Loic Lepiniec

List of Publications by Year
in descending order

126 papers	20,109 citations	25034 57 h-index	18130 120 g-index
129 all docs	129 docs citations	129 times ranked	15416 citing authors

#	Article	IF	Citations
1	MYB transcription factors in Arabidopsis. Trends in Plant Science, 2010, 15, 573-581.	8.8	2,987
2	Transcriptional control of flavonoid biosynthesis by MYBâ€“bHLHâ€“WDR complexes. Trends in Plant Science, 2015, 20, 176-185.	8.8	1,336
3	GENETICS AND BIOCHEMISTRY OF SEED FLAVONOIDS. Annual Review of Plant Biology, 2006, 57, 405-430.	18.7	1,056
4	TT2, TT8, and TTG1 synergistically specify the expression ofBANYULSand proanthocyanidin biosynthesis inArabidopsis thaliana. Plant Journal, 2004, 39, 366-380.	5.7	855
5	Flavonoid oxidation in plants: from biochemical properties to physiological functions. Trends in Plant Science, 2007, 12, 29-36.	8.8	758
6	LEAFY COTYLEDON2 encodes a B3 domain transcription factor that induces embryo development. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 11806-11811.	7.1	680
7	The TT8 Gene Encodes a Basic Helix-Loop-Helix Domain Protein Required for Expression of DFR and BAN Genes in Arabidopsis Siliques. Plant Cell, 2000, 12, 1863-1878.	6.6	679
8	The Arabidopsis <i>TT2</i> Gene Encodes an R2R3 MYB Domain Protein That Acts as a Key Determinant for Proanthocyanidin Accumulation in Developing Seed. Plant Cell, 2001, 13, 2099-2114.	6.6	667
9	MYBL2 is a new regulator of flavonoid biosynthesis in <i>Arabidopsis thaliana</i>. Plant Journal, 2008, 55, 940-953.	5.7	474
10	An integrated overview of seed development in Arabidopsis thaliana ecotype WS. Plant Physiology and Biochemistry, 2002, 40, 151-160.	5.8	418
11	WRINKLED1 specifies the regulatory action of LEAFY COTYLEDON2 towards fatty acid metabolism during seed maturation in Arabidopsis. Plant Journal, 2007, 50, 825-838.	5.7	408
12	Deciphering gene regulatory networks that control seed development and maturation in Arabidopsis. Plant Journal, 2008, 54, 608-620.	5.7	391
13	Identification and characterization of <scp>MYB</scp>â€b<scp>HLH</scp>â€<scp>WD</scp>40 regulatory complexes controlling proanthocyanidin biosynthesis in strawberry (<i><scp>F</scp>ragariaÂ</i>Ã—<i>Âananassa</i>) fruits. New Phytologist, 2013, 197, 454-467.	7.3	388
14	Physiological and developmental regulation of seed oil production. Progress in Lipid Research, 2010, 49, 235-249.	11.6	382
15	TRANSPARENT TESTA10 Encodes a Laccase-Like Enzyme Involved in Oxidative Polymerization of Flavonoids in Arabidopsis Seed Coat. Plant Cell, 2005, 17, 2966-2980.	6.6	380
16	Proanthocyanidin-Accumulating Cells in Arabidopsis Testa: Regulation of Differentiation and Role in Seed Development. Plant Cell, 2003, 15, 2514-2531.	6.6	359
17	Complexity and robustness of the flavonoid transcriptional regulatory network revealed by comprehensive analyses of <scp>MYB</scp>â€“b<scp>HLH</scp>â€“<scp>WDR</scp> complexes and their targets in <scp>A</scp>rabidopsis seed. New Phytologist, 2014, 202, 132-144.	7.3	338
18	The TRANSPARENT TESTA16 Locus Encodes the ARABIDOPSIS BSISTER MADS Domain Protein and Is Required for Proper Development and Pigmentation of the Seed Coat. Plant Cell, 2002, 14, 2463-2479.	6.6	333

#	Article	IF	Citations
19	TT8 controls its own expression in a feedback regulation involving TTG1 and homologous MYB and bHLH factors, allowing a strong and cell-specific accumulation of flavonoids inArabidopsis thaliana. Plant Journal, 2006, 46, 768-779.	5.7	288
