digestion. <i>Scientific Reports</i> , 2017, 7, 11462.	1.6	16
34	A time series transcriptome analysis of cassava ( <i>Manihot esculenta</i> Crantz) varieties challenged with Ugandan cassava brown streak virus. <i>Scientific Reports</i> , 2017, 7, 9747.	1.6	36
35	QTL associated with resistance to cassava brown streak and cassava mosaic diseases in a bi-parental cross of two Tanzanian farmer varieties, Namikonga and Albert. <i>Theoretical and Applied Genetics</i> , 2017, 130, 2069-2090.	1.8	39
36	Systems genetics reveals a transcriptional network associated with susceptibility in the maize "grey leaf spot" pathosystem. <i>Plant Journal</i> , 2017, 89, 746-763.	2.8	49

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37	QTL Mapping for Pest and Disease Resistance in Cassava and Coincidence of Some QTL with Introgression Regions Derived from <i>Manihot glaziovii</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 1168.	1.7	51
38	Localization and Transcriptional Responses of <i>Chrysosporthe austroafricana</i> in <i>Eucalyptus grandis</i> Identify Putative Pathogenicity Factors. <i>Frontiers in Microbiology</i> , 2016, 7, 1953.	1.5	4
39	Insect Gallers and Their Plant Hosts: From Omics Data to Systems Biology. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1891.	1.8	31
40	Dual RNA-Sequencing of <i>Eucalyptus nitens</i> during <i>Phytophthora cinnamomi</i> Challenge Reveals Pathogen and Host Factors Influencing Compatibility. <i>Frontiers in Plant Science</i> , 2016, 7, 191.	1.7	54
41	Functional network analysis of genes differentially expressed during xylogenesis in <i>woody Arabidopsis</i> plants. <i>Plant Journal</i> , 2016, 86, 376-390.	2.8	27
42	Systems genetics of wood formation. <i>Current Opinion in Plant Biology</i> , 2016, 30, 94-100.	3.5	46
43	The Arabidopsis Domain of Unknown Function 1218 (DUF1218) Containing Proteins, MODIFYING WALL LIGNIN-1 and 2 (At1g31720/MWL-1 and At4g19370/MWL-2) Function Redundantly to Alter Secondary Cell Wall Lignin Content. <i>PLoS ONE</i> , 2016, 11, e0150254.	1.1	14
44	Combined de novo and genome guided assembly and annotation of the <i>Pinus patula</i> juvenile shoot transcriptome. <i>BMC Genomics</i> , 2015, 16, 1057.	1.2	44
45	Foliar terpenoid levels and corresponding gene expression are systemically and differentially induced in <i>Eucalyptus grandis</i> clonal genotypes in response to <i>Chrysosporthe austroafricana</i> challenge. <i>Plant Pathology</i> , 2015, 64, 1320-1325.	1.2	5
46	Horsetails Are Ancient Polyploids: Evidence from <i>Equisetum giganteum</i> . <i>Plant Cell</i> , 2015, 27, 1567-1578.	3.1	78
47	Comparative interrogation of the developing xylem transcriptomes of two wood-forming species: <i>Populus trichocarpa</i> and <i>Eucalyptus grandis</i> . <i>New Phytologist</i> , 2015, 206, 1391-1405.	3.5	47
48	Genomic patterns of species diversity and divergence in <i>Eucalyptus</i> . <i>New Phytologist</i> , 2015, 206, 1378-1390.	3.5	20
49	Genome-wide analysis of the lignin toolbox of <i>Eucalyptus grandis</i> . <i>New Phytologist</i> , 2015, 206, 1297-1313.	3.5	113
50	High-Resolution Linkage Map and Chromosome-Scale Genome Assembly for Cassava ( <i>Manihot</i> )	8.8	100
51	Comprehensive Genome-Wide Analysis of the Aux/IAA Gene Family in <i>Eucalyptus</i> : Evidence for the Role of EgrIAA4 in Wood Formation. <i>Plant and Cell Physiology</i> , 2015, 56, 700-714.	1.5	37
52	Explosive Tandem and Segmental Duplications of Multigenic Families in <i>Eucalyptus grandis</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 1068-1081.	1.1	42
53	Transcriptome and hormone profiling reveals <i>Eucalyptus grandis</i> defence responses against <i>Chrysosporthe austroafricana</i> . <i>BMC Genomics</i> , 2015, 16, 319.	1.2	41
54	The Transcriptome and Terpene Profile of <i>Eucalyptus grandis</i> Reveals Mechanisms of Defense Against the Insect Pest, <i>Leptocybe invasa</i> . <i>Plant and Cell Physiology</i> , 2015, 56, 1418-1428.	1.5	55

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55	Comparative analysis of plant carbohydrate active enzymes and their role in xylogenesis. BMC Genomics, 2015, 16, 402.	1.2	23
