

# Henry T Nguyen

## List of Publications by Year in descending order

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251  
papers

20,669  
citations

10956

71  
h-index

12558

132  
g-index

262  
all docs

262  
docs citations

262  
times ranked

16328  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequence of the palaeopolyploid soybean. <i>Nature</i> , 2010, 463, 178-183.	13.7	3,854
2	Understanding regulatory networks and engineering for enhanced drought tolerance in plants. <i>Current Opinion in Plant Biology</i> , 2006, 9, 189-195.	3.5	695
3	Root growth maintenance during water deficits: physiology to functional genomics. <i>Journal of Experimental Botany</i> , 2004, 55, 2343-2351.	2.4	529
4	Neglecting legumes has compromised human health and sustainable food production. <i>Nature Plants</i> , 2016, 2, 16112.	4.7	529
5	Physiological and Molecular Approaches to Improve Drought Resistance in Soybean. <i>Plant and Cell Physiology</i> , 2009, 50, 1260-1276.	1.5	484
6	Comparative DNA Sequence Analysis of Wheat and Rice Genomes. <i>Genome Research</i> , 2003, 13, 1818-1827.	2.4	369
7	Molecular genetics of heat tolerance and heat shock proteins in cereals. <i>Plant Molecular Biology</i> , 2002, 48, 667-681.	2.0	303
8	The Organization and Rate of Evolution of Wheat Genomes Are Correlated With Recombination Rates Along Chromosome Arms. <i>Genome Research</i> , 2003, 13, 753-763.	2.4	298
9	Sorghum stay-green QTL individually reduce post-flowering drought-induced leaf senescence. <i>Journal of Experimental Botany</i> , 2006, 58, 327-338.	2.4	286
10	Breeding for Drought Resistance in Rice: Physiology and Molecular Genetics Considerations. <i>Crop Science</i> , 1997, 37, 1426-1434.	0.8	282
11	Genetic Analysis of Drought Resistance in Rice by Molecular Markers. <i>Crop Science</i> , 2003, 43, 1457-1469.	0.8	276
12	Application of genomics-assisted breeding for generation of climate resilient crops: progress and prospects. <i>Frontiers in Plant Science</i> , 2015, 6, 563.	1.7	243
13	Leaf Water Content and Gas Exchange Parameters of Two Wheat Genotypes Differing in Drought Resistance. <i>Crop Science</i> , 1990, 30, 105-111.	0.8	223
14	Global agricultural intensification during climate change: a role for genomics. <i>Plant Biotechnology Journal</i> , 2016, 14, 1095-1098.	4.1	221
15	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.	9.4	219
16	Integrating omic approaches for abiotic stress tolerance in soybean. <i>Frontiers in Plant Science</i> , 2014, 5, 244.	1.7	213
17	Cell Wall Proteome in the Maize Primary Root Elongation Zone. II. Region-Specific Changes in Water Soluble and Lightly Ionically Bound Proteins under Water Deficit. <i>Plant Physiology</i> , 2007, 145, 1533-1548.	2.3	196
18	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.	2.4	186

