

Stéphane Maury

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

2,755
citations

172207

29
h-index

205818

48
g-index

51
all docs

51
docs citations

51
times ranked

3506
citing authors

#	ARTICLE	IF	CITATIONS
1	Purification, Cloning, and Properties of an Acyltransferase Controlling Shikimate and Quinate Ester Intermediates in Phenylpropanoid Metabolism. <i>Journal of Biological Chemistry</i> , 2003, 278, 95-103.	1.6	345
2	Epigenetic regulation of adaptive responses of forest tree species to the environment. <i>Ecology and Evolution</i> , 2013, 3, 399-415.	0.8	271
3	Tobacco O-Methyltransferases Involved in Phenylpropanoid Metabolism. The Different Caffeoyl-Coenzyme A/5-Hydroxyferuloyl-Coenzyme A 3/5-O-Methyltransferase and Caffeic Acid/5-Hydroxyferulic Acid 3/5-O-Methyltransferase Classes Have Distinct Substrate Specificities and Expression Patterns. <i>Plant Physiology</i> , 1999, 121, 215-224.	2.3	135
4	Repression of O-methyltransferase genes in transgenic tobacco affects lignin synthesis and plant growth. <i>Phytochemistry</i> , 2001, 57, 1167-1176.	1.4	131
5	Differential accumulation of monolignol-derived compounds in elicited flax (<i>Linum usitatissimum</i>) cell suspension cultures. <i>Planta</i> , 2006, 223, 975-989.	1.6	123
6	Jasmonic acid elicitation of <i>Hypericum perforatum</i> L. cell suspensions and effects on the production of phenylpropanoids and naphthodianthrones. <i>Plant Cell, Tissue and Organ Culture</i> , 2007, 89, 1-13.	1.2	113
7	Tissue dependent variations of DNA methylation and endoreduplication levels during tomato fruit development and ripening. <i>Planta</i> , 2008, 228, 391-399.	1.6	105
8	The influence of salicylic acid elicitation of shoots, callus, and cell suspension cultures on production of naphthodianthrones and phenylpropanoids in <i>Hypericum perforatum</i> L.. <i>Plant Cell, Tissue and Organ Culture</i> , 2013, 113, 25-39.	1.2	101
9	cDNA cloning, substrate specificity and expression study of tobacco caffeoyl-CoA 3-O-methyltransferase, a lignin biosynthetic enzyme. <i>Plant Molecular Biology</i> , 1998, 36, 427-437.	2.0	98
10	Forest tree genomics: 10 achievements from the past 10 years and future prospects. <i>Annals of Forest Science</i> , 2016, 73, 77-103.	0.8	91
11	DNA methylating and demethylating treatments modify phenotype and cell wall differentiation state in sugarbeet cell lines. <i>Plant Physiology and Biochemistry</i> , 2005, 43, 681-691.	2.8	76
12	In search of markers for somatic embryo maturation in hybrid larch (<i>Larix laricina</i> × <i>eurolepis</i>): global DNA methylation and proteomic analyses. <i>Physiologia Plantarum</i> , 2014, 150, 271-291.	2.6	70
13	Chilling-responsive DEMETER-LIKE DNA demethylase mediates in poplar bud break. <i>Plant, Cell and Environment</i> , 2017, 40, 2236-2249.	2.8	69
14	Identification and quantification of hypericin and pseudohypericin in different <i>Hypericum perforatum</i> L. in vitro cultures. <i>Plant Physiology and Biochemistry</i> , 2005, 43, 591-601.	2.8	66
15	DNA methylation and histone acetylation: genotypic variations in hybrid poplars, impact of water deficit and relationships with productivity. <i>Annals of Forest Science</i> , 2010, 67, 208-208.	0.8	55
16	Epigenetics for Crop Improvement in Times of Global Change. <i>Biology</i> , 2021, 10, 766.	1.3	53
17	Changes in the epigenome and transcriptome of the poplar shoot apical meristem in response to water availability affect preferentially hormone pathways. <i>Journal of Experimental Botany</i> , 2018, 69, 537-551.	2.4	52
18	Winter-dormant shoot apical meristem in poplar trees shows environmental epigenetic memory. <i>Journal of Experimental Botany</i> , 2018, 69, 4821-4837.	2.4	52

