Jacqueline Grima-Pettenati

List of Publications by Year
in descending order

29 papers	3,500 citations	304743 22 h-index	477307 29 g-index
29 all docs	29 docs citations	29 times ranked	4070 citing authors

#	Article	IF	Citations
1	The genome of Eucalyptus grandis. Nature, 2014, 510, 356-362.	27.8	725
2	Downregulation of Cinnamoyl-Coenzyme A Reductase in Poplar: Multiple-Level Phenotyping Reveals Effects on Cell Wall Polymer Metabolism and Structure. Plant Cell, 2007, 19, 3669-3691.	6.6	352
3	EgMYB2, a new transcriptional activator from Eucalyptus xylem, regulates secondary cell wall formation and lignin biosynthesis. Plant Journal, 2005, 43, 553-567.	5.7	327
4	Lignins and lignocellulosics: a better control of synthesis for new and improved uses. Trends in Plant Science, 2003, 8, 576-581.	8.8	294
5	Down-regulation of Cinnamoyl-CoA Reductase induces significant changes of lignin profiles in transgenic tobacco plants. Plant Journal, 2002, 13, 71-83.	5.7	282
6	Cinnamoyl CoA reductase, the first committed enzyme of the lignin branch biosynthetic pathway: cloning, expression and phylogenetic relationships. Plant Journal, 1997, 11, 429-441.	5.7	271
7	EgMYB1, an R2R3 MYB transcription factor from eucalyptus negatively regulates secondary cell wall formation in Arabidopsis and poplar. New Phytologist, 2010, 188, 774-786.	7.3	180
8	Molecular characterization of EgMYB1, a putative transcriptional repressor of the lignin biosynthetic pathway. Plant Science, 2007, 173, 542-549.	3.6	123
9	Genomeâ€wide analysis of the lignin toolbox of <scp>E</scp>ucalyptus grandis. New Phytologist, 2015, 206, 1297-1313.	7.3	113
10	The <scp>E</scp>ucalyptus grandis <scp>R</scp>2<scp>R</scp>3â€<scp>MYB</scp> transcription factor family: evidence for woody growthâ€related evolution and function. New Phytologist, 2015, 206, 1364-1377.	7.3	107
11	Identification of novel transcription factors regulating secondary cell wall formation in Arabidopsis. Frontiers in Plant Science, 2013, 4, 189.	3.6	106
12	Identification of genes preferentially expressed during wood formation in Eucalyptus. Plant Molecular Biology, 2004, 55, 263-280.	3.9	99
13	Structural, evolutionary and functional analysis of the <scp>NAC</scp> domain protein family in Eucalyptus. New Phytologist, 2015, 206, 1337-1350.	7.3	69
14	Reference Genes for High-Throughput Quantitative Reverse Transcriptionâ€“PCR Analysis of Gene Expression in Organs and Tissues of Eucalyptus Grown in Various Environmental Conditions. Plant and Cell Physiology, 2012, 53, 2101-2116.	3.1	54
15	Eucalyptus hairy roots, a fast, efficient and versatile tool to explore function and expression of genes involved in wood formation. Plant Biotechnology Journal, 2016, 14, 1381-1393.	8.3	54
16	A systems biology view of wood formation in Eucalyptus grandis trees submitted to different potassium and water regimes. New Phytologist, 2019, 223, 766-782.	7.3	48
17	The Eucalyptus linker histone variant EgH1.3 cooperates with the transcription factor EgMYB1 to control lignin biosynthesis during wood formation. New Phytologist, 2017, 213, 287-299.	7.3	46
18	Genome-Wide Characterization and Expression Profiling of the AUXIN RESPONSE FACTOR (ARF) Gene Family in Eucalyptus grandis. PLoS ONE, 2014, 9, e108906.	2.5	45

#	Article	IF	Citations
19	Contrasting nitrogen fertilization treatments impact xylem gene expression and secondary cell wall lignification in Eucalyptus. BMC Plant Biology, 2014, 14, 256.	3.6	41
20	Comprehensive Genome-Wide Analysis of the Aux/IAA Gene Family in Eucalyptus: Evidence for the Role of EgrIAA4 in Wood Formation. Plant and Cell Physiology, 2015, 56, 700-714.	3.1	37
21	Implementing the CRISPR/Cas9 Technology in Eucalyptus Hairy Roots Using Wood-Related Genes. International Journal of Molecular Sciences, 2020, 21, 3408.	4.1	30
22	Long cold exposure induces transcriptional and biochemical remodelling of xylem secondary cell wall in Eucalyptus. Tree Physiology, 2018, 38, 409-422.	3.1	27
23	Overexpression of EgROP1, a Eucalyptus vascularâ€expressed Racâ€like small GTPase, affects secondary xylem formation in Arabidopsis thaliana. New Phytologist, 2009, 183, 1014-1029.	7.3	21
24	Genetic transformation of Eucalyptus globulus using the vascular-specific EgCCR as an alternative to the constitutive CaMV35S promoter. Plant Cell, Tissue and Organ Culture, 2014, 117, 77-84.	2.3	20
25	A Standardized Synthetic Eucalyptus Transcription Factor and Promoter Panel for Re-engineering Secondary Cell Wall Regulation in Biomass and Bioenergy Crops. ACS Synthetic Biology, 2019, 8, 463-465.	3.8	15
26	Wood Architecture and Composition Are Deeply Remodeled in Frost Sensitive Eucalyptus Overexpressing CBF/DREB1 Transcription Factors. International Journal of Molecular Sciences, 2020, 21, 3019.	4.1	7
27	Eucalyptus grandis AUX/INDOLE-3-ACETIC ACID 13 (EgrIAA13) is a novel transcriptional regulator of xylogenesis. Plant Molecular Biology, 2022, , 1.	3.9	3
28	Building up resources and knowledge to unravel transcriptomics dynamics underlying Eucalyptus globulusxylogenesis. BMC Proceedings, 2011, 5, .	1.6	2
29	Overexpression of EgrIAA20 from Eucalyptus grandis, a Non-Canonical Aux/IAA Gene, Specifically Decouples Lignification of the Different Cell-Types in Arabidopsis Secondary Xylem. International Journal of Molecular Sciences, 2022, 23, 5068.	4.1	2