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19	A reference-grade wild soybean genome. <i>Nature Communications</i> , 2019, 10, 1216.	5.8	183
20	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.	1.0	180
21	Soybean ( <i>Glycine max</i> ) SWEET gene family: insights through comparative genomics, transcriptome profiling and whole genome re-sequencing analysis. <i>BMC Genomics</i> , 2015, 16, 520.	1.2	173
22	Identification and mapping of the QTL for aluminum tolerance introgressed from the new source, <i>ORYZA RUFIPOGON</i> Griff., into indica rice ( <i>Oryza sativa</i> L.). <i>Theoretical and Applied Genetics</i> , 2003, 106, 583-593.	1.8	171
23	An Atlas of Soybean Small RNAs Identifies Phased siRNAs from Hundreds of Coding Genes. <i>Plant Cell</i> , 2014, 26, 4584-4601.	3.1	163
24	Genomic-assisted haplotype analysis and the development of high-throughput SNP markers for salinity tolerance in soybean. <i>Scientific Reports</i> , 2016, 6, 19199.	1.6	161
25	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.	1.8	160
26	Synteny perturbations between wheat homoeologous chromosomes caused by locus duplications and deletions correlate with recombination rates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 10836-10841.	3.3	159
27	Molecular Evolution of Lysin Motif-Type Receptor-Like Kinases in Plants. <i>Plant Physiology</i> , 2007, 144, 623-636.	2.3	159
28	Regulation of growth response to water stress in the soybean primary root. I. Proteomic analysis reveals region-specific regulation of phenylpropanoid metabolism and control of free iron in the elongation zone. <i>Plant, Cell and Environment</i> , 2010, 33, 223-243.	2.8	158
29	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.	2.8	156
30	Landscape of genomic diversity and trait discovery in soybean. <i>Scientific Reports</i> , 2016, 6, 23598.	1.6	151
31	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.	0.8	146
32	Molecular characterization of stress-inducible GmNAC genes in soybean. <i>Molecular Genetics and Genomics</i> , 2009, 281, 647-664.	1.0	138
33	Quantitative trait loci for root-penetration ability and root thickness in rice: Comparison of genetic backgrounds. <i>Genome</i> , 2000, 43, 53-61.	0.9	134
34	Silencing of GmFAD3 gene by siRNA leads to low $\hat{\pm}$ -linolenic acids (18:3) of fad3-mutant phenotype in soybean [ <i>Glycine max</i> (Merr.)]. <i>Transgenic Research</i> , 2008, 17, 839-850.	1.3	132
35	Prioritization of candidate genes in a QTL-hotspot region for drought tolerance in chickpea ( <i>Cicer</i> ) Tj ETQq1 1,0,784314,rgBT/O	1.6	131
36	Quantitative Phosphoproteomic Analysis of Soybean Root Hairs Inoculated with <i>Bradyrhizobium japonicum</i> . <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1140-1155.	2.5	126

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37	Use of Waxâ€etrolatum Layers for Screening Rice Root Penetration. <i>Crop Science</i> , 1995, 35, 684-687.	0.8	125
38	Genetic diversity of root system architecture in response to drought stress in grain legumes. <i>Journal of Experimental Botany</i> , 2018, 69, 3267-3277.	2.4	124
39	Use of RAPD markers to determine the genetic diversity of diploid, wheat genotypes. <i>Theoretical and Applied Genetics</i> , 1992, 84-84, 835-838.	1.8	122
40	QTL, additive and epistatic effects for SCN resistance in PI 437654. <i>Theoretical and Applied Genetics</i> , 2009, 118, 1093-1105.	1.8	118
41	Genetic diversity and genomic strategies for improving drought and waterlogging tolerance in soybeans. <i>Journal of Experimental Botany</i> , 2017, 68, erw433.	2.4	118
42	Heat Shock Protein Synthesis and Thermal Tolerance in Wheat. <i>Plant Physiology</i> , 1989, 90, 140-145.	2.3	117
43	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.	1.7	116
44	Evaluation of Candidate Reference Genes for Normalization of Quantitative RT-PCR in Soybean Tissues under Various Abiotic Stress Conditions. <i>PLoS ONE</i> , 2012, 7, e46487.	1.1	115
45	Pinpointing genes underlying the quantitative trait loci for root-knot nematode resistance in palaeopolyploid soybean by whole genome resequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 13469-13474.	3.3	113
46	Construction and comparison of three referenceâ€quality genome assemblies for soybean. <i>Plant Journal</i> , 2019, 100, 1066-1082.	2.8	113
47	Comparison of Measurement Methods of Osmotic Adjustment in Rice Cultivars. <i>Crop Science</i> , 1999, 39, 150-158.	0.8	109
48	RNAi-mediated disruption of squalene synthase improves drought tolerance and yield in rice. <i>Journal of Experimental Botany</i> , 2012, 63, 163-175.	2.4	108
49	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.	1.7	107
50	A chickpea genetic variation map based on the sequencing of 3,366 genomes. <i>Nature</i> , 2021, 599, 622-627.	13.7	106
51	Expanding Omics Resources for Improvement of Soybean Seed Composition Traits. <i>Frontiers in Plant Science</i> , 2015, 6, 1021.	1.7	105
52	SoyDB: a knowledge database of soybean transcription factors. <i>BMC Plant Biology</i> , 2010, 10, 14.	1.6	104
53	Expression profiling of rice segregating for drought tolerance QTLs using a rice genome array. <i>Functional and Integrative Genomics</i> , 2005, 5, 104-116.	1.4	103
54	Heat tolerance in spring wheat. I. Estimating cellular thermotolerance and its heritability. <i>Euphytica</i> , 1998, 104, 1-8.	0.6	102