56	The Eucalyptus terpene synthase gene family. BMC Genomics, 2015, 16, 450.	1.2	125
57	Plant scientists celebrate new woody plant genome. New Phytologist, 2015, 206, 1185-1187.	3.5	7
58	Genome-wide mapping of histone H3 lysine 4 trimethylation in Eucalyptus grandis developing xylem. BMC Plant Biology, 2015, 15, 117.	1.6	26
59	Protein domain evolution is associated with reproductive diversification and adaptive radiation in the genus Eucalyptus. New Phytologist, 2015, 206, 1328-1336.	3.5	19
60	Structural, evolutionary and functional analysis of the NAC domain protein family in Eucalyptus. New Phytologist, 2015, 206, 1337-1350.	3.5	69
61	Investigating the molecular underpinnings underlying morphology and changes in carbon partitioning during tension wood formation in Eucalyptus. New Phytologist, 2015, 206, 1351-1363.	3.5	27
62	The floral transcriptome of Eucalyptus grandis. New Phytologist, 2015, 206, 1406-1422.	3.5	61
63	The Eucalyptus grandis R2R3 MYB transcription factor family: evidence for woody growth-related evolution and function. New Phytologist, 2015, 206, 1364-1377.	3.5	107
64	Genome-Wide Characterization and Expression Profiling of the AUXIN RESPONSE FACTOR (ARF) Gene Family in Eucalyptus grandis. PLoS ONE, 2014, 9, e108906.	1.1	45
65	Cell Wall-Related Proteins of Unknown Function: Missing Links in Plant Cell Wall Development. Plant and Cell Physiology, 2014, 55, 1031-1043.	1.5	25
66	The genome of Eucalyptus grandis. Nature, 2014, 510, 356-362.	13.7	725
67	Uncovering the defence responses of Eucalyptus to pests and pathogens in the genomics age. Tree Physiology, 2014, 34, 931-943.	1.4	48
68	Recombinant hyperthermophilic enzyme expression in plants: a novel approach for lignocellulose digestion. Trends in Biotechnology, 2014, 32, 281-289.	4.9	21
69	Mapping QTL conferring resistance in maize to gray leaf spot disease caused by Cercospora zeina. BMC Genetics, 2014, 15, 60.	2.7	41
70	Transmission ratio distortion in an interspecific cross between Fusarium circinatum and Fusarium subglutinans. Genes and Genomics, 2013, 35, 177-183.	0.5	4
71	Induced somatic sector analysis of cellulose synthase (CesA) promoter regions in woody stem tissues. Planta, 2013, 237, 799-812.	1.6	14
72	Diversity and cis-element architecture of the promoter regions of cellulose synthase genes in Eucalyptus. Tree Genetics and Genomes, 2013, 9, 989-1004.	0.6	3

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73	Established and new technologies reduce increasing pest and pathogen threats to Eucalypt plantations. <i>Forest Ecology and Management</i> , 2013, 301, 35-42.	1.4	71
74	Chitosan application improves resistance to <i>Fusarium circinatum</i> in <i>Pinus patula</i> . <i>South African Journal of Botany</i> , 2013, 85, 70-78.	1.2	42
75	Pathogenicity associated genes in <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> race 4. <i>South African Journal of Science</i> , 2013, 109, 10.	0.3	32
76	Navigating the transcriptional roadmap regulating plant secondary cell wall deposition. <i>Frontiers in Plant Science</i> , 2013, 4, 325.	1.7	124
77	The identification and differential expression of <i>Eucalyptus grandis</i> pathogenesis-related genes in response to salicylic acid and methyl jasmonate. <i>Frontiers in Plant Science</i> , 2013, 4, 43.	1.7	31
78	Genetic dissection of growth, wood basic density and gene expression in interspecific backcrosses of <i>Eucalyptus grandis</i> and <i>E. urophylla</i> . <i>BMC Genetics</i> , 2012, 13, 60.	2.7	31
79	A reference linkage map for <i>Eucalyptus</i> . <i>BMC Genomics</i> , 2012, 13, 240.	1.2	33
80	Genomic Characterization of DArT Markers Based on High-Density Linkage Analysis and Physical Mapping to the <i>Eucalyptus</i> Genome. <i>PLoS ONE</i> , 2012, 7, e44684.	1.1	77
81	High synteny and colinearity among <i>Eucalyptus</i> genomes revealed by high-density comparative genetic mapping. <i>Tree Genetics and Genomes</i> , 2012, 8, 339-352.	0.6	49
82	Progress in Myrtaceae genetics and genomics: <i>Eucalyptus</i> as the pivotal genus. <i>Tree Genetics and Genomes</i> , 2012, 8, 463-508.	0.6	197
