

Lila O Vodkin

List of Publications by Year in descending order

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43
papers

2,763
citations

218381

26
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276539

41
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43
all docs

43
docs citations

43
times ranked

2579
citing authors

#	ARTICLE	IF	CITATIONS
1	Ca lectin gene insertion has the structural features of a transposable element. <i>Cell</i> , 1983, 34, 1023-1031.	13.5	299
2	Clustering of Microarray Data Reveals Transcript Patterns Associated with Somatic Embryogenesis in Soybean. <i>Plant Physiology</i> , 2003, 132, 118-136.	2.3	206
3	Tissue-Specific Gene Silencing Mediated by a Naturally Occurring Chalcone Synthase Gene Cluster in <i>Glycine max</i> [W]. <i>Plant Cell</i> , 2004, 16, 819-835.	3.1	192
4	Transcriptome changes in the phenylpropanoid pathway of <i>Glycine max</i> in response to <i>Pseudomonas syringae</i> infection. <i>BMC Plant Biology</i> , 2006, 6, 26.	1.6	160
5	An insertion sequence blocks the expression of a soybean lectin gene. <i>Cell</i> , 1983, 33, 465-475.	13.5	133
6	A compilation of soybean ESTs: generation and analysis. <i>Genome</i> , 2002, 45, 329-338.	0.9	133
7	Endogenous, Tissue-Specific Short Interfering RNAs Silence the Chalcone Synthase Gene Family in <i>Glycine max</i> Seed Coats. <i>Plant Cell</i> , 2009, 21, 3063-3077.	3.1	126
8	Using RNA-Seq to Profile Soybean Seed Development from Fertilization to Maturity. <i>PLoS ONE</i> , 2013, 8, e59270.	1.1	122
9	The wp Mutation of <i>Glycine max</i> Carries a Gene-Fragment-Rich Transposon of the CACTA Superfamily. <i>Plant Cell</i> , 2005, 17, 2619-2632.	3.1	117
10	Identification of soybean seed developmental stage-specific and tissue-specific miRNA targets by degradome sequencing. <i>BMC Genomics</i> , 2012, 13, 310.	1.2	115
11	Extraction of RNA from tissues containing high levels of procyanidins that bind RNA. <i>Plant Molecular Biology Reporter</i> , 1994, 12, 132-145.	1.0	102
12	Cloning of the Pleiotropic <i>T</i> Locus in Soybean and Two Recessive Alleles That Differentially Affect Structure and Expression of the Encoded Flavonoid 3-Hydroxylase. <i>Genetics</i> , 2003, 163, 295-309.	1.2	93
13	Features of a 103-kb gene-rich region in soybean include an inverted perfect repeat cluster of CHS genes comprising the <i>I</i> locus. <i>Genome</i> , 2004, 47, 819-831.	0.9	78
14	Genome-wide identification of binding sites for NAC and YABBY transcription factors and co-regulated genes during soybean seedling development by ChIP-Seq and RNA-Seq. <i>BMC Genomics</i> , 2013, 14, 477.	1.2	72
15	Flux of transcript patterns during soybean seed development. <i>BMC Genomics</i> , 2010, 11, 136.	1.2	58
16	Processing and localization of bovine β -casein expressed in transgenic soybean seeds under control of a soybean lectin expression cassette. <i>Plant Science</i> , 2001, 161, 323-335.	1.7	52
17	Isolation and Characterization of Messenger RNAs for Seed Lectin and Kunitz Trypsin Inhibitor in Soybeans. <i>Plant Physiology</i> , 1981, 68, 766-771.	2.3	51
18	Mutations in <i>Argonaute5</i> Illuminate Epistatic Interactions of the <i>K1</i> and <i>I</i> Loci Leading to Saddle Seed Color Patterns in <i>Glycine max</i> . <i>Plant Cell</i> , 2017, 29, 708-725.	3.1	51