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55	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.	6.5	102
56	Genome-wide transcriptome analysis of soybean primary root under varying water-deficit conditions. <i>BMC Genomics</i> , 2016, 17, 57.	1.2	99
57	Novel quantitative trait loci for broad-based resistance to soybean cyst nematode ( <i>Heterodera</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.8	98
58	Differential Expression of Isoflavone Biosynthetic Genes in Soybean During Water Deficits. <i>Plant and Cell Physiology</i> , 2010, 51, 936-948.	1.5	98
59	Mapping of Quantitative Trait Loci Associated with Resistance to <i>Phytophthora sojae</i> and Flooding Tolerance in Soybean. <i>Crop Science</i> , 2012, 52, 2481-2493.	0.8	96
60	SNP discovery by high-throughput sequencing in soybean. <i>BMC Genomics</i> , 2010, 11, 469.	1.2	94
61	Soybean Knowledge Base (SoyKB): a web resource for soybean translational genomics. <i>BMC Genomics</i> , 2012, 13, S15.	1.2	93
62	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.	4.1	93
63	RAPD (random amplified polymorphic DNA) analysis based intervarietal genetic relationships among hexaploid wheats. <i>Plant Science</i> , 1993, 93, 95-103.	1.7	91
64	Genomic resources in plant breeding for sustainable agriculture. <i>Journal of Plant Physiology</i> , 2021, 257, 153351.	1.6	90
65	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.	2.4	87
66	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.	1.0	85
67	Inheritance of the Stay Green Trait in Sorghum. <i>Crop Science</i> , 1994, 34, 970-972.	0.8	81
68	Establishment of a soybean ( <i>Glycine max</i> Merr. L) transposon-based mutagenesis repository. <i>Planta</i> , 2009, 229, 279-289.	1.6	81
69	Root xylem plasticity to improve water use and yield in water-stressed soybean. <i>Journal of Experimental Botany</i> , 2017, 68, erw472.	2.4	81
70	Genetic analysis of osmotic adjustment in crop plants. , 0, .		80
71	Trait associations in the pangenome of pigeon pea ( <i>Cajanus cajan</i> ). <i>Plant Biotechnology Journal</i> , 2020, 18, 1946-1954.	4.1	79
72	Genomic-assisted phylogenetic analysis and marker development for next generation soybean cyst nematode resistance breeding. <i>Plant Science</i> , 2016, 242, 342-350.	1.7	78

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73	Inheritance of Salt Tolerance in Wild Soybean ( <i>Glycine soja</i> Sieb. and Zucc.) Accession PI483463. <i>Journal of Heredity</i> , 2009, 100, 798-801.	1.0	77
74	Identification of Novel QTL Governing Root Architectural Traits in an Interspecific Soybean Population. <i>PLoS ONE</i> , 2015, 10, e0120490.	1.1	75
75	Drought Stress Causes a Reduction in the Biosynthesis of Ascorbic Acid in Soybean Plants. <i>Frontiers in Plant Science</i> , 2017, 8, 1042.	1.7	75
76	Adapting legume crops to climate change using genomic approaches. <i>Plant, Cell and Environment</i> , 2019, 42, 6-19.	2.8	74
77	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.	0.6	73
78	Genetic control of soybean seed isoflavone content: importance of statistical model and epistasis in complex traits. <i>Theoretical and Applied Genetics</i> , 2009, 119, 1069-1083.	1.8	67
79	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.	1.2	67
80	Sorghum Expressed Sequence Tags Identify Signature Genes for Drought, Pathogenesis, and Skotomorphogenesis from a Milestone Set of 16,801 Unique Transcripts. <i>Plant Physiology</i> , 2005, 139, 869-884.	2.3	66
81	Whole-genome re-sequencing 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.	4.1	65
82	Diversity among germplasm lines of the Ethiopian cereal tef [ <i>Eragrostis tef</i> (Zucc.) Trotter]. <i>Euphytica</i> , 1999, 106, 87-97.	0.6	63
83	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.	1.6	63
84	Classification of soybean leaf wilting due to drought stress using UAV-based imagery. <i>Computers and Electronics in Agriculture</i> , 2020, 175, 105576.	3.7	63
85	Heat tolerance in spring wheat. II. Grain filling. <i>Euphytica</i> , 1998, 104, 9-15.	0.6	61
86	Genetic engineering for abiotic stress resistance in crop plants. <i>In Vitro Cellular and Developmental Biology - Plant</i> , 2000, 36, 108-114.	0.9	61
87	Major locus and other novel additive and epistatic loci involved in modulation of isoflavone concentration in soybean seeds. <i>Theoretical and Applied Genetics</i> , 2011, 123, 1375-1385.	1.8	60
88	Large-Scale Analysis of Putative Soybean Regulatory Gene Expression Identifies a <i>Myb</i> Gene Involved in Soybean Nodule Development. <i>Plant Physiology</i> , 2009, 151, 1207-1220.	2.3	58
89	Single Feature Polymorphism Discovery in Rice. <i>PLoS ONE</i> , 2007, 2, e284.	1.1	57
90	Two MATE proteins play a role in iron efficiency in soybean. <i>Journal of Plant Physiology</i> , 2009, 166, 1453-1459.	1.6	56

