

Lewis Lukens

List of Publications by Year in descending order

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Version: 2024-02-01

44
papers

4,440
citations

304743

22
h-index

276875

41
g-index

45
all docs

45
docs citations

45
times ranked

5238
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetics, not environment, contributed to winter wheat yield gains in Ontario, Canada. <i>Theoretical and Applied Genetics</i> , 2022, , 1.	3.6	0
2	<i>Zea mays</i> RNA-seq estimated transcript abundances are strongly affected by read mapping bias. <i>BMC Genomics</i> , 2021, 22, 285.	2.8	3
3	The effects of crop attributes, selection, and recombination on Canadian bread wheat molecular variation. <i>Plant Genome</i> , 2021, 14, e20099.	2.8	1
4	Introgressed DNA within a <i>Zea mays</i> near-isogenic line displays lower levels of 24nt sRNA expression than the homologous region from the recurrent parent. <i>Genome</i> , 2021, 64, 1091-1098.	2.0	0
5	The Induction of the Isoflavone Biosynthesis Pathway Is Associated with Resistance to Common Bacterial Blight in <i>Phaseolus vulgaris</i> L.. <i>Metabolites</i> , 2021, 11, 433.	2.9	3
6	Patterns of stability and change in the maize genome: a case study of small RNA transcriptomes in two recombinant inbred lines and their progenitors. <i>Genome</i> , 2021, , 1-12.	2.0	1
7	Evidence for the Accumulation of Nonsynonymous Mutations and Favorable Pleiotropic Alleles During Wheat Breeding. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 4001-4011.	1.8	6
8	Genomic regions associated with important seed quality traits in food-grade soybeans. <i>BMC Plant Biology</i> , 2020, 20, 485.	3.6	12
9	Registration of the S2MET Barley Mapping Population for Multi-Environment Genomewide Selection. <i>Journal of Plant Registrations</i> , 2019, 13, 270-280.	0.5	11
10	Distinct gene networks modulate floral induction of autonomous maize and photoperiod-dependent teosinte. <i>Journal of Experimental Botany</i> , 2018, 69, 2937-2952.	4.8	39
11	Leaf Spectral Reflectance of Maize Seedlings and Its Relationship to Cold Tolerance. <i>Crop Science</i> , 2018, 58, 2569-2580.	1.8	9
12	Shared and genetically distinct <i>Zea mays</i> transcriptome responses to ongoing and past low temperature exposure. <i>BMC Genomics</i> , 2018, 19, 761.	2.8	29
13	Proanthocyanidin accumulation and transcriptional responses in the seed coat of cranberry beans (<i>Phaseolus vulgaris</i> L.) with different susceptibility to postharvest darkening. <i>BMC Plant Biology</i> , 2017, 17, 89.	3.6	32
14	Changes in light quality alter physiological responses of soybean to thiamethoxam. <i>Planta</i> , 2016, 244, 639-650.	3.2	5
15	Does the presence of neighbouring weeds alter the expression of adaptive plasticity to subsequent drought stress in soybean?. <i>Field Crops Research</i> , 2016, 192, 144-153.	5.1	7
16	<i>Brevis plant1</i> , a putative inositol polyphosphate 5-phosphatase, is required for internode elongation in maize. <i>Journal of Experimental Botany</i> , 2016, 67, 1577-1588.	4.8	29
17	Maize (<i>Zea mays</i>) seeds can detect above-ground weeds; thiamethoxam alters the view. <i>Pest Management Science</i> , 2015, 71, 1335-1345.	3.4	6
18	Detection of Neighboring Weeds Alters Soybean Seedling Roots and Nodulation. <i>Weed Science</i> , 2015, 63, 888-900.	1.5	11

