

David L Hyten

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

59
papers

8,758
citations

36
h-index

62
g-index

62
ext. papers

10,535
ext. citations

5.7
avg, IF

5.24
L-index

#	Paper	IF	Citations
59	Genome sequence of the palaeopolyploid soybean. <i>Nature</i> , 2010 , 463, 178-83	50.4	2997
58	A reference genome for common bean and genome-wide analysis of dual domestications. <i>Nature Genetics</i> , 2014 , 46, 707-13	36.3	772
57	A genome-wide association study of seed protein and oil content in soybean. <i>BMC Genomics</i> , 2014 , 15, 1	4.5	653
56	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, 16666-71	11.5	492
55	Development and evaluation of SoySNP50K, a high-density genotyping array for soybean. <i>PLoS ONE</i> , 2013 , 8, e54985	3.7	344
54	A soybean transcript map: gene distribution, haplotype and single-nucleotide polymorphism analysis. <i>Genetics</i> , 2007 , 176, 685-96	4	258
53	Abundance of SSR Motifs and Development of Candidate Polymorphic SSR Markers (BARCSOYSSR_1.0) in Soybean. <i>Crop Science</i> , 2010 , 50, 1950-1960	2.4	220
52	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	4.5	219
51	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	2.4	215
50	High-throughput genotyping with the GoldenGate assay in the complex genome of soybean. <i>Theoretical and Applied Genetics</i> , 2008 , 116, 945-52	6	195
49	Highly variable patterns of linkage disequilibrium in multiple soybean populations. <i>Genetics</i> , 2007 , 175, 1937-44	4	143
48	Structural variants in the soybean genome localize to clusters of biotic stress-response genes. <i>Plant Physiology</i> , 2012 , 159, 1295-308	6.6	140
47	Fingerprinting Soybean Germplasm and Its Utility in Genomic Research. <i>G3: Genes, Genomes, Genetics</i> , 2015 , 5, 1999-2006	3.2	138
46	Borrest 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	6	128
45	High-throughput SNP discovery and assay development in common bean. <i>BMC Genomics</i> , 2010 , 11, 475	4.5	120
44	Bulked Segregant Analysis Using the GoldenGate Assay to Locate the Rpp3 Locus that Confers Resistance to Soybean Rust in Soybean. <i>Crop Science</i> , 2009 , 49, 265-271	2.4	115
43	The composition and origins of genomic variation among individuals of the soybean reference cultivar Williams 82. <i>Plant Physiology</i> , 2011 , 155, 645-55	6.6	111

42	Map Location of the Rpp1 Locus That Confers Resistance to Soybean Rust in Soybean. <i>Crop Science</i> , 2007 , 47, 837-838	2.4	108
41	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, 2285-90 ²	3.2	95
40	Genome-Wide Association Analysis Identifies Candidate Genes Associated with Iron Deficiency Chlorosis in Soybean. <i>Plant Genome</i> , 2011 , 4, 154-164	4.4	82
39	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	2.4	76
38	Construction of high resolution genetic linkage maps to improve the soybean genome sequence assembly Glyma1.01. <i>BMC Genomics</i> , 2016 , 17, 33	4.5	73
37	Fine mapping the soybean aphid resistance gene Rag1 in soybean. <i>Theoretical and Applied Genetics</i> , 2010 , 120, 1063-71	6	69
36	Fine mapping of the soybean aphid-resistance gene Rag2 in soybean PI 200538. <i>Theoretical and Applied Genetics</i> , 2010 , 121, 599-610	6	68
35	Mapping and Confirmation of a New Allele at Rpp1 from Soybean PI 594538A Conferring RB LesionType Resistance to Soybean Rust. <i>Crop Science</i> , 2009 , 49, 783-790	2.4	68
34	Genetic Characterization of the Soybean Nested Association Mapping Population. <i>Plant Genome</i> , 2017 , 10, plantgenome2016.10.0109	4.4	67
33	Identification and validation of quantitative trait loci for seed yield, oil and protein contents in two recombinant inbred line populations of soybean. <i>Molecular Genetics and Genomics</i> , 2014 , 289, 935-49	3.1	59
32	Stacking Resistance Alleles from Wild and Domestic Soybean Sources Improves Soybean Cyst Nematode Resistance. <i>Crop Science</i> , 2011 , 51, 934-943	2.4	51
31	Genetic Architecture of Soybean Yield and Agronomic Traits. <i>G3: Genes, Genomes, Genetics</i> , 2018 , 8, 3367-3375	3.4	44
30	Molecular mapping and identification of soybean fatty acid modifier quantitative trait loci. <i>JAOCs, Journal of the American Oil Chemists Society</i> , 2004 , 81, 1115-1118	1.8	44
29	Identification of a second Asian soybean rust resistance gene in Hyuuga soybean. <i>Phytopathology</i> , 2011 , 101, 535-43	3.8	43
28	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> . <i>Plant Cell</i> , 2010 , 22, 2545-61 ^{11.6}	11.6	42
27	Fine Mapping of the SCN Resistance Locus rhg1-b from PI 88788. <i>Plant Genome</i> , 2010 , 3,	4.4	41
26	Molecular mapping of soybean rust resistance in soybean accession PI 561356 and SNP haplotype analysis of the Rpp1 region in diverse germplasm. <i>Theoretical and Applied Genetics</i> , 2012 , 125, 1339-52	6	38
25	Quantitative trait locus analysis of saturated fatty acids in a population of recombinant inbred lines of soybean. <i>Molecular Breeding</i> , 2012 , 30, 1163-1179	3.4	38