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91	Overexpression of AtDREB1D transcription factor improves drought tolerance in soybean. <i>Molecular Biology Reports</i> , 2014, 41, 7995-8008.	1.0	56
92	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.	1.8	55
93	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.	1.2	55
94	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.	1.7	53
95	Comparative analysis of the drought-responsive transcriptome in soybean lines contrasting for canopy wilting. <i>Plant Science</i> , 2015, 240, 65-78.	1.7	53
96	Avenues of the membrane transport system in adaptation of plants to abiotic stresses. <i>Critical Reviews in Biotechnology</i> , 2019, 39, 861-883.	5.1	53
97	Sequencing the USDA core soybean collection reveals gene loss during domestication and breeding. <i>Plant Genome</i> , 2022, 15, e20109.	1.6	53
98	Evaluation of diverse soybean germplasm for root growth and architecture. <i>Plant and Soil</i> , 2010, 330, 503-514.	1.8	52
99	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.	2.4	52
100	Automated segmentation of soybean plants from 3D point cloud using machine learning. <i>Computers and Electronics in Agriculture</i> , 2019, 162, 143-153.	3.7	50
101	Mobilizing Crop Biodiversity. <i>Molecular Plant</i> , 2020, 13, 1341-1344.	3.9	50
102	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.	1.9	50
103	The importance of slow canopy wilting in drought tolerance in soybean. <i>Journal of Experimental Botany</i> , 2020, 71, 642-652.	2.4	49
104	Impacts of genomic research on soybean improvement in East Asia. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1655-1678.	1.8	48
105	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.	4.1	48
106	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.	1.1	48
107	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.	2.8	47
108	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.	1.8	47

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109	Modelling predicts that soybean is poised to dominate crop production across Africa. <i>Plant, Cell and Environment</i> , 2019, 42, 373-385.	2.8	47
110	Functional Analysis of Water Stress-Responsive Soybean GmNAC003 and GmNAC004 Transcription Factors in Lateral Root Development in Arabidopsis. <i>PLoS ONE</i> , 2014, 9, e84886.	1.1	46
111	Identification of new loci for salt tolerance in soybean by high-resolution genome-wide association mapping. <i>BMC Genomics</i> , 2019, 20, 318.	1.2	46
112	Recent Advances in Breeding For Drought and Salt Stress Tolerance in Soybean. , 2007, , 739-773.		45
113	Advancements in breeding, genetics, and genomics for resistance to three nematode species in soybean. <i>Theoretical and Applied Genetics</i> , 2016, 129, 2295-2311.	1.8	44
114	Heat Shock Protein Gene Expression in Diploid Wheat Genotypes Differing in Thermal Tolerance. <i>Crop Science</i> , 1992, 32, 370-377.	0.8	43
115	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.	1.2	43
116	Evaluation of genetic variation among Brazilian soybean cultivars through genome resequencing. <i>BMC Genomics</i> , 2016, 17, 110.	1.2	43
117	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.	1.8	42
118	Breeding for disease resistance in soybean: a global perspective. <i>Theoretical and Applied Genetics</i> , 2022, 135, 3773-3872.	1.8	42
119	Cloning, functional expression and phylogenetic analysis of plant sterol 24C-methyltransferases involved in sitosterol biosynthesis. <i>Phytochemistry</i> , 2009, 70, 1982-1998.	1.4	40
120	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.	1.7	38
121	Genetic variation among 481 diverse soybean accessions, inferred from genomic re-sequencing. <i>Scientific Data</i> , 2021, 8, 50.	2.4	38
122	Primary Root Elongation Rate and Abscisic Acid Levels of Maize in Response to Water Stress. <i>Crop Science</i> , 2011, 51, 157-172.	0.8	37
123	Higher Plant Cytochrome b5 Polypeptides Modulate Fatty Acid Desaturation. <i>PLoS ONE</i> , 2012, 7, e31370.	1.1	37
124	Epigenetics and epigenomics: underlying mechanisms, relevance, and implications in crop improvement. <i>Functional and Integrative Genomics</i> , 2020, 20, 739-761.	1.4	37
125	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.	2.8	36
126	5' untranslated leader sequences of eukaryotic mRNAs encoding heat shock induced proteins. <i>Nucleic Acids Research</i> , 1995, 23, 541-549.	6.5	35