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19	The Effect of Linkage on Genetic Variances within Biparental Simulated and <i>Zea mays</i> Populations. <i>Crop Science</i> , 2014, 54, 2481-2491.	1.8	2
20	Delaying Weed Control Lengthens the Anthesis-Silking Interval in Maize. <i>Weed Science</i> , 2014, 62, 326-337.	1.5	11
21	Beyond the single gene: How epistasis and gene-by-environment effects influence crop domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6178-6183.	7.1	91
22	Current perspectives and the future of domestication studies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6139-6146.	7.1	594
23	Evidence for Selection on Gene Expression in Cultivated Rice (<i>Oryza sativa</i>). <i>Molecular Biology and Evolution</i> , 2014, 31, 1514-1525.	8.9	29
24	Protein-Coding cis-Natural Antisense Transcripts Have High and Broad Expression in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2013, 161, 2171-2180.	4.8	18
25	Bioinformatics Techniques for Understanding and Analyzing Tree Gene Expression Data. , 2012, , 17-38.		2
26	The Genetic Architecture of Flowering Time and Related Traits in Two Early Flowering Maize Lines. <i>Crop Science</i> , 2011, 51, 146-156.	1.8	9
27	Validation of mega-environment universal and specific QTL associated with seed yield and agronomic traits in soybeans. <i>Theoretical and Applied Genetics</i> , 2010, 120, 997-1003.	3.6	41
28	Timing, Effect, and Recovery from Intraspecific Competition in Maize. <i>Agronomy Journal</i> , 2010, 102, 1007-1013.	1.8	16
29	Identification of Novel miRNAs and miRNA Dependent Developmental Shifts of Gene Expression in <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , 2010, 5, e10157.	2.5	22
30	Development of public immortal mapping populations, molecular markers and linkage maps for rapid cycling <i>Brassica rapa</i> and <i>B. oleracea</i> . <i>Theoretical and Applied Genetics</i> , 2009, 120, 31-43.	3.6	94
31	The plant genome's methylation status and response to stress: implications for plant improvement. <i>Current Opinion in Plant Biology</i> , 2007, 10, 317-322.	7.1	173
32	Patterns of Sequence Loss and Cytosine Methylation within a Population of Newly Resynthesized <i>Brassica napus</i> Allopolyploids. <i>Plant Physiology</i> , 2006, 140, 336-348.	4.8	250
33	Islands of co-expressed neighbouring genes in <i>Arabidopsis thaliana</i> suggest higher-order chromosome domains. <i>Plant Journal</i> , 2006, 45, 347-357.	5.7	64
34	The origin of the naked grains of maize. <i>Nature</i> , 2005, 436, 714-719.	27.8	561
35	Segmental Structure of the <i>Brassica napus</i> Genome Based on Comparative Analysis With <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2005, 171, 765-781.	2.9	516
36	Sensitivity of 70-mer oligonucleotides and cDNAs for microarray analysis of gene expression in <i>Arabidopsis</i> and its related species. <i>Plant Biotechnology Journal</i> , 2004, 2, 45-57.	8.3	55

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37	Comparison of a <i>Brassica oleracea</i> Genetic Map With the Genome of <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2003, 164, 359-372.	2.9	139
38	Characterization and Effects of the Replicated Flowering Time Gene <i>FLC</i> in <i>Brassica rapa</i> . <i>Genetics</i> , 2002, 162, 1457-1468.	2.9	240
39	Molecular Evolution of the teosinte branched Gene Among Maize and Related Grasses. <i>Molecular Biology and Evolution</i> , 2001, 18, 627-638.	8.9	90
40	The limits of selection during maize domestication. <i>Nature</i> , 1999, 398, 236-239.	27.8	715
41	Transcriptional Regulators and the Evolution of Plant Form. <i>Plant Cell</i> , 1998, 10, 1075-1082.	6.6	416
42	Transcriptional Regulators and the Evolution of Plant Form. <i>Plant Cell</i> , 1998, 10, 1075.	6.6	30
43	Variation at the b Mating Type Locus of <i>Ustilago maydis</i> . <i>Phytopathology</i> , 1997, 87, 1233-1239.	2.2	25
44	Correlation of Genetic and Physical Maps at the <i>A</i> Mating-Type Locus of <i>Coprinus cinereus</i> . <i>Genetics</i> , 1996, 144, 1471-1477.	2.9	27