

David L Hyten

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/633923/david-l-hyten-publications-by-year.pdf>

Version: 2024-04-24

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	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
58	Genotyping Platforms for Genome-Wide Association Studies: Options and Practical Considerations. <i>Methods in Molecular Biology</i> , 2022 , 29-42	1.4	
57	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
56	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
55	Soybean BARCSoySNP6K: An assay for soybean genetics and breeding research. <i>Plant Journal</i> , 2020 , 104, 800-811	6.9	20
54	Generating High Density, Low Cost Genotype Data in Soybean [(L.) Merr.]. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 2153-2160	3.2	13
53	Soybean [Glycine max (L.) Merr.] Breeding: History, Improvement, Production and Future Opportunities 2019 , 431-516		14
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	2.4	11
51	Genetic Architecture of Soybean Yield and Agronomic Traits. <i>G3: Genes, Genomes, Genetics</i> , 2018 , 8, 3367-3375	3.375	44
50	Genome-wide Association Mapping of Qualitatively Inherited Traits in a Germplasm Collection. <i>Plant Genome</i> , 2017 , 10, plantgenome2016.06.0054	4.4	18
49	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
48	Genetic Characterization of the Soybean Nested Association Mapping Population. <i>Plant Genome</i> , 2017 , 10, plantgenome2016.10.0109	4.4	67
47	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
46	Molecular Characterization of Resistance to Soybean Rust (Phakopsora pachyrhizi Syd. & Syd.) in Soybean Cultivar DT 2000 (PI 635999). <i>PLoS ONE</i> , 2016 , 11, e0164493	3.7	13
45	Multi-Population Selective Genotyping to Identify Soybean [Glycine max (L.) Merr.] Seed Protein and Oil QTLs. <i>G3: Genes, Genomes, Genetics</i> , 2016 , 6, 1635-48	3.2	26
44	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	3.2	95
43	Fingerprinting Soybean Germplasm and Its Utility in Genomic Research. <i>G3: Genes, Genomes, Genetics</i> , 2015 , 5, 1999-2006	3.2	138

42	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
41	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
40	A reference genome for common bean and genome-wide analysis of dual domestications. <i>Nature Genetics</i> , 2014 , 46, 707-13	36.3	772
39	eQTL Networks Reveal Complex Genetic Architecture in the Immature Soybean Seed. <i>Plant Genome</i> , 2014 , 7, plantgenome2013.08.0027	4.4	11
38	Phytophthora Root Rot Resistance in Soybean E00003. <i>Crop Science</i> , 2014 , 54, 492-499	2.4	12
37	Detection and Confirmation of Quantitative Trait Loci for Soybean Seed Isoflavones. <i>Crop Science</i> , 2014 , 54, 595-606	2.4	13
36	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
35	A genome-wide association study of seed protein and oil content in soybean. <i>BMC Genomics</i> , 2014 , 15, 1	4.5	653
34	Mapping soybean aphid resistance genes in PI 567598B. <i>Theoretical and Applied Genetics</i> , 2013 , 126, 2086-91	2.8	28
33	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
32	Development and evaluation of SoySNP50K, a high-density genotyping array for soybean. <i>PLoS ONE</i> , 2013 , 8, e54985	3.7	344
31	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
30	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
29	Advances in Genome Sequencing and Genotyping Technology for Soybean Diversity Analysis 2012 , 45-52		
28	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
27	Mutational analysis of the major soybean UreF paralogue involved in urease activation. <i>Journal of Experimental Botany</i> , 2011 , 62, 3599-608	7	10
26	Identification of a second Asian soybean rust resistance gene in Hyuuga soybean. <i>Phytopathology</i> , 2011 , 101, 535-43	3.8	43
25	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

24	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
23	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
22	Genome sequence of the palaeopolyploid soybean. <i>Nature</i> , 2010 , 463, 178-83	50.4	2997
21	Fine Mapping of the SCN Resistance Locus rhg1-b from PI 88788. <i>Plant Genome</i> , 2010 , 3,	4.4	41
20	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
19	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
18	An integrative approach to genomic introgression mapping. <i>Plant Physiology</i> , 2010 , 154, 3-12	6.6	37
17	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}	4.2	42
16	Fine mapping the soybean aphid resistance gene Rag1 in soybean. <i>Theoretical and Applied Genetics</i> , 2010 , 120, 1063-71	6	69
15	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
14	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
13	High-throughput SNP discovery and assay development in common bean. <i>BMC Genomics</i> , 2010 , 11, 475	4.5	120
12	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
11	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
10	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
9	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
8	A soybean transcript map: gene distribution, haplotype and single-nucleotide polymorphism analysis. <i>Genetics</i> , 2007 , 176, 685-96	4	258
7	Highly variable patterns of linkage disequilibrium in multiple soybean populations. <i>Genetics</i> , 2007 , 175, 1937-44	4	143

6	Application of machine learning in SNP discovery. <i>BMC Bioinformatics</i> , 2006 , 7, 4	3.6	25
5	SNP-PHAGE--High throughput SNP discovery pipeline. <i>BMC Bioinformatics</i> , 2006 , 7, 468	3.6	23
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, 16666-71	11.5	492
3	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
2	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
1	High-throughput genotyping for a polymorphism linked to soybean cyst nematode resistance gene Rhg4 by using Taqman™ probes. <i>Molecular Breeding</i> , 2001 , 7, 63-71	3.4	30