

Henry T Nguyen

List of Publications by Year in descending order

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Version: 2024-02-01

251
papers

20,669
citations

10986

71
h-index

12597

132
g-index

262
all docs

262
docs citations

262
times ranked

16328
citing authors

#	ARTICLE	IF	CITATIONS
1	Sequencing the USDA core soybean collection reveals gene loss during domestication and breeding. <i>Plant Genome</i> , 2022, 15, e20109.	2.8	53
2	Chromosome-length genome assemblies of six legume species provide insights into genome organization, evolution, and agronomic traits for crop improvement. <i>Journal of Advanced Research</i> , 2022, 42, 315-329.	9.5	20
3	Haplotype mapping uncovers unexplored variation in wild and domesticated soybean at the major protein locus cqProt-003. <i>Theoretical and Applied Genetics</i> , 2022, 135, 1443-1455.	3.6	13
4	Root physiology and morphology of soybean in relation to stress tolerance. <i>Advances in Botanical Research</i> , 2022, , 77-103.	1.1	2
5	Differentiate Soybean Response to Off-Target Dicamba Damage Based on UAV Imagery and Machine Learning. <i>Remote Sensing</i> , 2022, 14, 1618.	4.0	8
6	Machine learning models outperform deep learning models, provide interpretation and facilitate feature selection for soybean trait prediction. <i>BMC Plant Biology</i> , 2022, 22, 180.	3.6	15
7	Mapping of partial resistance to <i>Phytophthora sojae</i> in soybean PIs using whole-genome sequencing reveals a major QTL. <i>Plant Genome</i> , 2022, 15, e20184.	2.8	11
8	Pangenomics in crop improvement—from coding structural variations to finding regulatory variants with pangenome graphs. <i>Plant Genome</i> , 2022, 15, e20177.	2.8	33
9	Screening of Soybean Genotypes Based on Root Morphology and Shoot Traits Using the Semi-Hydroponic Phenotyping Platform and Rhizobox Technique. <i>Agronomy</i> , 2022, 12, 56.	3.0	8
10	Differential responses of soybean genotypes to off-target dicamba damage. <i>Crop Science</i> , 2022, 62, 1472-1483.	1.8	5
11	Exploring Machine Learning Algorithms to Unveil Genomic Regions Associated With Resistance to Southern Root-Knot Nematode in Soybeans. <i>Frontiers in Plant Science</i> , 2022, 13, 883280.	3.6	4
12	QTL and Candidate Genes for Seed Tocopherol Content in "Forrest" by "Williams 82" Recombinant Inbred Line (RIL) Population of Soybean. <i>Plants</i> , 2022, 11, 1258.	3.5	3
13	Breeding for disease resistance in soybean: a global perspective. <i>Theoretical and Applied Genetics</i> , 2022, 135, 3773-3872.	3.6	42
14	Soybean (<i>Glycine max</i>) Haplotype Map (GmHapMap): a universal resource for soybean translational and functional genomics. <i>Plant Biotechnology Journal</i> , 2021, 19, 324-334.	8.3	48
15	Fine-mapping and characterization of qSCN18, a novel QTL controlling soybean cyst nematode resistance in PI 567516C. <i>Theoretical and Applied Genetics</i> , 2021, 134, 621-631.	3.6	13
16	Soybean transporter database: A comprehensive database for identification and exploration of natural variants in soybean transporter genes. <i>Physiologia Plantarum</i> , 2021, 171, 756-770.	5.2	12
17	Mapping QTL controlling soybean seed sucrose and oligosaccharides in a single family of soybean nested association mapping (SoyNAM) population. <i>Plant Breeding</i> , 2021, 140, 110-122.	1.9	7
18	High-Throughput Crop Phenotyping Systems for Controlled Environments. <i>Concepts and Strategies in Plant Sciences</i> , 2021, , 183-208.	0.5	0

