Veronique Storme

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	A Molecular Timetable for Apical Bud Formation and Dormancy Induction in Poplar. Plant Cell, 2007, 19, 2370-2390.	6.6	436
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	A Systems Biology View of Responses to Lignin Biosynthesis Perturbations in <i>Arabidopsis</i> Â. Plant Cell, 2012, 24, 3506-3529.	6.6	321
4	Lignin biosynthesis perturbations affect secondary cell wall composition and saccharification yield in Arabidopsis thaliana. Biotechnology for Biofuels, 2013, 6, 46.	6.2	251
5	Dense Genetic Linkage Maps of Three Populus Species (<i>Populus deltoides</i> , <i>P. nigra</i> and) Tj ETQq1 I	L 0,784314 2.9	t rgβŢ /Over
6	Capturing the phosphorylation and protein interaction landscape of the plant TOR kinase. Nature Plants, 2019, 5, 316-327.	9.3	205
7	Improved saccharification and ethanol yield from field-grown transgenic poplar deficient in cinnamoyl-CoA reductase. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 845-850.	7.1	186
8	GOLVEN Secretory Peptides Regulate Auxin Carrier Turnover during Plant Gravitropic Responses. Developmental Cell, 2012, 22, 678-685.	7.0	182
9	Leaf Responses to Mild Drought Stress in Natural Variants of Arabidopsis Â. Plant Physiology, 2015, 167, 800-816.	4.8	176
10	High–Level Secretion and Very Efficient Isotopic Labeling of Tick Anticoagulant Peptide (TAP) Expressed in the Methylotrophic Yeast, Pichia pastoris. Bio/technology, 1994, 12, 1119-1124.	1.5	161
11	Genetical metabolomics of flavonoid biosynthesis inPopulus: a case study. Plant Journal, 2006, 47, 224-237.	5.7	140
12	The ROS Wheel: Refining ROS Transcriptional Footprints. Plant Physiology, 2016, 171, 1720-1733.	4.8	137
13	Bud set in poplar – genetic dissection of a complex trait in natural and hybrid populations. New Phytologist, 2011, 189, 106-121.	7.3	125
14	Identification of AFLP molecular markers for resistance against Melampsora larici-populina in Populus. Theoretical and Applied Genetics, 1996, 93-93, 733-737.	3.6	118
15	Structure of the genetic diversity in black poplar (Populus nigra L.) populations across European river systems: Consequences for conservation and restoration. Forest Ecology and Management, 2008, 255, 1388-1399.	3.2	116
16	Engineering traditional monolignols out of lignin by concomitant up-regulation of F5H1 and down-regulation of COMT in Arabidopsis. Plant Journal, 2010, 64, 885-897.	5.7	114
17	A Spatiotemporal DNA Endoploidy Map of the Arabidopsis Root Reveals Roles for the Endocycle in Root Development and Stress Adaptation. Plant Cell, 2018, 30, 2330-2351.	6.6	107
18	Intraspecific and interspecific genetic and phylogenetic relationships in the genus Populus based on AFLP markers. Theoretical and Applied Genetics, 2005, 111, 1440-1456.	3.6	103

