

# Junyi Gai

## List of Publications by Year in descending order

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109  
papers

3,008  
citations

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docs citations

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2470  
citing authors

| #  | ARTICLE  | IF  | CITATIONS |
|----|--|-----|-----------|
| 1  | Discovery and characterization of differentially expressed soybean miRNAs and their targets during soybean mosaic virus infection unveils novel insight into Soybean-SMV interaction. BMC Genomics, 2022, 23, 171.                     | 2.8 | 1         |
| 2  | Evolutionary Variation of Accumulative Day Length and Accumulative Active Temperature Required for Growth Periods in Global Soybeans. Agronomy, 2022, 12, 962.   | 3.0 | 2         |
| 3  | Mapping Locus R and predicting candidate gene resistant to Soybean mosaic virus strain SC11 through linkage analysis combined with genome resequencing of the parents in soybean. Genomics, 2022, , 110387.                            | 2.9 | 2         |
| 4  | Evolutionary QTL-allele changes in main stem node number among geographic and seasonal subpopulations of Chinese cultivated soybeans. Molecular Genetics and Genomics, 2021, 296, 313-330.   | 2.1 | 5         |
| 5  | Identifying Wild Versus Cultivated Gene-Alleles Conferring Seed Coat Color and Days to Flowering in Soybean. International Journal of Molecular Sciences, 2021, 22, 1559.  | 4.1 | 6         |
| 6  | Comparative Analyses Reveal Peroxidases Play Important Roles in Soybean Tolerance to Aluminum Toxicity. Agronomy, 2021, 11, 670.   | 3.0 | 6         |
| 7  | The cloning and CRISPR/Cas9-mediated mutagenesis of a male sterility gene <i>MS1</i> of soybean. Plant Biotechnology Journal, 2021, 19, 1098-1100.   | 8.3 | 18        |
| 8  | Genetic dynamics of flowering date evolved from later to earlier in annual wild and cultivated soybean in China. Crop Science, 2021, 61, 2336-2354.  | 1.8 | 6         |
| 9  | QTL-allele system of main stem node number in recombinant inbred lines of soybean ( <i>Glycine max</i> ) using association versus linkage mapping. Plant Breeding, 2021, 140, 870.   | 1.9 | 4         |
| 10 | Confirmation of <i>GmPPR576</i> as a fertility restorer gene of cytoplasmic male sterility in soybean. Journal of Experimental Botany, 2021, 72, 7729-7742.  | 4.8 | 9         |
| 11 | Gm6PGDH1, a Cytosolic 6-Phosphogluconate Dehydrogenase, Enhanced Tolerance to Phosphate Starvation by Improving Root System Development and Modifying the Antioxidant System in Soybean. Frontiers in Plant Science, 2021, 12, 704983. | 3.6 | 4         |
| 12 | Transcription Factor GmWRKY46 Enhanced Phosphate Starvation Tolerance and Root Development in Transgenic Plants. Frontiers in Plant Science, 2021, 12, 700651.   | 3.6 | 10        |
| 13 | A small RNA of miR2119b from soybean CMS line acts as a negative regulator of male fertility in transgenic Arabidopsis. Plant Physiology and Biochemistry, 2021, 167, 210-221.   | 5.8 | 7         |
| 14 | Comparative analysis of mitochondrial genomes of soybean cytoplasmic male-sterile lines and their maintainer lines. Functional and Integrative Genomics, 2021, 21, 43-57.  | 3.5 | 8         |
| 15 | Natural variation in the promoter of <i>GsERD15B</i> affects salt tolerance in soybean. Plant Biotechnology Journal, 2021, 19, 1155-1169.  | 8.3 | 34        |
| 16 | Growth period QTL-allele constitution of global soybeans and its differential evolution changes in geographic adaptation versus maturity group extension. Plant Journal, 2021, 108, 1624-1643.   | 5.7 | 9         |
| 17 | Two TGA Transcription Factor Members from Hyper-Susceptible Soybean Exhibiting Significant Basal Resistance to Soybean mosaic virus. International Journal of Molecular Sciences, 2021, 22, 11329.                                     | 4.1 | 5         |
| 18 | Optimizing RNAi-Target by Nicotiana benthamiana-Soybean Mosaic Virus System Drives Broad Resistance to Soybean Mosaic Virus in Soybean. Frontiers in Plant Science, 2021, 12, 739971.  | 3.6 | 1         |