20	Flavonoid diversity and biosynthesis in seed of Arabidopsis thaliana. Planta, 2006, 224, 96-107.	3.2	249
21	FLAGdb/FST: a database of mapped flanking insertion sites (FSTs) of Arabidopsis thaliana T-DNA transformants. Nucleic Acids Research, 2002, 30, 94-97.	14.5	220
22	WRINKLED Transcription Factors Orchestrate Tissue-Specific Regulation of Fatty Acid Biosynthesis in <i>Arabidopsis</i> Â. Plant Cell, 2013, 24, 5007-5023.	6.6	219
23	Role of WRINKLED1 in the transcriptional regulation of glycolytic and fatty acid biosynthetic genes in Arabidopsis. Plant Journal, 2009, 60, 933-947.	5.7	216
24	The TAG1 locus of Arabidopsis encodes for a diacylglycerol acyltransferase. Plant Physiology and Biochemistry, 1999, 37, 831-840.	5.8	210
25	Storage Reserve Accumulation in Arabidopsis: Metabolic and Developmental Control of Seed Filling. The Arabidopsis Book, 2008, 6, e0113.	0.5	202
26	LEAFY COTYLEDON 2 activation is sufficient to trigger the accumulation of oil and seed specific mRNAs inArabidopsisleaves. FEBS Letters, 2005, 579, 4666-4670.	2.8	193
27	Multifunctional acetyl-CoA carboxylase 1 is essential for very long chain fatty acid elongation and embryo development in Arabidopsis. Plant Journal, 2003, 33, 75-86.	5.7	190
28	Regulation of de novo fatty acid synthesis in maturing oilseeds of Arabidopsis. Plant Physiology and Biochemistry, 2009, 47, 448-455.	5.8	189
29	Phosphoenolpyruvate carboxylase: structure, regulation and evolution. Plant Science, 1994, 99, 111-124.	3.6	177
30	Tâ€ĐNA integration into the Arabidopsis genome depends on sequences of preâ€insertion sites. EMBO Reports, 2002, 3, 1152-1157.	4.5	162
31	Arabidopsis seed secrets unravelled after a decade of genetic and omicsâ€driven research. Plant Journal, 2010, 61, 971-981.	5.7	161
32	The <i>Arabidopsis PILZ</i> group genes encode tubulin-folding cofactor orthologs required for cell division but not cell growth. Genes and Development, 2002, 16, 959-971.	5.9	157
33	Null Mutation ofAtCUL1Causes Arrest in Early Embryogenesis inArabidopsis. Molecular Biology of the Cell, 2002, 13, 1916-1928.	2.1	153
34	The AtSUC5 sucrose transporter specifically expressed in the endosperm is involved in early seed development in Arabidopsis. Plant Journal, 2005, 43, 824-836.	5.7	152
35	Function of plastidial pyruvate kinases in seeds of <i>Arabidopsis thaliana</i>^{â€}. Plant Journal, 2007, 52, 405-419.	5.7	141
36	Arabidopsis glucosidase I mutants reveal a critical role of N-glycan trimming in seed development. EMBO Journal, 2001, 20, 1010-1019.	7.8	138

#	Article	IF	Citations
37	Metabolite profiling and quantitative genetics of natural variation for flavonoids in Arabidopsis. Journal of Experimental Botany, 2012, 63, 3749-3764.	4.8	131
38	Transcriptional Regulation of <i>Arabidopsis LEAFY COTYLEDON2</i> Involves <i>RLE</i>, a <i>cis</i>-Element That Regulates Trimethylation of Histone H3 at Lysine-27. Plant Cell, 2011, 23, 4065-4078.	6.6	120
39	The Regulation of Flavonoid Biosynthesis. , 2006, , 97-122.		115
40	Regulation of flavonoid biosynthesis involves an unexpected complex transcriptional regulation of <i><scp>TT</scp>8</i> expression, in <scp>A</scp>rabidopsis. New Phytologist, 2013, 198, 59-70.	7.3	111