83	Cellulose factories: advancing bioenergy production from forest trees. <i>New Phytologist</i> , 2012, 194, 54-62.	3.5	82
84	High-density genetic linkage maps with over 2,400 sequence-anchored DArT markers for genetic dissection in an F2 pseudo-backcross of <i>Eucalyptus grandis</i> Å— <i>E. urophylla</i> . <i>Tree Genetics and Genomes</i> , 2012, 8, 163-175.	0.6	39
85	Genetic analysis of growth, morphology and pathogenicity in the F1 progeny of an interspecific cross between <i>Fusarium circinatum</i> and <i>Fusarium subglutinans</i> . <i>Fungal Biology</i> , 2011, 115, 902-908.	1.1	15
86	Population genetic analysis and phylogeny reconstruction in <i>Eucalyptus</i> (Myrtaceae) using high-throughput, genome-wide genotyping. <i>Molecular Phylogenetics and Evolution</i> , 2011, 59, 206-224.	1.2	102
87	SND2, a NAC transcription factor gene, regulates genes involved in secondary cell wall development in <i>Arabidopsis</i> fibres and increases fibre cell area in <i>Eucalyptus</i> . <i>BMC Plant Biology</i> , 2011, 11, 173.	1.6	164
88	Maize microarray annotation database. <i>Plant Methods</i> , 2011, 7, 31.	1.9	9
89	The <i>Eucalyptus grandis</i> Genome Project: Genome and transcriptome resources for comparative analysis of woody plant biology. <i>BMC Proceedings</i> , 2011, 5, .	1.8	25
90	The <i>Eucalyptus</i> genome integrative explorer (EucGenIE): a resource for <i>Eucalyptus</i> genomics and transcriptomics. <i>BMC Proceedings</i> , 2011, 5, .	1.8	18

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91	Genetic dissection of transcript, metabolite, growth and wood property traits in an F2 pseudo-backcross pedigree of <i>Eucalyptus grandis</i> x <i>E. urophylla</i> . BMC Proceedings, 2011, 5, .	1.8	3
92	Characterising the role of the <i>Eucalyptus grandis</i> SND2 promoter in secondary cell wall biosynthesis. BMC Proceedings, 2011, 5, .	1.8	2
93	The role of SND2 in the regulation of Arabidopsis fibre secondary cell wall formation. BMC Proceedings, 2011, 5, .	1.8	14
94	Optimization of a plant regeneration and genetic transformation protocol for <i>Eucalyptus</i> clonal genotypes. BMC Proceedings, 2011, 5, .	1.8	4
95	Development of <i>Eucalyptus</i> tissue culture conditions for improved in vitro plant health and transformability. BMC Proceedings, 2011, 5, P153.	1.8	5
96	In silico comparative analysis of glycoside hydrolase (GH) family 10 endo-(1-4)-beta-xylanase genes from <i>Eucalyptus grandis</i> and <i>Arabidopsis thaliana</i> . BMC Proceedings, 2011, 5, .	1.8	0
97	Genomic characterization, high-density mapping and anchoring of DArT markers to the reference genome of <i>Eucalyptus</i> . BMC Proceedings, 2011, 5, .	1.8	3
98	Investigating <i>Eucalyptus</i> ’ pathogen and pest interactions to dissect broad spectrum defense mechanisms. BMC Proceedings, 2011, 5, .	1.8	1
99	Comparison of different control-pollination techniques for small-flowered eucalypts. New Forests, 2010, 39, 75-88.	0.7	10
100	Diurnal and circadian patterns of gene expression in the developing xylem of <i>Eucalyptus</i> trees. South African Journal of Botany, 2010, 76, 425-439.	1.2	32
101	De novo assembled expressed gene catalog of a fast-growing <i>Eucalyptus</i> tree produced by Illumina mRNA-Seq. BMC Genomics, 2010, 11, 681.	1.2	150
102	A high-density Diversity Arrays Technology (DArT) microarray for genome-wide genotyping in <i>Eucalyptus</i> . Plant Methods, 2010, 6, 16.	1.9	110
103	Genomics, Domestication, and Evolution of Forest Trees. Cold Spring Harbor Symposia on Quantitative Biology, 2009, 74, 303-317.	2.0	13
104	Microsatellite diversity and genetic structure of the commercially important tropical tree species <i>Eucalyptus urophylla</i> , endemic to seven islands in eastern Indonesia. Tree Genetics and Genomes, 2008, 4, 519-530.	0.6	41
105	Relationship between hybrid performance and AFLP based genetic distance in highland maize inbred lines. Euphytica, 2008, 162, 313-323.	0.6	33