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19	Genomic resources in plant breeding for sustainable agriculture. <i>Journal of Plant Physiology</i> , 2021, 257, 153351.	3.5	90
20	Genetic variation among 481 diverse soybean accessions, inferred from genomic re-sequencing. <i>Scientific Data</i> , 2021, 8, 50.	5.3	38
21	Development of an automated plant phenotyping system for evaluation of salt tolerance in soybean. <i>Computers and Electronics in Agriculture</i> , 2021, 182, 106001.	7.7	13
22	Dissecting nematode resistance regions in soybean revealed pleiotropic effect of soybean cyst and reniform nematode resistance genes. <i>Plant Genome</i> , 2021, 14, e20083.	2.8	12
23	Identification and characterization of novel QTL conferring internal detoxification of aluminium in soybean. <i>Journal of Experimental Botany</i> , 2021, 72, 4993-5009.	4.8	12
24	Yield estimation of soybean breeding lines under drought stress using unmanned aerial vehicle-based imagery and convolutional neural network. <i>Biosystems Engineering</i> , 2021, 204, 90-103.	4.3	50
25	A major quantitative trait locus resistant to southern root-knot nematode sustains soybean yield under nematode pressure. <i>Crop Science</i> , 2021, 61, 1773-1782.	1.8	15
26	OsGERLP: A novel aluminum tolerance rice gene isolated from a local cultivar in Indonesia. <i>Plant Physiology and Biochemistry</i> , 2021, 162, 86-99.	5.8	7
27	TILLING-by-Sequencing+ Reveals the Role of Novel Fatty Acid Desaturases (GmFAD2-2s) in Increasing Soybean Seed Oleic Acid Content. <i>Cells</i> , 2021, 10, 1245.	4.1	19
28	Qualification of Soybean Responses to Flooding Stress Using UAV-Based Imagery and Deep Learning. <i>Plant Phenomics</i> , 2021, 2021, 9892570.	5.9	21
29	Genome-wide identification and analysis of soybean acyl-ACP thioesterase gene family reveals the role of GmFAT to improve fatty acid composition in soybean seed. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3611-3623.	3.6	20
30	Omics advances and integrative approaches for the simultaneous improvement of seed oil and protein content in soybean (<i>Glycine max</i> L.). <i>Critical Reviews in Plant Sciences</i> , 2021, 40, 398-421.	5.7	17
31	The Soybean High Density "Forrest" by "Williams 82" SNP-Based Genetic Linkage Map Identifies QTL and Candidate Genes for Seed Isoflavone Content. <i>Plants</i> , 2021, 10, 2029.	3.5	10
32	Classification methods and identification of reniform nematode resistance in known soybean cyst nematode resistant soybean genotypes. <i>Plant Disease</i> , 2021, , .	1.4	3
33	Genetic characterization of qSCN10 from an exotic soybean accession PI 567516C reveals a novel source conferring broad-spectrum resistance to soybean cyst nematode. <i>Theoretical and Applied Genetics</i> , 2021, 134, 859-874.	3.6	10
34	A chickpea genetic variation map based on the sequencing of 3,366 genomes. <i>Nature</i> , 2021, 599, 622-627.	27.8	106
35	Characterization of Root System Architecture Traits in Diverse Soybean Genotypes Using a Semi-Hydroponic System. <i>Plants</i> , 2021, 10, 2781.	3.5	19
36	Direct Infusion Metabolomics of the Photosystem and Chlorophyll Related Metabolites within a Drought Tolerant Plant Introduction of <i>Glycine max</i> . <i>Metabolites</i> , 2021, 11, 843.	2.9	0