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19	Fluorescent in situ hybridization to soybean metaphase chromosomes. <i>Plant Molecular Biology</i> , 1991, 17, 101-109.	2.0	49
20	Improved Sensitivity of DNA Microarrays Using Photonic Crystal Enhanced Fluorescence. <i>Analytical Chemistry</i> , 2010, 82, 6854-6861.	3.2	49
21	Methylation Affects Transposition and Splicing of a Large CACTA Transposon from a MYB Transcription Factor Regulating Anthocyanin Synthase Genes in Soybean Seed Coats. <i>PLoS ONE</i> , 2014, 9, e111959.	1.1	48
22	Duplications That Suppress and Deletions That Restore Expression from a Chalcone Synthase Multigene Family. <i>Plant Cell</i> , 1996, 8, 687.	3.1	41
23	Structural Features of the Endogenous <i>CHS</i> Silencing and Target Loci in the Soybean Genome. <i>Crop Science</i> , 2008, 48, S-49.	0.8	40
24	Variation of proline rich cell wall proteins in soybean lines with anthocyanin mutations. <i>Plant Molecular Biology</i> , 1993, 21, 145-156.	2.0	38
25	Cassettes for seed-specific expression tested in transformed embryogenic cultures of soybean. <i>Plant Molecular Biology Reporter</i> , 1995, 13, 255-269.	1.0	38
26	Specific elements of the glyoxylate pathway play a significant role in the functional transition of the soybean cotyledon during seedling development. <i>BMC Genomics</i> , 2007, 8, 468.	1.2	34
27	Cosegregation of Purple Throat Flower Color with Dihydroflavonol Reductase Polymorphism in Soybean. <i>Crop Science</i> , 1995, 35, 1028-1031.	0.8	29
28	Sequence and structure of a phenylalanine ammonia-lyase gene from <i>Glycine max</i> . <i>DNA Sequence</i> , 1991, 1, 335-346.	0.7	26
29	Expression of soybean lectin gene deletions in tobacco. <i>Genesis</i> , 1990, 11, 160-167.	3.1	23
30	A defective seed coat pattern (Net) is correlated with the post-transcriptional abundance of soluble proline-rich cell wall proteins. <i>Plant Molecular Biology</i> , 1999, 40, 603-613.	2.0	23
31	The Transition from Primary siRNAs to Amplified Secondary siRNAs That Regulate Chalcone Synthase During Development of <i>Glycine max</i> Seed Coats. <i>PLoS ONE</i> , 2013, 8, e76954.	1.1	22
32	Localization of β -glucuronidase in protein bodies of transgenic tobacco seed by fusion to an amino terminal sequence of the soybean lectin gene. <i>Plant Science</i> , 1998, 137, 191-204.	1.7	21
33	Ribosome profiling reveals changes in translational status of soybean transcripts during immature cotyledon development. <i>PLoS ONE</i> , 2018, 13, e0194596.	1.1	20
34	Genetic length polymorphisms create size variation in proline-rich proteins of the cell wall. <i>Plant Journal</i> , 1994, 6, 177-186.	2.8	18
35	Transcript profiling reveals expression differences in wild-type and glabrous soybean lines. <i>BMC Plant Biology</i> , 2011, 11, 145.	1.6	18
36	RNA-Seq Profiling of a Defective Seed Coat Mutation in <i>Glycine max</i> Reveals Differential Expression of Proline-Rich and Other Cell Wall Protein Transcripts. <i>PLoS ONE</i> , 2014, 9, e96342.	1.1	16

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37	Nonallelic homologous recombination events responsible for copy number variation within an RNA silencing locus. <i>Plant Direct</i> , 2019, 3, e00162.	0.8	14
38	Direct Detection of Transcription Factors in Cotyledons during Seedling Development Using Sensitive Silicon-Substrate Photonic Crystal Protein Arrays A. <i>Plant Physiology</i> , 2015, 167, 639-649.	2.3	13
39	Unstable genes affecting chloroplast development in soybean. <i>Genesis</i> , 1989, 10, 532-541.	3.1	9
40	Transcription factors and glyoxylate cycle genes prominent in the transition of soybean cotyledons to the first functional leaves of the seedling. <i>Functional and Integrative Genomics</i> , 2014, 14, 683-696.	1.4	9
41	Overexpression of an ethylene-forming ACC oxidase (ACO) gene precedes the Minute Hilum seed coat phenotype in <i>Glycine max</i> . <i>BMC Genomics</i> , 2020, 21, 716.	1.2	3
42	An embryo lethal transgenic line manifests global expression changes and elevated protein/oil ratios in heterozygous soybean plants. <i>PLoS ONE</i> , 2020, 15, e0233721.	1.1	2
43	Tissue-Specific Regulation of Gene Expression by siRNAs in Soybean. , 2012, , 111-127.		0