

David L Hyten

List of Publications by Year in descending order

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58
papers

12,046
citations

81900

39
h-index

144013

57
g-index

62
all docs

62
docs citations

62
times ranked

10156
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequence of the palaeopolyploid soybean. <i>Nature</i> , 2010, 463, 178-183.	27.8	3,854
2	A genome-wide association study of seed protein and oil content in soybean. <i>BMC Genomics</i> , 2014, 15, 1.	2.8	1,312
3	A reference genome for common bean and genome-wide analysis of dual domestications. <i>Nature Genetics</i> , 2014, 46, 707-713.	21.4	1,159
4	Impacts of genetic bottlenecks on soybean genome diversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 16666-16671.	7.1	633
5	Development and Evaluation of SoySNP50K, a High-Density Genotyping Array for Soybean. <i>PLoS ONE</i> , 2013, 8, e54985.	2.5	490
6	A Soybean Transcript Map: Gene Distribution, Haplotype and Single-Nucleotide Polymorphism Analysis. <i>Genetics</i> , 2007, 176, 685-696.	2.9	285
7	Abundance of SSR Motifs and Development of Candidate Polymorphic SSR Markers (BARCSOYSSR_1.0) in Soybean. <i>Crop Science</i> , 2010, 50, 1950-1960.	1.8	282
8	A High Density Integrated Genetic Linkage Map of Soybean and the Development of a 1536 Universal Soy Linkage Panel for Quantitative Trait Locus Mapping. <i>Crop Science</i> , 2010, 50, 960-968.	1.8	247
9	High-throughput SNP discovery through deep resequencing of a reduced representation library to anchor and orient scaffolds in the soybean whole genome sequence. <i>BMC Genomics</i> , 2010, 11, 38.	2.8	242
10	Fingerprinting Soybean Germplasm and Its Utility in Genomic Research. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1999-2006.	1.8	212
11	High-throughput genotyping with the GoldenGate assay in the complex genome of soybean. <i>Theoretical and Applied Genetics</i> , 2008, 116, 945-952.	3.6	210
12	Highly Variable Patterns of Linkage Disequilibrium in Multiple Soybean Populations. <i>Genetics</i> , 2007, 175, 1937-1944.	2.9	182
13	Structural Variants in the Soybean Genome Localize to Clusters of Biotic Stress-Response Genes. <i>Plant Physiology</i> , 2012, 159, 1295-1308.	4.8	175
14	Forrest resistance to the soybean cyst nematode is bigenic: saturation mapping of the Rhg1 and Rhg4 loci. <i>Theoretical and Applied Genetics</i> , 2001, 103, 710-717.	3.6	156
15	SNP Assay Development for Linkage Map Construction, Anchoring Whole-Genome Sequence, and Other Genetic and Genomic Applications in Common Bean. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2285-2290.	1.8	147
16	Genetic Mapping and Confirmation of Quantitative Trait Loci for Seed Protein and Oil Contents and Seed Weight in Soybean. <i>Crop Science</i> , 2013, 53, 765-774.	1.8	146
17	Bulked Segregant Analysis Using the GoldenGate Assay to Locate the <i>Rpp3</i> Locus that Confers Resistance to Soybean Rust in Soybean. <i>Crop Science</i> , 2009, 49, 265-271.	1.8	138
18	The Composition and Origins of Genomic Variation among Individuals of the Soybean Reference Cultivar Williams 82. <i>Plant Physiology</i> , 2011, 155, 645-655.	4.8	137

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19	Construction of high resolution genetic linkage maps to improve the soybean genome sequence assembly Glyma1.01. BMC Genomics, 2016, 17, 33.	2.8	137
20	High-throughput SNP discovery and assay development in common bean. BMC Genomics, 2010, 11, 475.	2.8	134
21	Map Location of the <i>Rpp1</i> Locus That Confers Resistance to Soybean Rust in Soybean. Crop Science, 2007, 47, 837-838.	1.8	132
22	Genetic Characterization of the Soybean Nested Association Mapping Population. Plant Genome, 2017, 10, plantgenome2016.10.0109.	2.8	114
23	Genome-Wide Association Analysis Identifies Candidate Genes Associated with Iron Deficiency Chlorosis in Soybean. Plant Genome, 2011, 4, 154-164.	2.8	106
24	Genetic Architecture of Soybean Yield and Agronomic Traits. G3: Genes, Genomes, Genetics, 2018, 8, 3367-3375.	1.8	98
25	Identification and validation of quantitative trait loci for seed yield, oil and protein contents in two recombinant inbred line populations of soybean. Molecular Genetics and Genomics, 2014, 289, 935-949.	2.1	95
26	Fine mapping the soybean aphid resistance gene Rag1 in soybean. Theoretical and Applied Genetics, 2010, 120, 1063-1071.	3.6	87
27	Mapping and Confirmation of a New Allele at <i>Rpp1</i> from Soybean PI 594538A Conferring RB Lesion- <i>T</i> Type Resistance to Soybean Rust. Crop Science, 2009, 49, 783-790.	1.8	82
28	Fine mapping of the soybean aphid-resistance gene Rag2 in soybean PI 200538. Theoretical and Applied Genetics, 2010, 121, 599-610.	3.6	76
29	Stacking Resistance Alleles from Wild and Domestic Soybean Sources Improves Soybean Cyst Nematode Resistance. Crop Science, 2011, 51, 934-943.	1.8	61
30	Structural and Functional Divergence of a 1-Mb Duplicated Region in the Soybean (<i>Glycine max</i>) Genome and Comparison to an Orthologous Region from <i>Phaseolus vulgaris</i> . Plant Cell, 2010, 22, 2545-2561.	6.6	60
31	Soybean BARCSoySNP6K: An assay for soybean genetics and breeding research. Plant Journal, 2020, 104, 800-811.	5.7	60
32	Fine Mapping of the SCN Resistance Locus <i>rhg1</i> from PI 88788. Plant Genome, 2010, 3, .	2.8	56
33	Identification of a Second Asian Soybean Rust Resistance Gene in Hyuuga Soybean. Phytopathology, 2011, 101, 535-543.	2.2	53
34	Quantitative trait locus analysis of saturated fatty acids in a population of recombinant inbred lines of soybean. Molecular Breeding, 2012, 30, 1163-1179.	2.1	52
35	Molecular mapping and identification of soybean fatty acid modifier quantitative trait loci. JAOCS, Journal of the American Oil Chemists' Society, 2004, 81, 1115-1118.	1.9	51
36	Molecular mapping of soybean rust resistance in soybean accession PI 561356 and SNP haplotype analysis of the <i>Rpp1</i> region in diverse germplasm. Theoretical and Applied Genetics, 2012, 125, 1339-1352.	3.6	47