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37	The importance of slow canopy wilting in drought tolerance in soybean. <i>Journal of Experimental Botany</i> , 2020, 71, 642-652.	4.8	49
38	Impacts of genomic research on soybean improvement in East Asia. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1655-1678.	3.6	48
39	Whole-genome resequencing identifies quantitative trait loci associated with mycorrhizal colonization of soybean. <i>Theoretical and Applied Genetics</i> , 2020, 133, 409-417.	3.6	19
40	Genome-wide association mapping of flooding tolerance in soybean. <i>Molecular Breeding</i> , 2020, 40, 1.	2.1	25
41	Epigenetics and epigenomics: underlying mechanisms, relevance, and implications in crop improvement. <i>Functional and Integrative Genomics</i> , 2020, 20, 739-761.	3.5	37
42	Mobilizing Crop Biodiversity. <i>Molecular Plant</i> , 2020, 13, 1341-1344.	8.3	50
43	Mapping Quantitative Trait Loci for Soybean Seedling Shoot and Root Architecture Traits in an Inter-Specific Genetic Population. <i>Frontiers in Plant Science</i> , 2020, 11, 1284.	3.6	19
44	Analysis of Whole Transcriptome RNA-seq Data Reveals Many Alternative Splicing Events in Soybean Roots under Drought Stress Conditions. <i>Genes</i> , 2020, 11, 1520.	2.4	15
45	Classification of soybean leaf wilting due to drought stress using UAV-based imagery. <i>Computers and Electronics in Agriculture</i> , 2020, 175, 105576.	7.7	63
46	Trait associations in the pangenome of pigeon pea (<i>Cajanus cajan</i>). <i>Plant Biotechnology Journal</i> , 2020, 18, 1946-1954.	8.3	79
47	Registration of 'S14' soybean, a high-yielding RR1 cultivar with high oil content and broad disease resistance and adaptation. <i>Journal of Plant Registrations</i> , 2020, 14, 35-42.	0.5	9
48	Molecular and genetic bases of heat stress responses in crop plants and breeding for increased resilience and productivity. <i>Journal of Experimental Botany</i> , 2020, 71, 3780-3802.	4.8	186
49	Breeding and Molecular Approaches for Evolving Drought-Tolerant Soybeans. , 2020, , 83-130.		3
50	Reproductive success of soybean (<i>Glycine max</i> L. Merrill) cultivars and exotic lines under high daytime temperature. <i>Plant, Cell and Environment</i> , 2019, 42, 321-336.	5.7	33
51	Understanding genetic control of root system architecture in soybean: Insights into the genetic basis of lateral root number. <i>Plant, Cell and Environment</i> , 2019, 42, 212-229.	5.7	36
52	Avenues of the membrane transport system in adaptation of plants to abiotic stresses. <i>Critical Reviews in Biotechnology</i> , 2019, 39, 861-883.	9.0	53
53	Construction and comparison of three reference-quality genome assemblies for soybean. <i>Plant Journal</i> , 2019, 100, 1066-1082.	5.7	113
54	Quantifying Variation in Soybean Due to Flood Using a Low-Cost 3D Imaging System. <i>Sensors</i> , 2019, 19, 2682.	3.8	11

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55	Genome-wide transcriptional profiling for elucidating the effects of brassinosteroids on <i>Glycine max</i> during early vegetative development. <i>Scientific Reports</i> , 2019, 9, 16085.	3.3	12
56	Whole-genome resequencing reveals the impact of the interaction of copy number variants of the <i>rhg1</i> and <i>Rhg4</i> genes on broad-based resistance to soybean cyst nematode. <i>Plant Biotechnology Journal</i> , 2019, 17, 1595-1611.	8.3	65
57	Resequencing of 429 chickpea accessions from 45 countries provides insights into genome diversity, domestication and agronomic traits. <i>Nature Genetics</i> , 2019, 51, 857-864.	21.4	219
58	Automated segmentation of soybean plants from 3D point cloud using machine learning. <i>Computers and Electronics in Agriculture</i> , 2019, 162, 143-153.	7.7	50
59	Identification of new loci for salt tolerance in soybean by high-resolution genome-wide association mapping. <i>BMC Genomics</i> , 2019, 20, 318.	2.8	46
60	Registration of "S11-20124"™ Soybean with High Yield Potential, Multiple Nematode Resistance, and Salt Tolerance. <i>Journal of Plant Registrations</i> , 2019, 13, 154-160.	0.5	14
61	A reference-grade wild soybean genome. <i>Nature Communications</i> , 2019, 10, 1216.	12.8	183
62	GmBZL3 acts as a major BR signaling regulator through crosstalk with multiple pathways in <i>Glycine max</i> . <i>BMC Plant Biology</i> , 2019, 19, 86.	3.6	10
63	Genome reorganization of the GmSHMT gene family in soybean showed a lack of functional redundancy in resistance to soybean cyst nematode. <i>Scientific Reports</i> , 2019, 9, 1506.	3.3	24
64	Approaches, Applicability, and Challenges for Development of Climate-Smart Soybean. , 2019, , 1-74.		7
65	Progress Toward Development of Climate-Smart Flax: A Perspective on Omics-Assisted Breeding. , 2019, , 239-274.		10
66	Assessment of Phenotypic Variations and Correlation among Seed Composition Traits in Mutagenized Soybean Populations. <i>Genes</i> , 2019, 10, 975.	2.4	18
67	Legumesâ€”The art and science of environmentally sustainable agriculture. <i>Plant, Cell and Environment</i> , 2019, 42, 1-5.	5.7	28
68	Molecular characterization of genomic regions for resistance to <i>Pythium ultimum</i> var. <i>ultimum</i> in the soybean cultivar Magellan. <i>Theoretical and Applied Genetics</i> , 2019, 132, 405-417.	3.6	25
69	Modelling predicts that soybean is poised to dominate crop production across Africa. <i>Plant, Cell and Environment</i> , 2019, 42, 373-385.	5.7	47
70	Characterization of Select Wild Soybean Accessions in the USDA Germplasm Collection for Seed Composition and Agronomic Traits. <i>Crop Science</i> , 2019, 59, 233-251.	1.8	29
71	Adapting legume crops to climate change using genomic approaches. <i>Plant, Cell and Environment</i> , 2019, 42, 6-19.	5.7	74
72	Genetic diversity of root system architecture in response to drought stress in grain legumes. <i>Journal of Experimental Botany</i> , 2018, 69, 3267-3277.	4.8	124

