

# Loic Lepiniec

## List of Publications by Year in descending order

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126  
papers

20,109  
citations

25034

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docs citations

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times ranked

15416  
citing authors

#	ARTICLE	IF	CITATIONS
1	Plant monounsaturated fatty acids: Diversity, biosynthesis, functions and uses. <i>Progress in Lipid Research</i> , 2022, 85, 101138.	11.6	27
2	Untargeted metabolomic analyses reveal the diversity and plasticity of the specialized metabolome in seeds of different <i>Camelina sativa</i> genotypes. <i>Plant Journal</i> , 2022, 110, 147-165.	5.7	9
3	<i>Camelina</i> [ <i>Camelina sativa</i> (L.) Crantz] seeds as a multi-purpose feedstock for bio-based applications. <i>Industrial Crops and Products</i> , 2022, 182, 114944.	5.2	9
4	Specialized metabolites in seeds. <i>Advances in Botanical Research</i> , 2021, , 35-70.	1.1	6
5	The Seed Development Factors TT2 and MYB5 Regulate Heat Stress Response in <i>Arabidopsis</i> . <i>Genes</i> , 2021, 12, 746.	2.4	13
6	Genetic and Molecular Control of Somatic Embryogenesis. <i>Plants</i> , 2021, 10, 1467.	3.5	48
7	Docking of acetyl-CoA carboxylase to the plastid envelope membrane attenuates fatty acid production in plants. <i>Nature Communications</i> , 2020, 11, 6191.	12.8	23
8	Differential Activation of Partially Redundant $\Delta^9$ Stearoyl-ACP Desaturase Genes Is Critical for Omega-9 Monounsaturated Fatty Acid Biosynthesis During Seed Development in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2020, 32, 3613-3637.	6.6	35
9	Specialized phenolic compounds in seeds: structures, functions, and regulations. <i>Plant Science</i> , 2020, 296, 110471.	3.6	62
10	AtMYB92 enhances fatty acid synthesis and suberin deposition in leaves of <i>Nicotiana benthamiana</i> . <i>Plant Journal</i> , 2020, 103, 660-676.	5.7	39
11	Variation in Expression of the HECT E3 Ligase <i>UPL3</i> Modulates LEC2 Levels, Seed Size, and Crop Yields in <i>Brassica napus</i> . <i>Plant Cell</i> , 2019, 31, 2370-2385.	6.6	38
12	Deposition of a cutin apoplastic barrier separating seed maternal and zygotic tissues. <i>BMC Plant Biology</i> , 2019, 19, 304.	3.6	17
13	Regulation of <i>FUSCA3</i> Expression During Seed Development in <i>Arabidopsis</i> . <i>Plant and Cell Physiology</i> , 2019, 60, 476-487.	3.1	22
14	A TRANSPARENT TESTA Transcriptional Module Regulates Endothelium Polarity. <i>Frontiers in Plant Science</i> , 2019, 10, 1801.	3.6	4
15	LEC1 (NF-YB9) directly interacts with LEC2 to control gene expression in seed. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2018, 1861, 443-450.	1.9	20
16	Molecular and epigenetic regulations and functions of the LAFL transcriptional regulators that control seed development. <i>Plant Reproduction</i> , 2018, 31, 291-307.	2.2	71
17	Seeds as perfect factories for developing sustainable agriculture. <i>Plant Reproduction</i> , 2018, 31, 201-202.	2.2	4
18	Seed coats as an alternative molecular factory: thinking outside the box. <i>Plant Reproduction</i> , 2018, 31, 327-342.	2.2	24