41	Specialization of Oleosins in Oil Body Dynamics during Seed Development in Arabidopsis Seeds Â. Plant Physiology, 2014, 164, 1866-1878.	4.8	104
42	Cellularisation in the endosperm of Arabidopsis thaliana is coupled to mitosis and shares multiple components with cytokinesis. Development (Cambridge), 2002, 129, 5567-5576.	2.5	103
43	Promoter DNA Hypermethylation and Gene Repression in Undifferentiated Arabidopsis Cells. PLoS ONE, 2008, 3, e3306.	2.5	99
44	Sorghum phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution. Plant Molecular Biology, 1993, 21, 487-502.	3.9	88
45	Structural Characterization of the Major Flavonoid Glycosides fromArabidopsis thalianaSeeds. Journal of Agricultural and Food Chemistry, 2006, 54, 6603-6612.	5.2	83
46	Improved PCR-Walking for Large-Scale Isolation of Plant T-DNA Borders. BioTechniques, 2001, 30, 496-504.	1.8	78
47	A comprehensive overview of grain development in Brachypodium distachyon variety Bd21. Journal of Experimental Botany, 2012, 63, 739-755.	4.8	75
48	gurke and pasticcino3 mutants affected in embryo development are impaired in acetylâ€CoA carboxylase. EMBO Reports, 2004, 5, 515-520.	4.5	74
49	Isolation and Characterization of High Temperature-Resistant Germination Mutants of Arabidopsis thaliana. Plant and Cell Physiology, 2006, 47, 1081-1094.	3.1	73
50	Transcriptional regulation of fatty acid production in higher plants: Molecular bases and biotechnological outcomes. European Journal of Lipid Science and Technology, 2014, 116, 1332-1343.	1.5	73
51	The phosphoenolpyruvate carboxylase gene family of Sorghum: promoter structures, amino acid sequences and expression of genes. Gene, 1991, 99, 87-94.	2.2	72
52	MYB118 Represses Endosperm Maturation in Seeds of <i>Arabidopsis</i> Â Â. Plant Cell, 2014, 26, 3519-3537.	6.6	72
53	Molecular and epigenetic regulations and functions of the LAFL transcriptional regulators that control seed development. Plant Reproduction, 2018, 31, 291-307.	2.2	71
54	Endosperm and Nucellus Develop Antagonistically in Arabidopsis Seeds. Plant Cell, 2016, 28, 1343-1360.	6.6	69

#	Article	IF	Citations
55	The Arabidopsis AtEPR1 extensin-like gene is specifically expressed in endosperm during seed germination. Plant Journal, 2000, 23, 643-652.	5.7	64
56	Deciphering and modifying LAFL transcriptional regulatory network in seed for improving yield and quality of storage compounds. Plant Science, 2016, 250, 198-204.	3.6	62
57	Specialized phenolic compounds in seeds: structures, functions, and regulations. Plant Science, 2020, 296, 110471.	3.6	62
58	Regulation and evolution of the interaction of the seed B3 transcription factors with NF-Y subunits. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2017, 1860, 1069-1078.	1.9	61
59	Geographic distribution and evolution of yellow fever viruses based on direct sequencing of genomic cDNA fragments. Journal of General Virology, 1994, 75, 417-423.	2.9	60
60	Analysis of the DNA-Binding Activities of the Arabidopsis R2R3-MYB Transcription Factor Family by One-Hybrid Experiments in Yeast. PLoS ONE, 2015, 10, e0141044.	2.5	60
61	Primary structure of sorghum malate dehydrogenase (NADP) deduced from cDNA sequence. Homology with malate dehydrogenase (NAD). FEBS Journal, 1990, 192, 299-303.	0.2	59
62	Characterization of anArabidopsis thalianacDNA homologue to animal poly(ADP-ribose) polymerase. FEBS Letters, 1995, 364, 103-108.	2.8	59