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73	A major natural genetic variation associated with root system architecture and plasticity improves waterlogging tolerance and yield in soybean. <i>Plant, Cell and Environment</i> , 2018, 41, 2169-2182.	5.7	47
74	Dissecting genomic hotspots underlying seed protein, oil, and sucrose content in an interspecific mapping population of soybean using high-density linkage mapping. <i>Plant Biotechnology Journal</i> , 2018, 16, 1939-1953.	8.3	93
75	Comparative genome analysis to identify SNPs associated with high oleic acid and elevated protein content in soybean. <i>Genome</i> , 2018, 61, 217-222.	2.0	6
76	Accelerating genetic gains in legumes for the development of prosperous smallholder agriculture: integrating genomics, phenotyping, systems modelling and agronomy. <i>Journal of Experimental Botany</i> , 2018, 69, 3293-3312.	4.8	87
77	Mapping and confirmation of loci for salt tolerance in a novel soybean germplasm, Fiskeby III. <i>Theoretical and Applied Genetics</i> , 2018, 131, 513-524.	3.6	42
78	Prediction of Soybean Root Response in the Field Using Nondestructive Seedling Three-Dimensional Root Features. <i>The Plant Phenome Journal</i> , 2018, 1, 1-15.	2.0	6
79	Evaluation of Soybean Germplasm for Resistance to Multiple Nematode Species: <i>Heterodera glycines</i> , <i>Meloidogyne incognita</i> , and <i>Rotylenchulus reniformis</i> . <i>Crop Science</i> , 2018, 58, 2511-2522.	1.8	21
80	Characterization of the XTH Gene Family: New Insight to the Roles in Soybean Flooding Tolerance. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2705.	4.1	47
81	Heat in Wheat: Exploit Reverse Genetic Techniques to Discover New Alleles Within the <i>Triticum durum</i> sHsp26 Family. <i>Frontiers in Plant Science</i> , 2018, 9, 1337.	3.6	38
82	Advances in Genetics and Breeding of Salt Tolerance in Soybean. , 2018, , 217-237.		4
83	Identification of drought-inducible regulatory factors in <i>Lablab purpureus</i> by a comparative genomic approach. <i>Crop and Pasture Science</i> , 2018, 69, 632.	1.5	7
84	Development of an automated phenotyping platform for quantifying soybean dynamic responses to salinity stress in greenhouse environment. <i>Computers and Electronics in Agriculture</i> , 2018, 151, 319-330.	7.7	33
85	A seed change in our understanding of legume biology from genomics to the efficient cooperation between nodulation and arbuscular mycorrhizal fungi. <i>Plant, Cell and Environment</i> , 2018, 41, 1949-1954.	5.7	3
86	Genetic diversity and genomic strategies for improving drought and waterlogging tolerance in soybeans. <i>Journal of Experimental Botany</i> , 2017, 68, erw433.	4.8	118
87	Root xylem plasticity to improve water use and yield in water-stressed soybean. <i>Journal of Experimental Botany</i> , 2017, 68, erw472.	4.8	81
88	Genetic mapping and haplotype analysis of a locus for quantitative resistance to <i>Fusarium graminearum</i> in soybean accession PI 567516C. <i>Theoretical and Applied Genetics</i> , 2017, 130, 999-1010.	3.6	35
89	From Hype to Hope: Genome-Wide Association Studies in Soybean. <i>Compendium of Plant Genomes</i> , 2017, , 95-109.	0.5	0
90	Molecular mapping and genomics of soybean seed protein: a review and perspective for the future. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1975-1991.	3.6	160