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19	Combining laser-assisted microdissection (LAM) and RNA-seq allows to perform a comprehensive transcriptomic analysis of epidermal cells of Arabidopsis embryo. <i>Plant Methods</i> , 2018, 14, 10.	4.3	19
20	Overexpression of MYB115, AAD2, or AAD3 in Arabidopsis thaliana seeds yields contrasting omega-7 contents. <i>PLoS ONE</i> , 2018, 13, e0192156.	2.5	11
21	Growth of the Arabidopsis sub-epidermal integument cell layers might require an endosperm signal. <i>Plant Signaling and Behavior</i> , 2017, 12, e1339000.	2.4	8
22	TRANSPARENT TESTA 16 and 15 act through different mechanisms to control proanthocyanidin accumulation in Arabidopsis testa. <i>Journal of Experimental Botany</i> , 2017, 68, 2859-2870.	4.8	30
23	Developmental patterning of the sub-epidermal integument cell layer in Arabidopsis seeds. <i>Development (Cambridge)</i> , 2017, 144, 1490-1497.	2.5	23
24	Regulation and evolution of the interaction of the seed B3 transcription factors with NF-Y subunits. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2017, 1860, 1069-1078.	1.9	61
25	Profiling the onset of somatic embryogenesis in Arabidopsis. <i>BMC Genomics</i> , 2017, 18, 998.	2.8	50
26	Developmental patterning of sub-epidermal cells in the outer integument of Arabidopsis seeds. <i>PLoS ONE</i> , 2017, 12, e0188148.	2.5	20
27	Deciphering and modifying LAFL transcriptional regulatory network in seed for improving yield and quality of storage compounds. <i>Plant Science</i> , 2016, 250, 198-204.	3.6	62
28	Endosperm and Nucellus Develop Antagonistically in Arabidopsis Seeds. <i>Plant Cell</i> , 2016, 28, 1343-1360.	6.6	69
29	Deciphering the molecular mechanisms underpinning the transcriptional control of gene expression by L-AFL proteins in Arabidopsis seed.. <i>Plant Physiology</i> , 2016, 171, pp.00034.2016.	4.8	53
30	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. <i>Plant Cell</i> , 2016, 28, 2666-2682.	6.6	46
31	The Physcomitrella patens System for Transient Gene Expression Assays. <i>Methods in Molecular Biology</i> , 2016, 1482, 151-161.	0.9	11
32	Fast and Efficient Cloning of Cis-Regulatory Sequences for High-Throughput Yeast One-Hybrid Analyses of Transcription Factors. <i>Methods in Molecular Biology</i> , 2016, 1482, 139-149.	0.9	2
33	TWS1, a Novel Small Protein, Regulates Various Aspects of Seed and Plant Development. <i>Plant Physiology</i> , 2016, 172, 1732-1745.	4.8	28
34	New insights on the organization and regulation of the fatty acid biosynthetic network in the model higher plant Arabidopsis thaliana. <i>Biochimie</i> , 2016, 120, 3-8.	2.6	45
35	Overview of the Regulatory Network of Plant Seed Development (SeeDev) Task at the BioNLP Shared Task 2016.. , 2016, , .		17
36	Chromodomain, Helicase and DNA-binding CHD1 protein, CHR5, are involved in establishing active chromatin state of seed maturation genes. <i>Plant Biotechnology Journal</i> , 2015, 13, 811-820.	8.3	37

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37	Transcriptional control of flavonoid biosynthesis by MYB–bHLH–WDR complexes. Trends in Plant Science, 2015, 20, 176-185.	8.8	1,336
38	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
39	New insights toward the transcriptional engineering of proanthocyanidin biosynthesis. Plant Signaling and Behavior, 2014, 9, e28736.	2.4	25
40	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
41	Complexity and robustness of the flavonoid transcriptional regulatory network revealed by comprehensive analyses of MYB–bHLH–WDR complexes and their targets in Arabidopsis seed. New Phytologist, 2014, 202, 132-144.	7.3	338
42	MYB118 Represses Endosperm Maturation in Seeds of Arabidopsis. Plant Cell, 2014, 26, 3519-3537.	6.6	72
43	Integrating bioinformatic resources to predict transcription factors interacting with cis-sequences conserved in co-regulated genes. BMC Genomics, 2014, 15, 317.	2.8	19
44	Specialization of Oleosins in Oil Body Dynamics during Seed Development in Arabidopsis Seeds. Plant Physiology, 2014, 164, 1866-1878.	4.8	104
45	Identification and characterization of MYB–bHLH–WDR 40 regulatory complexes controlling proanthocyanidin biosynthesis in strawberry (Fragaria)–Ananassa fruits. New Phytologist, 2013, 197, 454-467.	7.3	388
46	Regulation of flavonoid biosynthesis involves an unexpected complex transcriptional regulation of TT8 expression, in Arabidopsis. New Phytologist, 2013, 198, 59-70.	7.3	111
47	WRINKLED Transcription Factors Orchestrate Tissue-Specific Regulation of Fatty Acid Biosynthesis in Arabidopsis. Plant Cell, 2013, 24, 5007-5023.	6.6	219
48	A comprehensive overview of grain development in Brachypodium distachyon variety Bd21. Journal of Experimental Botany, 2012, 63, 739-755.	4.8	75
49	Metabolite profiling and quantitative genetics of natural variation for flavonoids in Arabidopsis. Journal of Experimental Botany, 2012, 63, 3749-3764.	4.8	131
50	Controlling lipid accumulation in cereal grains. Plant Science, 2012, 185-186, 33-39.	3.6	51
51	Expression variation in connected recombinant populations of Arabidopsis thaliana highlights distinct transcriptome architectures. BMC Genomics, 2012, 13, 117.	2.8	34
52	A new system for fast and quantitative analysis of heterologous gene expression in plants. New Phytologist, 2012, 193, 504-512.	7.3	43
53	Transcriptional Regulation of Arabidopsis LEAFY COTYLEDON2 Involves RLE, a cis-Element That Regulates Trimethylation of Histone H3 at Lysine-27. Plant Cell, 2011, 23, 4065-4078.	6.6	120
54	Arabidopsis seed secrets unravelled after a decade of genetic and omics-driven research. Plant Journal, 2010, 61, 971-981.	5.7	161