63	Site-directed mutagenesis of the phosphorylatable serine (Ser8) in C4 phosphoenolpyruvate carboxylase from sorghum. The effect of negative charge at position 8.. Journal of Biological Chemistry, 1992, 267, 16759-16762.	3.4	59
64	Site-directed mutagenesis of the phosphorylatable serine (Ser8) in C4 phosphoenolpyruvate carboxylase from sorghum. The effect of negative charge at position 8. Journal of Biological Chemistry, 1992, 267, 16759-62.	3.4	56
65	Deciphering the molecular mechanisms underpinning the transcriptional control of gene expression by L-AFL proteins in Arabidopsis seed.. Plant Physiology, 2016, 171, pp.00034.2016.	4.8	53
66	Controlling lipid accumulation in cereal grains. Plant Science, 2012, 185-186, 33-39.	3.6	51
67	Seed Coat Development and Dormancy. , 0, , 25-49.		50
68	Profiling the onset of somatic embryogenesis in Arabidopsis. BMC Genomics, 2017, 18, 998.	2.8	50
69	Kinetic Analysis of the Non-Phosphorylated, in Vitro Phosphorylated, and Phosphorylation-Site-Mutant (Asp8) Forms of Intact Recombinant C4 Phosphoenolpyruvate Carboxylase from Sorghum. FEBS Journal, 1995, 228, 92-95.	0.2	50
70	Purification and characterization of pea thioredoxin f expressed in Escherichia coli. Plant Molecular Biology, 1994, 26, 225-234.	3.9	49
71	PII is induced by WRINKLED1 and fine-tunes fatty acid composition in seeds of Arabidopsis thaliana. Plant Journal, 2010, 64, 291-303.	5.7	49
72	Genetic and Molecular Control of Somatic Embryogenesis. Plants, 2021, 10, 1467.	3.5	48

#	Article	IF	Citations
73	Regulation of HSD1 in Seeds of Arabidopsis thaliana. Plant and Cell Physiology, 2009, 50, 1463-1478.	3.1	47
74	Transcriptional Activation of Two Delta-9 Palmitoyl-ACP Desaturase Genes by MYB115 and MYB118 Is Critical for Biosynthesis of Omega-7 Monounsaturated Fatty Acids in the Endosperm of Arabidopsis Seeds. Plant Cell, 2016, 28, 2666-2682.	6.6	46
75	The promoter of the Arabidopsis thaliana BAN gene is active in proanthocyanidin-accumulating cells of the Brassica napus seed coat. Plant Cell Reports, 2009, 28, 601-617.	5.6	45
76	New insights on the organization and regulation of the fatty acid biosynthetic network in the model higher plant Arabidopsis thaliana. Biochimie, 2016, 120, 3-8.	2.6	45
77	A new system for fast and quantitative analysis of heterologous gene expression in plants. New Phytologist, 2012, 193, 504-512.	7.3	43
78	AtMYB92 enhances fatty acid synthesis and suberin deposition in leaves of <i>Nicotiana benthamiana</i>. Plant Journal, 2020, 103, 660-676.	5.7	39
79	Variation in Expression of the HECT E3 Ligase <i>UPL3</i> Modulates LEC2 Levels, Seed Size, and Crop Yields in <i>Brassica napus</i>. Plant Cell, 2019, 31, 2370-2385.	6.6	38
80	The Arabidopsis TT2 Gene Encodes and R2R3 MYB Domain Protein That Acts as a Key Determinant for Proanthocyanidin Accumulation in Developing Seed. Plant Cell, 2001, 13, 2099.	6.6	37
81	Chromodomain, Helicase and DNAâ€binding CHD1 protein, CHR5, are involved in establishing active chromatin state of seed maturation genes. Plant Biotechnology Journal, 2015, 13, 811-820.	8.3	37
82	Complete cDNA sequence of sorghum phosphoenolpyruvate carboxylase involved in C4 photosynthesis. Nucleic Acids Research, 1990, 18, 658-658.	14.5	35
83	Differential Activation of Partially Redundant Î”9 Stearoyl-ACP Desaturase Genes Is Critical for Omega-9 Monounsaturated Fatty Acid Biosynthesis During Seed Development in Arabidopsis. Plant Cell, 2020, 32, 3613-3637.	6.6	35