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91	Evaluation and development of flood-tolerant soybean cultivars. <i>Plant Breeding</i> , 2017, 136, 913-923.	1.9	19
92	Ultrasound Accuracy in Diagnosing Appendicitis in Obese Pediatric Patients. <i>American Surgeon</i> , 2017, 83, 1063-1067.	0.8	6
93	Drought Stress Causes a Reduction in the Biosynthesis of Ascorbic Acid in Soybean Plants. <i>Frontiers in Plant Science</i> , 2017, 8, 1042.	3.6	75
94	Editorial: Aquaporins: Dynamic Role and Regulation. <i>Frontiers in Plant Science</i> , 2017, 8, 1420.	3.6	28
95	Development of SNP Genotyping Assays for Seed Composition Traits in Soybean. <i>International Journal of Plant Genomics</i> , 2017, 2017, 1-12.	2.2	34
96	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
97	Comprehensive Analysis of the Soybean (<i>Glycine max</i>) GmLAX Auxin Transporter Gene Family. <i>Frontiers in Plant Science</i> , 2016, 7, 282.	3.6	18
98	Identification and Comparative Analysis of Differential Gene Expression in Soybean Leaf Tissue under Drought and Flooding Stress Revealed by RNA-Seq. <i>Frontiers in Plant Science</i> , 2016, 7, 1044.	3.6	116
99	Soybean TIP Gene Family Analysis and Characterization of GmTIP1;5 and GmTIP2;5 Water Transport Activity. <i>Frontiers in Plant Science</i> , 2016, 7, 1564.	3.6	30
100	Evaluation of high yielding soybean germplasm under water limitation. <i>Journal of Integrative Plant Biology</i> , 2016, 58, 475-491.	8.5	29
101	Landscape of genomic diversity and trait discovery in soybean. <i>Scientific Reports</i> , 2016, 6, 23598.	3.3	151
102	Small RNA profiles in soybean primary root tips under water deficit. <i>BMC Systems Biology</i> , 2016, 10, 126.	3.0	33
103	Genomic-assisted haplotype analysis and the development of high-throughput SNP markers for salinity tolerance in soybean. <i>Scientific Reports</i> , 2016, 6, 19199.	3.3	161
104	Genome-wide transcriptome analysis of soybean primary root under varying water-deficit conditions. <i>BMC Genomics</i> , 2016, 17, 57.	2.8	99
105	Global agricultural intensification during climate change: a role for genomics. <i>Plant Biotechnology Journal</i> , 2016, 14, 1095-1098.	8.3	221
106	Novel constructs for efficient cloning of sRNA-encoding DNA and uniform silencing of plant genes employing artificial trans-acting small interfering RNA. <i>Plant Cell Reports</i> , 2016, 35, 2137-2150.	5.6	7
107	Genetic analysis of shoot fresh weight in a cross of wild (<i>G. soja</i>) and cultivated (<i>G. max</i>) soybean. <i>Molecular Breeding</i> , 2016, 36, 1.	2.1	16
108	Advancements in breeding, genetics, and genomics for resistance to three nematode species in soybean. <i>Theoretical and Applied Genetics</i> , 2016, 129, 2295-2311.	3.6	44