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55	PII is induced by WRINKLED1 and fine-tunes fatty acid composition in seeds of <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2010, 64, 291-303.	5.7	49
56	Seed Development. , 2010, , 341-359.		4
57	Physiological and developmental regulation of seed oil production. <i>Progress in Lipid Research</i> , 2010, 49, 235-249.	11.6	382
58	MYB transcription factors in <i>Arabidopsis</i> . <i>Trends in Plant Science</i> , 2010, 15, 573-581.	8.8	2,987
59	NOF1 Encodes an <i>Arabidopsis</i> Protein Involved in the Control of rRNA Expression. <i>PLoS ONE</i> , 2010, 5, e12829.	2.5	32
60	Regulation of HSD1 in Seeds of <i>Arabidopsis thaliana</i> . <i>Plant and Cell Physiology</i> , 2009, 50, 1463-1478.	3.1	47
61	The promoter of the <i>Arabidopsis thaliana</i> BAN gene is active in proanthocyanidin-accumulating cells of the <i>Brassica napus</i> seed coat. <i>Plant Cell Reports</i> , 2009, 28, 601-617.	5.6	45
62	Role of WRINKLED1 in the transcriptional regulation of glycolytic and fatty acid biosynthetic genes in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2009, 60, 933-947.	5.7	216
63	Regulation of de novo fatty acid synthesis in maturing oilseeds of <i>Arabidopsis</i> . <i>Plant Physiology and Biochemistry</i> , 2009, 47, 448-455.	5.8	189
64	Deciphering gene regulatory networks that control seed development and maturation in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2008, 54, 608-620.	5.7	391
65	MYBL2 is a new regulator of flavonoid biosynthesis in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2008, 55, 940-953.	5.7	474
66	Liver and colon DNA oxidative damage and gene expression profiles of rats fed <i>Arabidopsis thaliana</i> mutant seeds containing contrasted flavonoids. <i>Food and Chemical Toxicology</i> , 2008, 46, 1213-1220.	3.6	25
67	Compared analysis of the regulatory systems controlling lipogenesis in hepatocytes of mice and in maturing oilseeds of <i>Arabidopsis</i> . <i>Comptes Rendus - Biologies</i> , 2008, 331, 737-745.	0.2	9
68	Study of AtSUS2 Localization in Seeds Reveals a Strong Association with Plastids. <i>Plant and Cell Physiology</i> , 2008, 49, 1621-1626.	3.1	25
69	Storage Reserve Accumulation in <i>Arabidopsis</i> : Metabolic and Developmental Control of Seed Filling. <i>The Arabidopsis Book</i> , 2008, 6, e0113.	0.5	202
70	Promoter DNA Hypermethylation and Gene Repression in Undifferentiated <i>Arabidopsis</i> Cells. <i>PLoS ONE</i> , 2008, 3, e3306.	2.5	99
71	Flavonoid oxidation in plants: from biochemical properties to physiological functions. <i>Trends in Plant Science</i> , 2007, 12, 29-36.	8.8	758
72	At5g50600 encodes a member of the short-chain dehydrogenase reductase superfamily with 11 $\beta$ - and 17 $\beta$ -hydroxysteroid dehydrogenase activities associated with <i>Arabidopsis thaliana</i> seed oil bodies. <i>Biochimie</i> , 2007, 89, 222-229.	2.6	34