84	At5g50600 encodes a member of the short-chain dehydrogenase reductase superfamily with 11Î²- and 17Î²-hydroxysteroid dehydrogenase activities associated with Arabidopsis thaliana seed oil bodies. Biochimie, 2007, 89, 222-229.	2.6	34
85	Expression variation in connected recombinant populations of Arabidopsis thaliana highlights distinct transcriptome architectures. BMC Genomics, 2012, 13, 117.	2.8	34
86	NOF1 Encodes an Arabidopsis Protein Involved in the Control of rRNA Expression. PLoS ONE, 2010, 5, e12829.	2.5	32
87	TRANSPARENT TESTA 16 and 15 act through different mechanisms to control proanthocyanidin accumulation in Arabidopsis testa. Journal of Experimental Botany, 2017, 68, 2859-2870.	4.8	30
88	Isolation, characterization and nucleotide sequence of a full-length pea cDNA encoding thioredoxin-f. Plant Molecular Biology, 1992, 18, 1023-1025.	3.9	29
89	TWS1, a Novel Small Protein, Regulates Various Aspects of Seed and Plant Development. Plant Physiology, 2016, 172, 1732-1745.	4.8	28
90	Plant monounsaturated fatty acids: Diversity, biosynthesis, functions and uses. Progress in Lipid Research, 2022, 85, 101138.	11.6	27

#	Article	IF	Citations
91	Liver and colon DNA oxidative damage and gene expression profiles of rats fed Arabidopsis thaliana mutant seeds containing contrasted flavonoids. Food and Chemical Toxicology, 2008, 46, 1213-1220.	3.6	25
92	Study of AtSUS2 Localization in Seeds Reveals a Strong Association with Plastids. Plant and Cell Physiology, 2008, 49, 1621-1626.	3.1	25
93	New insights toward the transcriptional engineering of proanthocyanidin biosynthesis. Plant Signaling and Behavior, 2014, 9, e28736.	2.4	25
94	Seed coats as an alternative molecular factory: thinking outside the box. Plant Reproduction, 2018, 31, 327-342.	2.2	24
95	Production inEscherichia coli of activeSorghum phosphoenolpyruvate carboxylase which can be phosphorylated. Plant Molecular Biology, 1991, 17, 83-88.	3.9	23
96	Developmental patterning of the sub-epidermal integument cell layer in <i>Arabidopsis</i> seeds. Development (Cambridge), 2017, 144, 1490-1497.	2.5	23
97	Docking of acetyl-CoA carboxylase to the plastid envelope membrane attenuates fatty acid production in plants. Nature Communications, 2020, 11, 6191.	12.8	23
98	Regulation of<i>FUSCA3</i>Expression During Seed Development in Arabidopsis. Plant and Cell Physiology, 2019, 60, 476-487.	3.1	22
99	From enzyme activity to plant biotechnology: 30 years of research on phosphoenolpyruvate carboxylase. Plant Physiology and Biochemistry, 2003, 41, 533-539.	5.8	21
100	Complete nucleotide sequence of one member of theSorghum phosphoenolpyruvate carboxylase gene family. Plant Molecular Biology, 1991, 17, 1077-1079.	3.9	20
101	Kinetic Analysis of the Non-Phosphorylated, in Vitro Phosphorylated, and Phosphorylation-Site-Mutant (Asp8) Forms of Intact Recombinant C4 Phosphoenolpyruvate Carboxylase from Sorghum. FEBS Journal, 1995, 228, 92-95.	0.2	20
102	LEC1 (NF-YB9) directly interacts with LEC2 to control gene expression in seed. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2018, 1861, 443-450.	1.9	20
103	Developmental patterning of sub-epidermal cells in the outer integument of Arabidopsis seeds. PLoS ONE, 2017, 12, e0188148.	2.5	20