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19	Advances and Promises of Epigenetics for Forest Trees. <i>Forests</i> , 2020, 11, 976.	0.9	49
20	Effects of Polysaccharide Elicitors on Secondary Metabolite Production and Antioxidant Response in <i>Hypericum perforatum</i> L. Shoot Cultures. <i>Scientific World Journal</i> , The, 2014, 2014, 1-10.	0.8	47
21	Methylome of DNase I sensitive chromatin in <i>Populus trichocarpa</i> shoot apical meristematic cells: a simplified approach revealing characteristics of genome-wide DNA methylation in open chromatin state. <i>New Phytologist</i> , 2013, 197, 416-430.	3.5	44
22	Fungal elicitor-mediated enhancement in phenylpropanoid and naphthodianthrone contents of <i>Hypericum perforatum</i> L. cell cultures. <i>Plant Cell, Tissue and Organ Culture</i> , 2015, 122, 213-226.	1.2	39
23	Folivory elicits a strong defense reaction in <i>Catharanthus roseus</i> : metabolomic and transcriptomic analyses reveal distinct local and systemic responses. <i>Scientific Reports</i> , 2017, 7, 40453.	1.6	39
24	Phytohormone and Chromatin Crosstalk: The Missing Link For Developmental Plasticity?. <i>Frontiers in Plant Science</i> , 2019, 10, 395.	1.7	39
25	Polysaccharide elicitors enhance phenylpropanoid and naphthodianthrone production in cell suspension cultures of <i>Hypericum perforatum</i> . <i>Plant Cell, Tissue and Organ Culture</i> , 2015, 122, 649-663.	1.2	38
26	Epigenetics in Forest Trees. <i>Advances in Botanical Research</i> , 2018, 88, 387-453.	0.5	37
27	Time course and amplitude of DNA methylation in the shoot apical meristem are critical points for bolting induction in sugar beet and bolting tolerance between genotypes. <i>Journal of Experimental Botany</i> , 2011, 62, 2585-2597.	2.4	36
28	Deciphering the Epigenetic Alphabet Involved in Transgenerational Stress Memory in Crops. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7118.	1.8	36
29	Biological invasion: The influence of the hidden side of the (epi)genome. <i>Functional Ecology</i> , 2020, 34, 385-400.	1.7	34
30	Epigenomics and bolting tolerance in sugar beet genotypes. <i>Journal of Experimental Botany</i> , 2016, 67, 207-225.	2.4	31
31	RNAi suppression of DNA methylation affects the drought stress response and genome integrity in transgenic poplar. <i>New Phytologist</i> , 2021, 232, 80-97.	3.5	31
32	Relationship between DNA methylation and histone acetylation levels, cell redox and cell differentiation states in sugarbeet lines. <i>Planta</i> , 2006, 224, 812-827.	1.6	29
33	Identification of differentially methylated regions during vernalization revealed a role for RNA methyltransferases in bolting. <i>Journal of Experimental Botany</i> , 2013, 64, 651-663.	2.4	25
34	Poplars with a PtDDM1-RNAi transgene have reduced DNA methylation and show aberrant post-dormancy morphology. <i>Planta</i> , 2013, 237, 1483-1493.	1.6	24
35	Identification of the Enzymatic Active Site of Tobacco Caffeoyl-coenzyme A O-Methyltransferase by Site-directed Mutagenesis. <i>Journal of Biological Chemistry</i> , 2001, 276, 36831-36838.	1.6	23
36	O-methyltransferase(s)-suppressed plants produce lower amounts of phenolic vir inducers and are less susceptible to <i>Agrobacterium tumefaciens</i> infection. <i>Planta</i> , 2010, 232, 975-986.	1.6	23

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37	In silico study of wall-associated kinase family reveals large-scale genomic expansion potentially connected with functional diversification in <i>Populus</i> . <i>Tree Genetics and Genomes</i> , 2014, 10, 1135-1147.	0.6	17
38	Narrow-sense heritability and PST estimates of DNA methylation in three <i>Populus nigra</i> L. populations under contrasting water availability. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	15
39	Developmental Methylome of the Medicinal Plant <i>Catharanthus roseus</i> Unravels the Tissue-Specific Control of the Monoterpene Indole Alkaloid Pathway by DNA Methylation. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6028.	1.8	14
40	Genic DNA methylation changes during in vitro organogenesis: organ specificity and conservation between parental lines of epialleles. <i>Physiologia Plantarum</i> , 2012, 146, 321-335.	2.6	13
41	Impact of drought and leaf development stage on enzymatic antioxidant system of two <i>Populus deltoides</i> —nigra clones. <i>Annals of Forest Science</i> , 2006, 63, 323-327.	0.8	13
42	Hypomethylation of the aquatic invasive plant, <i>Ludwigia grandiflora</i> subsp. <i>hexapetala</i> mimics the adaptive transition into the terrestrial morphotype. <i>Physiologia Plantarum</i> , 2020, 170, 280-298.	2.6	12
43	Assessing Global DNA Methylation Changes Associated with Plasticity in Seven Highly Inbred Lines of Snapdragon Plants (<i>Antirrhinum majus</i>). <i>Genes</i> , 2019, 10, 256.	1.0	11
44	Characterization of Epigenetic Biomarkers Using New Molecular Approaches. , 2007, , 351-370.		9
45	Developmental, genetic and environmental variations of global DNA methylation in the first leaves emerging from the shoot apical meristem in poplar trees. <i>Plant Signaling and Behavior</i> , 2019, 14, 1596717.	1.2	7
46	From Methylome to Integrative Analysis of Tissue Specificity. <i>Methods in Molecular Biology</i> , 2022, , 223-240.	0.4	4
47	Augmenter le niveau de production de biomasse des cultures ligneuses d'œuvres ou semi-d'œuvres. Principaux enseignements du projet SYLVABIOM. <i>Revue Forestière Française</i> , 2015, , 249.	0.0	3
48	Zebularine, a DNA Methylation Inhibitor, Activates Anthocyanin Accumulation in Grapevine Cells. <i>Genes</i> , 2022, 13, 1256.	1.0	3