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73	WRINKLED1 specifies the regulatory action of LEAFY COTYLEDON2 towards fatty acid metabolism during seed maturation in Arabidopsis. <i>Plant Journal</i> , 2007, 50, 825-838.	5.7	408
74	Function of plastidial pyruvate kinases in seeds of <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2007, 52, 405-419.	5.7	141
75	GENETICS AND BIOCHEMISTRY OF SEED FLAVONOIDS. <i>Annual Review of Plant Biology</i> , 2006, 57, 405-430.	18.7	1,056
76	The Regulation of Flavonoid Biosynthesis. , 2006, , 97-122.		115
77	Structural Characterization of the Major Flavonoid Glycosides from <i>Arabidopsis thaliana</i> Seeds. <i>Journal of Agricultural and Food Chemistry</i> , 2006, 54, 6603-6612.	5.2	83
78	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 in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2006, 46, 768-779.	5.7	288
79	Flavonoid diversity and biosynthesis in seed of <i>Arabidopsis thaliana</i> . <i>Planta</i> , 2006, 224, 96-107.	3.2	249
80	Isolation and Characterization of High Temperature-Resistant Germination Mutants of <i>Arabidopsis thaliana</i> . <i>Plant and Cell Physiology</i> , 2006, 47, 1081-1094.	3.1	73
81	The AtSUC5 sucrose transporter specifically expressed in the endosperm is involved in early seed development in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2005, 43, 824-836.	5.7	152
82	TRANSPARENT TESTA10 Encodes a Laccase-Like Enzyme Involved in Oxidative Polymerization of Flavonoids in <i>Arabidopsis</i> Seed Coat. <i>Plant Cell</i> , 2005, 17, 2966-2980.	6.6	380
83	LEAFY COTYLEDON 2 activation is sufficient to trigger the accumulation of oil and seed specific mRNAs in <i>Arabidopsis</i> leaves. <i>FEBS Letters</i> , 2005, 579, 4666-4670.	2.8	193
84	TT2, TT8, and TTG1 synergistically specify the expression of BANYULS and proanthocyanidin biosynthesis in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2004, 39, 366-380.	5.7	855
85	gurke and pasticcino3 mutants affected in embryo development are impaired in acetyl-CoA carboxylase. <i>EMBO Reports</i> , 2004, 5, 515-520.	4.5	74
86	From enzyme activity to plant biotechnology: 30 years of research on phosphoenolpyruvate carboxylase. <i>Plant Physiology and Biochemistry</i> , 2003, 41, 533-539.	5.8	21
87	Multifunctional acetyl-CoA carboxylase 1 is essential for very long chain fatty acid elongation and embryo development in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2003, 33, 75-86.	5.7	190
88	Proanthocyanidin-Accumulating Cells in <i>Arabidopsis</i> Testa: Regulation of Differentiation and Role in Seed Development. <i>Plant Cell</i> , 2003, 15, 2514-2531.	6.6	359
89	Cellularisation in the endosperm of <i>Arabidopsis thaliana</i> is coupled to mitosis and shares multiple components with cytokinesis. <i>Development (Cambridge)</i> , 2002, 129, 5567-5576.	2.5	103
90	The TRANSPARENT TESTA16 Locus Encodes the ARABIDOPSIS BSISTER MADS Domain Protein and Is Required for Proper Development and Pigmentation of the Seed Coat. <i>Plant Cell</i> , 2002, 14, 2463-2479.	6.6	333