104	Integrating bioinformatic resources to predict transcription factors interacting with cis-sequences conserved in co-regulated genes. BMC Genomics, 2014, 15, 317.	2.8	19
105	Combining laser-assisted microdissection (LAM) and RNA-seq allows to perform a comprehensive transcriptomic analysis of epidermal cells of Arabidopsis embryo. Plant Methods, 2018, 14, 10.	4.3	19
106	Transcription of a sorghum phosphoenolpyruvate carboxylase gene in transgenic tobacco leaves: maturation of monocot PRE-mRNA by dicot cells. Plant Cell Reports, 1991, 9, 688-690.	5.6	18
107	Complete nucleotide sequence of a sorghum gene coding for the phosphoenolpyruvate carboxylase involved in C4 photosynthesis. Plant Molecular Biology, 1992, 19, 339-342.	3.9	17
108	An Engineered Change in the L-Malate Sensitivity of a Site-Directed Mutant of Sorghum Phosphoenolpyruvate Carboxylase: The Effect of Sequential Mutagenesis and S-Carboxymethylation at Position 8. Archives of Biochemistry and Biophysics, 1993, 306, 272-276.	3.0	17

#	Article	IF	Citations
109	Deposition of a cutin apoplastic barrier separating seed maternal and zygotic tissues. BMC Plant Biology, 2019, 19, 304.	3.6	17
110	Overview of the Regulatory Network of Plant Seed Development (SeeDev) Task at the BioNLP Shared Task 2016.. , 2016, , .		17
111	The TT8 Gene Encodes a Basic Helix-Loop-Helix Domain Protein Required for Expression of DFR and BAN Genes in Arabidopsis Siliques. Plant Cell, 2000, 12, 1863.	6.6	14
112	The Seed Development Factors TT2 and MYB5 Regulate Heat Stress Response in Arabidopsis. Genes, 2021, 12, 746.	2.4	13
113	The Physcomitrella patens System for Transient Gene Expression Assays. Methods in Molecular Biology, 2016, 1482, 151-161.	0.9	11
114	Overexpression of MYB115, AAD2, or AAD3 in Arabidopsis thaliana seeds yields contrasting omega-7 contents. PLoS ONE, 2018, 13, e0192156.	2.5	11
115	Compared analysis of the regulatory systems controlling lipogenesis in hepatocytes of mice and in maturing oilseeds of Arabidopsis. Comptes Rendus - Biologies, 2008, 331, 737-745.	0.2	9
116	Untargeted metabolomic analyses reveal the diversity and plasticity of the specialized metabolome in seeds of different <i>Camelina sativa</i> genotypes. Plant Journal, 2022, 110, 147-165.	5.7	9
117	Camelina [Camelina sativa (L.) Crantz] seeds as a multi-purpose feedstock for bio-based applications. Industrial Crops and Products, 2022, 182, 114944.	5.2	9
118	Growth of the Arabidopsis sub-epidermal integument cell layers might require an endosperm signal. Plant Signaling and Behavior, 2017, 12, e1339000.	2.4	8
119	Specialized metabolites in seeds. Advances in Botanical Research, 2021, , 35-70.	1.1	6
120	Seed Development. , 2010, , 341-359.		4
121	Seeds as perfect factories for developing sustainable agriculture. Plant Reproduction, 2018, 31, 201-202.	2.2	4
122	A TRANSPARENT TESTA Transcriptional Module Regulates Endothelium Polarity. Frontiers in Plant Science, 2019, 10, 1801.	3.6	4
123	Fast and Efficient Cloning of Cis-Regulatory Sequences for High-Throughput Yeast One-Hybrid Analyses of Transcription Factors. Methods in Molecular Biology, 2016, 1482, 139-149.	0.9	2
124	Genes of malate and pyruvate metabolism. Plant Molecular Biology Reporter, 1994, 12, S43-S44.	1.8	1
125	La germination vient en dormant. Biofutur, 1998, 1998, 32-35.	0.0	0
126	Interactions of nitrogen and carbon metabolism: implications of PEP carboxylase and isocitrate dehydrogenase. , 1995, , 19-28.		0