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|----|---|-----|-----------|
| 19 | Natural variation and selection in <i>GmSWEET39</i> affect soybean seed oil content. <i>New Phytologist</i> , 2020, 225, 1651-1666.   | 7.3 | 73        |
| 20 | Geographic differentiation and phylogeographic relationships among world soybean populations. <i>Crop Journal</i> , 2020, 8, 260-272.   | 5.2 | 16        |
| 21 | Comparative Transcriptomics Analysis and Functional Study Reveal Important Role of High-Temperature Stress Response Gene <i>GmHSFA2</i> During Flower Bud Development of CMS-Based F1 in Soybean. <i>Frontiers in Plant Science</i> , 2020, 11, 600217.   | 3.6 | 20        |
| 22 | The soybean U-box gene <i>GmPUB6</i> regulates drought tolerance in <i>Arabidopsis thaliana</i> . <i>Plant Physiology and Biochemistry</i> , 2020, 155, 284-296.  | 5.8 | 21        |
| 23 | Molecular characterization of QTL-allele system for drought tolerance at seedling stage and optimal genotype design using multi-locus multi-allele genome-wide association analysis in a half-sib population of soybean ( <i>Glycine max</i> (L.) Merr.). <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2020, 18, 295-306. | 0.8 | 3         |
| 24 | Identification of Additive and Epistatic QTLs Conferring Seed Traits in Soybean Using Recombinant Inbred Lines. <i>Frontiers in Plant Science</i> , 2020, 11, 566056.   | 3.6 | 10        |
| 25 | Bi-Phenotypic Trait May Be Conferred by Multiple Alleles in a Germplasm Population. <i>Frontiers in Genetics</i> , 2020, 11, 559.   | 2.3 | 4         |
| 26 | Comparative Transcriptome Analysis of Two Contrasting Soybean Varieties in Response to Aluminum Toxicity. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4316.  | 4.1 | 16        |
| 27 | miR156b from Soybean CMS Line Modulates Floral Organ Development. <i>Journal of Plant Biology</i> , 2020, 63, 141-153.  | 2.1 | 16        |
| 28 | Genetic dynamics of earlier maturity group emergence in south-to-north extension of Northeast China soybeans. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1839-1857.   | 3.6 | 12        |
| 29 | Exploring the QTL-allele constitution of main stem node number and its differentiation among maturity groups in a Northeast China soybean population. <i>Crop Science</i> , 2020, 60, 1223-1238.  | 1.8 | 12        |
| 30 | Double mutation of two homologous genes <i>YL1</i> and <i>YL2</i> results in a leaf yellowing phenotype in soybean [ <i>Glycine max</i> (L.) Merr.]. <i>Plant Molecular Biology</i> , 2020, 103, 527-543.   | 3.9 | 11        |
| 31 | Overexpression of Peroxidase Gene <i>GsPRX9</i> Confers Salt Tolerance in Soybean. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3745.   | 4.1 | 53        |
| 32 | Molecular mapping of a novel male-sterile gene <i>msNJ</i> in soybean [ <i>Glycine max</i> (L.) Merr.]. <i>Plant Reproduction</i> , 2019, 32, 371-380.  | 2.2 | 18        |
| 33 | Deciphering the Genetic Architecture of Plant Height in Soybean Using Two RIL Populations Sharing a Common M8206 Parent. <i>Plants</i> , 2019, 8, 373.  | 3.5 | 14        |
| 34 | Metabolomics Studies on Cytoplasmic Male Sterility during Flower Bud Development in Soybean. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2869.   | 4.1 | 28        |
| 35 | Using the RTM-GWAS procedure to detect the drought tolerance QTL-allele system at the seedling stage under sand culture in a half-sib population of soybean [ <i>Glycine max</i> (L.) Merr.]. <i>Canadian Journal of Plant Science</i> , 2019, 99, 801-814.   | 0.9 | 7         |
| 36 | <i>Agrobacterium rhizogenes</i> -induced soybean hairy roots versus Soybean mosaic virus (ARISHR-SMV) is an efficient pathosystem for studying soybean-virus interactions. <i>Plant Methods</i> , 2019, 15, 56.   | 4.3 | 7         |