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19	Altered expression of maize PLASTOCHRON1 enhances biomass and seed yield by extending cell division duration. Nature Communications, 2017, 8, 14752.	12.8	89
20	From network to phenotype: the dynamic wiring of an Arabidopsis transcriptional network induced by osmotic stress. Molecular Systems Biology, 2017, 13, 961.	7.2	86
21	The reduction in maize leaf growth under mild drought affects the transition between cell division and cell expansion and cannot be restored by elevated gibberellic acid levels. Plant Biotechnology Journal, 2018, 16, 615-627.	8.3	73
22	Chloroplasts Are Central Players in Sugar-Induced Leaf Growth. Plant Physiology, 2016, 171, 590-605.	4.8	67
23	Ex-situ conservation of Black poplar in Europe: genetic diversity in nine gene bank collections and their value for nature development. Theoretical and Applied Genetics, 2004, 108, 969-981.	3.6	65
24	Forever Young: The Role of Ubiquitin Receptor DA1 and E3 Ligase BIG BROTHER in Controlling Leaf Growth and Development. Plant Physiology, 2017, 173, 1269-1282.	4.8	55
25	The Transcription Factor MYB29 Is a Regulator of <i>ALTERNATIVE OXIDASE1a</i> . Plant Physiology, 2017, 173, 1824-1843.	4.8	46
26	Integrative inference of transcriptional networks in Arabidopsis yields novel ROS signalling regulators. Nature Plants, 2021, 7, 500-513.	9.3	43
27	Highâ€resolution timeâ€resolved imaging of <i>in vitro</i> Arabidopsis rosette growth. Plant Journal, 2014, 80, 172-184.	5.7	41
28	Combining growth-promoting genes leads to positive epistasis in Arabidopsis thaliana. ELife, 2014, 3, e02252.	6.0	38
29	Postglacial migration of Populus nigra L.: lessons learnt from chloroplast DNA. Forest Ecology and Management, 2005, 206, 71-90.	3.2	36
30	Genomic regions involved in productivity of two interspecific poplar families in Europe. 1. Stem height, circumference and volume. Tree Genetics and Genomes, 2009, 5, 147-164.	1.6	35
31	Fine Mapping and Identification of Nucleotide Binding Site/Leucine-Rich Repeat Sequences at the MER Locus in Populus deltoides †S9-2'. Phytopathology, 2001, 91, 1069-1073.	2.2	32
32	Transcriptional coordination between leaf cell differentiation and chloroplast development established by TCP20 and the subgroup Ib bHLH transcription factors. Plant Molecular Biology, 2014, 85, 233-245.	3.9	31
33	A user-friendly platform for yeast two-hybrid library screening using next generation sequencing. PLoS ONE, 2018, 13, e0201270.	2.5	30
34	Seedling developmental defects upon blocking CINNAMATEâ€4â€HYDROXYLASE are caused by perturbations in auxin transport. New Phytologist, 2021, 230, 2275-2291.	7.3	27
35	Paternity analysis ofPopulus nigraL. offspring in a Belgian plantation of native and exotic poplars. Annals of Forest Science, 2006, 63, 783-790.	2.0	25
36	Comparative transcriptomics enables the identification of functional orthologous genes involved in early leaf growth. Plant Biotechnology Journal, 2020, 18, 553-567.	8.3	24

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37	The â€TranSeq' 3′â€end sequencing method for highâ€throughput transcriptomics and gene space refine in plant genomes. Plant Journal, 2018, 96, 223-232.	ment	23
38	Plant cell wall profiling by fast maximum likelihood reconstruction (FMLR) and region-of-interest (ROI) segmentation of solution-state 2D 1H–13C NMR spectra. Biotechnology for Biofuels, 2013, 6, 45.	6.2	18
39	Natural Variation of Molecular and Morphological Gibberellin Responses. Plant Physiology, 2017, 173, 703-714.	4.8	16
40	Nonselective Chemical Inhibition of Sec7 Domain-Containing ARF GTPase Exchange Factors. Plant Cell, 2018, 30, 2573-2593.	6.6	16
41	Genomic regions involved in productivity of two interspecific poplar families in Europe. 2. Biomass production and its relationships with tree architecture and phenology. Tree Genetics and Genomes, 2010, 6, 533-554.	1.6	12
42	Nanobody-Dependent Delocalization of Endocytic Machinery in Arabidopsis Root Cells Dampens Their Internalization Capacity. Frontiers in Plant Science, 2021, 12, 538580.	3.6	6
43	Emergent adaptive behaviour of GRN-controlled simulated robots in a changing environment. PeerJ, 2016, 4, e2812.	2.0	4
44	Genetic Variability of Arabidopsis thaliana Mature Root System Architecture and Genome-Wide Association Study. Frontiers in Plant Science, 2021, 12, 814110.	3.6	3
45	Science, society and biosafety of a field trial with transgenic biofuel poplars. BMC Proceedings, 2011, 5, I23.	1.6	2
46	Functional analysis of Arabidopsis and maize transgenic lines overexpressing the ADP-ribose/NADH pyrophosphohydrolase, AtNUDX7. International Journal of Developmental Biology, 2019, 63, 45-55.	0.6	1