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127	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.	1.8	35
128	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.	1.0	34
129	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
130	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.	1.8	33
131	Small RNA profiles in soybean primary root tips under water deficit. <i>BMC Systems Biology</i> , 2016, 10, 126.	3.0	33
132	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.	3.7	33
133	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.	2.8	33
134	Pangenomics in crop improvement—from coding structural variations to finding regulatory variants with pangenome graphs. <i>Plant Genome</i> , 2022, 15, e20177.	1.6	33
135	A novel approach for efficient plant regeneration from long-term suspension culture of wheat. <i>Plant Cell Reports</i> , 1990, 8, 639-642.	2.8	32
136	Amplified Fragment Length Polymorphism Analysis of Tef [ <i>Eragrostis tef</i> (Zucc.) Trotter]. <i>Crop Science</i> , 1999, 39, 819-824.	0.8	31
137	Genetic Characterization of two <i>Eragrostis</i> Species using AFLP and Morphological Traits. <i>Hereditas</i> , 2004, 130, 33-40.	0.5	31
138	A Bayesian model for detection of high-order interactions among genetic variants in genome-wide association studies. <i>BMC Genomics</i> , 2015, 16, 1011.	1.2	31
139	Genomic differences between cultivated soybean, <i>G. max</i> and its wild relative <i>G. soja</i> . <i>BMC Genomics</i> , 2013, 14, S5.	1.2	30
140	Molecular characterization of <i>Glycine max</i> squalene synthase genes in seed phytosterol biosynthesis. <i>Plant Physiology and Biochemistry</i> , 2013, 73, 23-32.	2.8	30
141	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.	1.7	30
142	Effects of water deficit on gas-exchange parameters and ribulose 1,5-bisphosphate carboxylase activation in wheat. <i>Environmental and Experimental Botany</i> , 1992, 32, 403-410.	2.0	29
143	Title is missing!. <i>Euphytica</i> , 2000, 112, 15-22.	0.6	29
144	Evaluation of high yielding soybean germplasm under water limitation. <i>Journal of Integrative Plant Biology</i> , 2016, 58, 475-491.	4.1	29

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145	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.	0.8	29
146	Quantifying Acquired Thermal Tolerance in Winter Wheat. <i>Crop Science</i> , 1994, 34, 1686-1689.	0.8	28
147	Differential display-mediated rapid identification of different members of a multigene family, HSP16.9 in wheat. <i>Plant Molecular Biology</i> , 1996, 31, 575-584.	2.0	28
148	Diversity for osmotic adjustment and root depth in TEF [ <i>Eragrostis tef</i> (Zucc) Trotter]. <i>Euphytica</i> , 2001, 121, 237-249.	0.6	28
149	Identification of quantitative trait loci controlling linolenic acid concentration in PI483463 ( <i>Glycine</i> ) Tj ETQq1 1 0.784314 rgBT/Overl	1.8	28
150	Identification and characterization of a stachyose synthase gene controlling reduced stachyose content in soybean. <i>Theoretical and Applied Genetics</i> , 2015, 128, 2167-2176.	1.8	28
151	Editorial: Aquaporins: Dynamic Role and Regulation. <i>Frontiers in Plant Science</i> , 2017, 8, 1420.	1.7	28
152	Legumesâ€”The art and science of environmentally sustainable agriculture. <i>Plant, Cell and Environment</i> , 2019, 42, 1-5.	2.8	28
153	A <i>Triticum aestivum</i> cDNA clone encoding a low-molecular-weight heat shock protein. <i>Plant Molecular Biology</i> , 1991, 17, 273-275.	2.0	27
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