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37	An Integrative Approach to Genomic Introgression Mapping. <i>Plant Physiology</i> , 2010, 154, 3-12.	4.8	45
38	Multi-Population Selective Genotyping to Identify Soybean [<i>Glycine max</i> (L.) Merr.] Seed Protein and Oil QTLs. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1635-1648.	1.8	45
39	Application of machine learning in SNP discovery. <i>BMC Bioinformatics</i> , 2006, 7, 4.	2.6	43
40	Genome-wide Association Mapping of Qualitatively Inherited Traits in a Germplasm Collection. <i>Plant Genome</i> , 2017, 10, plantgenome2016.06.0054.	2.8	37
41	Soybean [<i>Glycine max</i> (L.) Merr.] Breeding: History, Improvement, Production and Future Opportunities. , 2019, , 431-516.		36
42	Title is missing!. <i>Molecular Breeding</i> , 2001, 7, 63-71.	2.1	35
43	Mapping soybean aphid resistance genes in PI 567598B. <i>Theoretical and Applied Genetics</i> , 2013, 126, 2081-2091.	3.6	32
44	SNP-PHAGE-High throughput SNP discovery pipeline. <i>BMC Bioinformatics</i> , 2006, 7, 468.	2.6	29
45	Quantitative trait locus analysis of unsaturated fatty acids in a recombinant inbred population of soybean. <i>Molecular Breeding</i> , 2014, 33, 281-296.	2.1	29
46	Mapping the low palmitate <i>fap1</i> mutation and validation of its effects in soybean oil and agronomic traits in three soybean populations. <i>Theoretical and Applied Genetics</i> , 2014, 127, 97-111.	3.6	22
47	Generating High Density, Low Cost Genotype Data in Soybean [<i>Glycine max</i> (L.) Merr.]. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2153-2160.	1.8	19
48	Molecular Characterization of Resistance to Soybean Rust (<i>Phakopsora pachyrhizi</i> Syd. & Syd.) in Soybean Cultivar DT 2000 (PI 635999). <i>PLoS ONE</i> , 2016, 11, e0164493.	2.5	18
49	Phytophthora Root Rot Resistance in Soybean E00003. <i>Crop Science</i> , 2014, 54, 492-499.	1.8	16
50	Detection and Confirmation of Quantitative Trait Loci for Soybean Seed Isoflavones. <i>Crop Science</i> , 2014, 54, 595-606.	1.8	16
51	eQTL Networks Reveal Complex Genetic Architecture in the Immature Soybean Seed. <i>Plant Genome</i> , 2014, 7, plantgenome2013.08.0027.	2.8	15
52	Context-specific Genomic Selection Strategies Outperform Phenotypic Selection for Soybean Quantitative Traits in the Progeny Row Stage. <i>Crop Science</i> , 2019, 59, 54-67.	1.8	15
53	A bumper crop of SNPs in soybean through high-density genotyping-by-sequencing (HD-GBS). <i>Plant Biotechnology Journal</i> , 2021, 19, 860-862.	8.3	13
54	Mutational analysis of the major soybean <i>UreF</i> paralogue involved in urease activation. <i>Journal of Experimental Botany</i> , 2011, 62, 3599-3608.	4.8	10

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55	Identifying and exploring significant genomic regions associated with soybean yield, seed fatty acids, protein and oil. <i>Journal of Crop Science and Biotechnology</i> , 2017, 20, 243-253.	1.5	9
56	Comparing a Mixed Model Approach to Traditional Stability Estimators for Mapping Genotype by Environment Interactions and Yield Stability in Soybean [<i>Glycine max</i> (L.) Merr.]. <i>Frontiers in Plant Science</i> , 2021, 12, 630175.	3.6	7
57	Candidate Genes Modulating Reproductive Timing in Elite US Soybean Lines Identified in Soybean Alleles of <i>Arabidopsis</i> Flowering Orthologs With Divergent Latitude Distribution. <i>Frontiers in Plant Science</i> , 2022, 13, 889066.	3.6	4
58	Advances in Genome Sequencing and Genotyping Technology for Soybean Diversity Analysis. , 2012, , 45-52.		1