

Lila O Vodkin

List of Publications by Year in descending order

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218381

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times ranked

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citing authors

#	ARTICLE	IF	CITATIONS
1	Overexpression of an ethylene-forming ACC oxidase (ACO) gene precedes the Minute Hilum seed coat phenotype in <i>Glycine max</i> . BMC Genomics, 2020, 21, 716.	1.2	3
2	An embryo lethal transgenic line manifests global expression changes and elevated protein/oil ratios in heterozygous soybean plants. PLoS ONE, 2020, 15, e0233721.	1.1	2
3	Nonallelic homologous recombination events responsible for copy number variation within an RNA silencing locus. Plant Direct, 2019, 3, e00162.	0.8	14
4	Ribosome profiling reveals changes in translational status of soybean transcripts during immature cotyledon development. PLoS ONE, 2018, 13, e0194596.	1.1	20
5	Mutations in <i>Argonaute5</i> illuminate Epistatic Interactions of the <i>K1</i> and <i>I1</i> Loci Leading to Saddle Seed Color Patterns in <i>Glycine max</i> . Plant Cell, 2017, 29, 708-725.	3.1	51
6	Direct Detection of Transcription Factors in Cotyledons during Seedling Development Using Sensitive Silicon-Substrate Photonic Crystal Protein Arrays. Plant Physiology, 2015, 167, 639-649.	2.3	13
7	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. PLoS ONE, 2014, 9, e96342.	1.1	16
8	Methylation Affects Transposition and Splicing of a Large CACTA Transposon from a MYB Transcription Factor Regulating Anthocyanin Synthase Genes in Soybean Seed Coats. PLoS ONE, 2014, 9, e111959.	1.1	48
9	Transcription factors and glyoxylate cycle genes prominent in the transition of soybean cotyledons to the first functional leaves of the seedling. Functional and Integrative Genomics, 2014, 14, 683-696.	1.4	9
10	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. BMC Genomics, 2013, 14, 477.	1.2	72
11	Using RNA-Seq to Profile Soybean Seed Development from Fertilization to Maturity. PLoS ONE, 2013, 8, e59270.	1.1	122
12	The Transition from Primary siRNAs to Amplified Secondary siRNAs That Regulate Chalcone Synthase During Development of <i>Glycine max</i> Seed Coats. PLoS ONE, 2013, 8, e76954.	1.1	22
13	Identification of soybean seed developmental stage-specific and tissue-specific miRNA targets by degradome sequencing. BMC Genomics, 2012, 13, 310.	1.2	115
14	Tissue-Specific Regulation of Gene Expression by siRNAs in Soybean. , 2012, , 111-127.		0
15	Transcript profiling reveals expression differences in wild-type and glabrous soybean lines. BMC Plant Biology, 2011, 11, 145.	1.6	18
16	Improved Sensitivity of DNA Microarrays Using Photonic Crystal Enhanced Fluorescence. Analytical Chemistry, 2010, 82, 6854-6861.	3.2	49
17	Flux of transcript patterns during soybean seed development. BMC Genomics, 2010, 11, 136.	1.2	58
18	Endogenous, Tissue-Specific Short Interfering RNAs Silence the Chalcone Synthase Gene Family in <i>Glycine max</i> Seed Coats. Plant Cell, 2009, 21, 3063-3077.	3.1	126

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19	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
20	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
21	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
22	The <i>wp</i> 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
23	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
24	Features of a 103-kb gene-rich region in soybean include an inverted perfect repeat cluster of <i>CHS</i> genes comprising the <i>l</i> locus. <i>Genome</i> , 2004, 47, 819-831.	0.9	78
25	Clustering of Microarray Data Reveals Transcript Patterns Associated with Somatic Embryogenesis in Soybean. <i>Plant Physiology</i> , 2003, 132, 118-136.	2.3	206
26	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
27	A compilation of soybean ESTs: generation and analysis. <i>Genome</i> , 2002, 45, 329-338.	0.9	133
28	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
29	A defective seed coat pattern (<i>Net</i>) 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
30	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
31	Duplications That Suppress and Deletions That Restore Expression from a Chalcone Synthase Multigene Family. <i>Plant Cell</i> , 1996, 8, 687.	3.1	41
32	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
33	Cosegregation of Purple-Throat Flower Color with Dihydroflavonol Reductase Polymorphism in Soybean. <i>Crop Science</i> , 1995, 35, 1028-1031.	0.8	29
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	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
36	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

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37	Fluorescent in situ hybridization to soybean metaphase chromosomes. <i>Plant Molecular Biology</i> , 1991, 17, 101-109.	2.0	49
38	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
39	Expression of soybean lectin gene deletions in tobacco. <i>Genesis</i> , 1990, 11, 160-167.	3.1	23
40	Unstable genes affecting chloroplast development in soybean. <i>Genesis</i> , 1989, 10, 532-541.	3.1	9
41	An insertion sequence blocks the expression of a soybean lectin gene. <i>Cell</i> , 1983, 33, 465-475.	13.5	133
42	Ca lectin gene insertion has the structural features of a transposable element. <i>Cell</i> , 1983, 34, 1023-1031.	13.5	299
43	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