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109	Neglecting legumes has compromised human health and sustainable food production. <i>Nature Plants</i> , 2016, 2, 16112.	9.3	529
110	PGen: large-scale genomic variations analysis workflow and browser in SoyKB. <i>BMC Bioinformatics</i> , 2016, 17, 337.	2.6	27
111	Evaluation of genetic variation among Brazilian soybean cultivars through genome resequencing. <i>BMC Genomics</i> , 2016, 17, 110.	2.8	43
112	Genomic-assisted phylogenetic analysis and marker development for next generation soybean cyst nematode resistance breeding. <i>Plant Science</i> , 2016, 242, 342-350.	3.6	78
113	Application of Digital PCR in the Analysis of Transgenic Soybean Plants. <i>Advances in Bioscience and Biotechnology (Print)</i> , 2016, 07, 403-417.	0.7	17
114	Prioritization of candidate genes in a QTL-hotspot region for drought tolerance in chickpea (<i>Cicer</i>) Tj ETQq0 0.0 r gBT /Overlock 10	3.3	131
115	Genome-wide analysis and expression profiling of the PIN auxin transporter gene family in soybean (<i>Glycine max</i>). <i>BMC Genomics</i> , 2015, 16, 951.	2.8	55
116	A Bayesian model for detection of high-order interactions among genetic variants in genome-wide association studies. <i>BMC Genomics</i> , 2015, 16, 1011.	2.8	31
117	Application of genomics-assisted breeding for generation of climate resilient crops: progress and prospects. <i>Frontiers in Plant Science</i> , 2015, 6, 563.	3.6	243
118	Identification of Novel QTL Governing Root Architectural Traits in an Interspecific Soybean Population. <i>PLoS ONE</i> , 2015, 10, e0120490.	2.5	75
119	Comparative analysis of endogenous hormones level in two soybean (<i>Glycine max</i> L.) lines differing in waterlogging tolerance. <i>Frontiers in Plant Science</i> , 2015, 6, 714.	3.6	107
120	Expanding Omics Resources for Improvement of Soybean Seed Composition Traits. <i>Frontiers in Plant Science</i> , 2015, 6, 1021.	3.6	105
121	A Simple Analytical Method for High-Throughput Screening of Major Sugars from Soybean by Normal-Phase HPLC with Evaporative Light Scattering Detection. <i>Chromatography Research International</i> , 2015, 2015, 1-8.	0.4	19
122	Genome-wide expression analysis of soybean NF-Y genes reveals potential function in development and drought response. <i>Molecular Genetics and Genomics</i> , 2015, 290, 1095-1115.	2.1	85
123	Genotyping-by-sequencing based intra-specific genetic map refines a QTL-hotspot region for drought tolerance in chickpea. <i>Molecular Genetics and Genomics</i> , 2015, 290, 559-571.	2.1	180
124	Whole-genome gene expression profiling revealed genes and pathways potentially involved in regulating interactions of soybean with cyst nematode (<i>Heterodera glycines</i> Ichinohe). <i>BMC Genomics</i> , 2015, 16, 148.	2.8	43
125	Genetic variants in root architecture-related genes in a <i>Glycine soja</i> accession, a potential resource to improve cultivated soybean. <i>BMC Genomics</i> , 2015, 16, 132.	2.8	67
126	Soybean (<i>Glycine max</i>) SWEET gene family: insights through comparative genomics, transcriptome profiling and whole genome re-sequence analysis. <i>BMC Genomics</i> , 2015, 16, 520.	2.8	173