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91	The <i>Arabidopsis</i> PILZ group genes encode tubulin-folding cofactor orthologs required for cell division but not cell growth. <i>Genes and Development</i> , 2002, 16, 959-971.	5.9	157
92	Null Mutation of <i>AtCUL1</i> Causes Arrest in Early Embryogenesis in <i>Arabidopsis</i> . <i>Molecular Biology of the Cell</i> , 2002, 13, 1916-1928.	2.1	153
93	FLAGdb/FST: a database of mapped flanking insertion sites (FSTs) of <i>Arabidopsis thaliana</i> T-DNA transformants. <i>Nucleic Acids Research</i> , 2002, 30, 94-97.	14.5	220
94	An integrated overview of seed development in <i>Arabidopsis thaliana</i> ecotype WS. <i>Plant Physiology and Biochemistry</i> , 2002, 40, 151-160.	5.8	418
95	T-DNA integration into the <i>Arabidopsis</i> genome depends on sequences of pre-insertion sites. <i>EMBO Reports</i> , 2002, 3, 1152-1157.	4.5	162
96	Improved PCR-Walking for Large-Scale Isolation of Plant T-DNA Borders. <i>BioTechniques</i> , 2001, 30, 496-504.	1.8	78
97	<i>Arabidopsis</i> glucosidase I mutants reveal a critical role of N-glycan trimming in seed development. <i>EMBO Journal</i> , 2001, 20, 1010-1019.	7.8	138
98	The <i>Arabidopsis</i> TT2 Gene Encodes an R2R3 MYB Domain Protein That Acts as a Key Determinant for Proanthocyanidin Accumulation in Developing Seed. <i>Plant Cell</i> , 2001, 13, 2099.	6.6	37
99	The <i>Arabidopsis</i> TT2 Gene Encodes an R2R3 MYB Domain Protein That Acts as a Key Determinant for Proanthocyanidin Accumulation in Developing Seed. <i>Plant Cell</i> , 2001, 13, 2099-2114.	6.6	667
100	LEAFY COTYLEDON2 encodes a B3 domain transcription factor that induces embryo development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 11806-11811.	7.1	680
101	The TT8 Gene Encodes a Basic Helix-Loop-Helix Domain Protein Required for Expression of DFR and BAN Genes in <i>Arabidopsis</i> Siliques. <i>Plant Cell</i> , 2000, 12, 1863.	6.6	14
102	The <i>Arabidopsis</i> <i>AtEPR1</i> extensin-like gene is specifically expressed in endosperm during seed germination. <i>Plant Journal</i> , 2000, 23, 643-652.	5.7	64
103	The TT8 Gene Encodes a Basic Helix-Loop-Helix Domain Protein Required for Expression of DFR and BAN Genes in <i>Arabidopsis</i> Siliques. <i>Plant Cell</i> , 2000, 12, 1863-1878.	6.6	679
104	The TAG1 locus of <i>Arabidopsis</i> encodes for a diacylglycerol acyltransferase. <i>Plant Physiology and Biochemistry</i> , 1999, 37, 831-840.	5.8	210
105	La germination vient en dormant. <i>Biofutur</i> , 1998, 1998, 32-35.	0.0	0
106	Kinetic Analysis of the Non-Phosphorylated, in Vitro Phosphorylated, and Phosphorylation-Site-Mutant (Asp8) Forms of Intact Recombinant C4 Phosphoenolpyruvate Carboxylase from Sorghum. <i>FEBS Journal</i> , 1995, 228, 92-95.	0.2	20
107	Characterization of an <i>Arabidopsis thaliana</i> cDNA homologue to animal poly(ADP-ribose) polymerase. <i>FEBS Letters</i> , 1995, 364, 103-108.	2.8	59
108	Kinetic Analysis of the Non-Phosphorylated, in Vitro Phosphorylated, and Phosphorylation-Site-Mutant (Asp8) Forms of Intact Recombinant C4 Phosphoenolpyruvate Carboxylase from Sorghum. <i>FEBS Journal</i> , 1995, 228, 92-95.	0.2	50

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109	Interactions of nitrogen and carbon metabolism: implications of PEP carboxylase and isocitrate dehydrogenase. , 1995, , 19-28.		0
110	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
111	Purification and characterization of pea thioredoxin f expressed in Escherichia coli. Plant Molecular Biology, 1994, 26, 225-234.	3.9	49
112	Genes of malate and pyruvate metabolism. Plant Molecular Biology Reporter, 1994, 12, S43-S44.	1.8	1
113	Phosphoenolpyruvate carboxylase: structure, regulation and evolution. Plant Science, 1994, 99, 111-124.	3.6	177
114	Sorghum phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution. Plant Molecular Biology, 1993, 21, 487-502.	3.9	88
115	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
116	Isolation, characterization and nucleotide sequence of a full-length pea cDNA encoding thioredoxin-f. Plant Molecular Biology, 1992, 18, 1023-1025.	3.9	29
117	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
118	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
119	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
120	The phosphoenolpyruvate carboxylase gene family of Sorghum: promoter structures, amino acid sequences and expression of genes. Gene, 1991, 99, 87-94.	2.2	72
121	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
122	Production in Escherichia coli of active Sorghum phosphoenolpyruvate carboxylase which can be phosphorylated. Plant Molecular Biology, 1991, 17, 83-88.	3.9	23
123	Complete nucleotide sequence of one member of the Sorghum phosphoenolpyruvate carboxylase gene family. Plant Molecular Biology, 1991, 17, 1077-1079.	3.9	20
124	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
125	Complete cDNA sequence of sorghum phosphoenolpyruvate carboxylase involved in C4 photosynthesis. Nucleic Acids Research, 1990, 18, 658-658.	14.5	35
126	Seed Coat Development and Dormancy. , 0, , 25-49.		50