24	An integrative approach to genomic introgression mapping. <i>Plant Physiology</i> , 2010 , 154, 3-12	6.6	37
23	High-throughput genotyping for a polymorphism linked to soybean cyst nematode resistance gene Rhg4 by using Taqman TM probes. <i>Molecular Breeding</i> , 2001 , 7, 63-71	3.4	30
22	Mapping soybean aphid resistance genes in PI 567598B. <i>Theoretical and Applied Genetics</i> , 2013 , 126, 2086-91		28
21	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, 1635-48	3.2	26
20	Application of machine learning in SNP discovery. <i>BMC Bioinformatics</i> , 2006 , 7, 4	3.6	25
19	Quantitative trait locus analysis of unsaturated fatty acids in a recombinant inbred population of soybean. <i>Molecular Breeding</i> , 2014 , 33, 281-296	3.4	24
18	SNP-PHAGE--High throughput SNP discovery pipeline. <i>BMC Bioinformatics</i> , 2006 , 7, 468	3.6	23
17	Soybean BARCSoySNP6K: An assay for soybean genetics and breeding research. <i>Plant Journal</i> , 2020 , 104, 800-811	6.9	20
16	Genome-wide Association Mapping of Qualitatively Inherited Traits in a Germplasm Collection. <i>Plant Genome</i> , 2017 , 10, plantgenome2016.06.0054	4.4	18
15	Mapping the low palmitate fap1 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	6	18
14	Soybean [<i>Glycine max</i> (L.) Merr.] Breeding: History, Improvement, Production and Future Opportunities 2019 , 431-516		14
13	Generating High Density, Low Cost Genotype Data in Soybean [(L.) Merr.]. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 2153-2160	3.2	13
12	Detection and Confirmation of Quantitative Trait Loci for Soybean Seed Isoflavones. <i>Crop Science</i> , 2014 , 54, 595-606	2.4	13
11	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	3.7	13
10	Phytophthora Root Rot Resistance in Soybean E00003. <i>Crop Science</i> , 2014 , 54, 492-499	2.4	12
9	eQTL Networks Reveal Complex Genetic Architecture in the Immature Soybean Seed. <i>Plant Genome</i> , 2014 , 7, plantgenome2013.08.0027	4.4	11
8	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	2.4	11
7	Mutational analysis of the major soybean UreF paralogue involved in urease activation. <i>Journal of Experimental Botany</i> , 2011 , 62, 3599-608	7	10

6	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	1.2	8
5	A bumper crop of SNPs in soybean through high-density genotyping-by-sequencing (HD-GBS). <i>Plant Biotechnology Journal</i> , 2021 , 19, 860-862	11.6	4
4	Comparing a Mixed Model Approach to Traditional Stability Estimators for Mapping Genotype by Environment Interactions and Yield Stability in Soybean [(L.) Merr.]. <i>Frontiers in Plant Science</i> , 2021 , 12, 630175	6.2	1
3	Candidate Genes Modulating Reproductive Timing in Elite US Soybean Lines Identified in Soybean Alleles of Flowering Orthologs With Divergent Latitude Distribution.. <i>Frontiers in Plant Science</i> , 2022 , 13, 889066	6.2	0
2	Advances in Genome Sequencing and Genotyping Technology for Soybean Diversity Analysis 2012 , 45-52		
1	Genotyping Platforms for Genome-Wide Association Studies: Options and Practical Considerations. <i>Methods in Molecular Biology</i> , 2022 , 29-42	1.4	