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127	Identification of quantitative trait loci underlying resistance to southern root-knot and reniform nematodes in soybean accession PI 567516C. <i>Molecular Breeding</i> , 2015, 35, 131.	2.1	34
128	Identification and characterization of a stachyose synthase gene controlling reduced stachyose content in soybean. <i>Theoretical and Applied Genetics</i> , 2015, 128, 2167-2176.	3.6	28
129	High-throughput and functional SNP detection assays for oleic and linolenic acids in soybean. <i>Molecular Breeding</i> , 2015, 35, 1.	2.1	20
130	Soybean transcription factor ORFeome associated with drought resistance: a valuable resource to accelerate research on abiotic stress resistance. <i>BMC Genomics</i> , 2015, 16, 596.	2.8	17
131	Core clock, <i>SUB1</i> , and <i>ABAR</i> genes mediate flooding and drought responses via alternative splicing in soybean. <i>Journal of Experimental Botany</i> , 2015, 66, 7129-7149.	4.8	52
132	Comparative analysis of the drought-responsive transcriptome in soybean lines contrasting for canopy wilting. <i>Plant Science</i> , 2015, 240, 65-78.	3.6	53
133	Understanding abiotic stress tolerance mechanisms in soybean: A comparative evaluation of soybean response to drought and flooding stress. <i>Plant Physiology and Biochemistry</i> , 2015, 86, 109-120.	5.8	156
134	Identification and evaluation of quantitative trait loci underlying resistance to multiple HG types of soybean cyst nematode in soybean PI 437655. <i>Theoretical and Applied Genetics</i> , 2015, 128, 15-23.	3.6	33
135	A Sweetpotato Geranylgeranyl Pyrophosphate Synthase Gene, <i>IbGGPS</i> , Increases Carotenoid Content and Enhances Osmotic Stress Tolerance in <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , 2015, 10, e0137623.	2.5	48
136	Reaction of Soybean Cyst Nematode Resistant Plant Introductions to Root-Knot and Reniform Nematodes. <i>Plant Breeding and Biotechnology</i> , 2015, 3, 346-354.	0.9	12
137	Potential of Association Mapping and Genomic Selection to Explore PI 88788 Derived Soybean Cyst Nematode Resistance. <i>Plant Genome</i> , 2014, 7, plantgenome2013.11.0039.	2.8	63
138	Functional Analysis of Water Stress-Responsive Soybean <i>GmNAC003</i> and <i>GmNAC004</i> Transcription Factors in Lateral Root Development in <i>Arabidopsis</i> . <i>PLoS ONE</i> , 2014, 9, e84886.	2.5	46
139	Expression of Root-Related Transcription Factors Associated with Flooding Tolerance of Soybean (<i>Glycine max</i>). <i>International Journal of Molecular Sciences</i> , 2014, 15, 17622-17643.	4.1	55
140	An Atlas of Soybean Small RNAs Identifies Phased siRNAs from Hundreds of Coding Genes. <i>Plant Cell</i> , 2014, 26, 4584-4601.	6.6	163
141	Integrating omic approaches for abiotic stress tolerance in soybean. <i>Frontiers in Plant Science</i> , 2014, 5, 244.	3.6	213
142	Soybean knowledge base (SoyKB): a web resource for integration of soybean translational genomics and molecular breeding. <i>Nucleic Acids Research</i> , 2014, 42, D1245-D1252.	14.5	102
143	Overexpression of <i>AtDREB1D</i> transcription factor improves drought tolerance in soybean. <i>Molecular Biology Reports</i> , 2014, 41, 7995-8008.	2.3	56
144	Identification of quantitative trait loci controlling linolenic acid concentration in PI483463 (<i>Glycine</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	3.6	28

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145	Two Soybean Plant Introductions Display Slow Leaf Wilting and Reduced Yield Loss under Drought. <i>Journal of Agronomy and Crop Science</i> , 2014, 200, 231-236.	3.5	53
146	Effect of High-oleic Acid Soybean on Seed Oil, Protein Concentration, and Yield. <i>Crop Science</i> , 2014, 54, 2054-2062.	1.8	16
147	Root Characters. , 2013, , 67-131.		11
148	Genomic differences between cultivated soybean, <i>G. max</i> and its wild relative <i>G. soja</i> . <i>BMC Genomics</i> , 2013, 14, S5.	2.8	30
149	Genetic mapping of quantitative trait loci conditioning salt tolerance in wild soybean (<i>Glycine soja</i>) PI 483463. <i>Euphytica</i> , 2013, 193, 79-88.	1.2	73
150	Molecular characterization of <i>Glycine max</i> squalene synthase genes in seed phytosterol biosynthesis. <i>Plant Physiology and Biochemistry</i> , 2013, 73, 23-32.	5.8	30
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