106	Comparative analysis of orthologous cellulose synthase promoters from <i>Arabidopsis</i> , <i>Populus</i> and <i>Eucalyptus</i> : evidence of conserved regulatory elements in angiosperms. New Phytologist, 2008, 179, 722-737.	3.5	49
107	Resistance genes in the Triticeae and the dynamics of divergence before duplication. South African Journal of Botany, 2008, 74, 51-64.	1.2	3
108	Forest and fibre genomics: biotechnology tools for applied tree improvement. Southern Forests, 2008, 70, 59-68.	0.2	5

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109	Chloroplast DNA phylogeography reveals the island colonisation route of <i>Eucalyptus urophylla</i> (Myrtaceae). <i>Australian Journal of Botany</i> , 2007, 55, 673.	0.3	25
110	Complete genetic linkage maps from an interspecific cross between <i>Fusarium circinatum</i> and <i>Fusarium subglutinans</i> . <i>Fungal Genetics and Biology</i> , 2007, 44, 701-714.	0.9	33
111	<i>Eucalypts.</i> , 2007, , 115-160.		15
112	Genetic diversity of African maize inbred lines revealed by SSR markers. <i>Hereditas</i> , 2007, 144, 10-17.	0.5	83
113	Comparative genetic analysis of highland maize inbred lines using AFLP and SSR markers. <i>South African Journal of Plant and Soil</i> , 2006, 23, 99-104.	0.4	0
114	Genetic Diversity Among Traditional Ethiopian Highland Maize Accessions Assessed by Simple Sequence Repeat (SSR) Markers. <i>Genetic Resources and Crop Evolution</i> , 2006, 53, 1579-1588.	0.8	23
115	Genetic diversity in traditional Ethiopian highland maize accessions assessed by AFLP markers and morphological traits. <i>Biodiversity and Conservation</i> , 2006, 15, 2655-2671.	1.2	25
116	Within-tree transcriptome profiling in wood-forming tissues of a fast-growing <i>Eucalyptus</i> tree. <i>Tree Physiology</i> , 2006, 26, 365-375.	1.4	26
117	Six new cellulose synthase genes from <i>Eucalyptus</i> are associated with primary and secondary cell wall biosynthesis. <i>Tree Physiology</i> , 2006, 26, 545-556.	1.4	89
118	Genetic diversity analysis of CIMMYT-mid-altitude maize inbred lines using AFLP markers. <i>South African Journal of Plant and Soil</i> , 2006, 23, 49-53.	0.4	1
119	Genetic Architecture of Transcript-Level Variation in Differentiating Xylem of a <i>Eucalyptus</i> Hybrid. <i>Genetics</i> , 2005, 169, 2295-2303.	1.2	107
120	Phenotypic diversity for morphological and agronomic traits in traditional Ethiopian highland maize accessions. <i>South African Journal of Plant and Soil</i> , 2005, 22, 100-105.	0.4	10
121	Genetic diversity in traditional Ethiopian highland maize accessions assessed by AFLP markers and morphological traits. , 2005, , 315-331.		1
122	Coordinated Genetic Regulation of Growth and Lignin Revealed by Quantitative Trait Locus Analysis of cDNA Microarray Data in an Interspecific Backcross of <i>Eucalyptus</i> . <i>Plant Physiology</i> , 2004, 135, 2368-2378.	2.3	205
123	Genetics of Postzygotic Isolation in <i>Eucalyptus</i> : Whole-Genome Analysis of Barriers to Introgression in a Wide Interspecific Cross of <i>Eucalyptus grandis</i> and <i>E. globulus</i> . <i>Genetics</i> , 2004, 166, 1405-1418.	1.2	61
124	Development and assessment of microarray-based DNA fingerprinting in <i>Eucalyptus grandis</i> . <i>Theoretical and Applied Genetics</i> , 2004, 109, 1329-1336.	1.8	45
125	<i>Genetic Mapping in Forest Trees: Markers, Linkage Analysis and Genomics.</i> , 2004, 26, 105-141.		8
126	Comparative genetic linkage maps of <i>Eucalyptus grandis</i> , <i>Eucalyptus globulus</i> and their F1 hybrid based on a double pseudo-backcross mapping approach. <i>Theoretical and Applied Genetics</i> , 2003, 107, 1028-1042.	1.8	75



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127	High-Throughput AFLP Analysis Using Infrared Dye-Labeled Primers and an Automated DNA Sequencer. <i>BioTechniques</i> , 2001, 30, 348-357.	0.8	88
128	Development of RAPD and SCAR markers linked to the Russian wheat aphid resistance gene Dn2 in wheat. <i>Theoretical and Applied Genetics</i> , 1998, 96, 1162-1169.	1.8	35
129	Identification and Genetic Distance Analysis of Wheat Cultivars using RAPD Fingerprinting. <i>Cereal Research Communications</i> , 1997, 25, 875-882.	0.8	10