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|----|---|-----|-----------|
| 37 | Dynamic Transcriptome Changes Related to Oil Accumulation in Developing Soybean Seeds. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2202.   | 4.1 | 26        |
| 38 | An efficient <i>Agrobacterium</i> -mediated soybean transformation method using green fluorescent protein as a selectable marker. <i>Plant Signaling and Behavior</i> , 2019, 14, 1612682.  | 2.4 | 14        |
| 39 | Differentiation and evolution among geographic and seasonal eco-populations of soybean germplasm in Southern China. <i>Crop and Pasture Science</i> , 2019, 70, 121.  | 1.5 | 2         |
| 40 | Genome-Wide Detection of Major and Epistatic Effect QTLs for Seed Protein and Oil Content in Soybean Under Multiple Environments Using High-Density Bin Map. <i>International Journal of Molecular Sciences</i> , 2019, 20, 979.      | 4.1 | 27        |
| 41 | Genetic Analysis and Gene Mapping for a Short-Petiole Mutant in Soybean ( <i>Glycine max</i> (L.) Merr.). <i>Agronomy</i> , 2019, 9, 709.   | 3.0 | 5         |
| 42 | Establishment of Plot-Yield Prediction Models in Soybean Breeding Programs Using UAV-Based Hyperspectral Remote Sensing. <i>Remote Sensing</i> , 2019, 11, 2752.  | 4.0 | 44        |
| 43 | Exploration of miRNA-mediated fertility regulation network of cytoplasmic male sterility during flower bud development in soybean. <i>3 Biotech</i> , 2019, 9, 22.  | 2.2 | 12        |
| 44 | GmWRKY45 Enhances Tolerance to Phosphate Starvation and Salt Stress, and Changes Fertility in Transgenic Arabidopsis. <i>Frontiers in Plant Science</i> , 2019, 10, 1714.   | 3.6 | 25        |
| 45 | Detecting the QTL-Allele System of Seed Oil Traits Using Multi-Locus Genome-Wide Association Analysis for Population Characterization and Optimal Cross Prediction in Soybean. <i>Frontiers in Plant Science</i> , 2018, 9, 1793.     | 3.6 | 19        |
| 46 | Comparative analysis of circular RNAs between soybean cytoplasmic male-sterile line NJCMS1A and its maintainer NJCMS1B by high-throughput sequencing. <i>BMC Genomics</i> , 2018, 19, 663.  | 2.8 | 35        |
| 47 | Genome-wide analysis of DNA methylation to identify genes and pathways associated with male sterility in soybean. <i>Molecular Breeding</i> , 2018, 38, 1.  | 2.1 | 7         |
| 48 | Efficient QTL detection of flowering date in a soybean RIL population using the novel restricted two-stage multi-locus GWAS procedure. <i>Theoretical and Applied Genetics</i> , 2018, 131, 2581-2599.                                | 3.6 | 31        |
| 49 | Analysis of QTL-allele system conferring drought tolerance at seedling stage in a nested association mapping population of soybean [ <i>Glycine max</i> (L.) Merr.] using a novel GWAS procedure. <i>Planta</i> , 2018, 248, 947-962. | 3.2 | 34        |
| 50 | Cloning and functional analysis of two GmDeg genes in soybean [ <i>Glycine max</i> (L.) Merr.]. <i>Journal of Plant Biology</i> , 2017, 60, 48-56.  | 2.1 | 0         |
| 51 | Development of a cytoplasmic male-sterile line <i>NJCMS</i> 4A for hybrid soybean production. <i>Plant Breeding</i> , 2017, 136, 516-525.   | 1.9 | 20        |
| 52 | Transcriptome comparative analysis between the cytoplasmic male sterile line and fertile line in soybean ( <i>Glycine max</i> (L.) Merr.). <i>Genes and Genomics</i> , 2017, 39, 1117-1127.   | 1.4 | 7         |
| 53 | Functional Mapping of Multiple Dynamic Traits. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2017, 22, 60-75.  | 1.4 | 2         |
| 54 | Inheritance, fine-mapping, and candidate gene analyses of resistance to soybean mosaic virus strain SC5 in soybean. <i>Molecular Genetics and Genomics</i> , 2017, 292, 811-822.  | 2.1 | 35        |

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|----|---|-----|-----------|
| 55 | Chicken Toes-Like Leaf and Petalody Flower (CTP) is a novel regulator that controls leaf and flower development in soybean. <i>Journal of Experimental Botany</i> , 2017, 68, 5565-5581.                                | 4.8 | 7         |
| 56 | An innovative procedure of genome-wide association analysis fits studies on germplasm population and plant breeding. <i>Theoretical and Applied Genetics</i> , 2017, 130, 2327-2343.                                    | 3.6 | 121       |
| 57 | Detecting the QTL-allele system conferring flowering date in a nested association mapping population of soybean using a novel procedure. <i>Theoretical and Applied Genetics</i> , 2017, 130, 2297-2314.                | 3.6 | 70        |
| 58 | Characterization of a soybean mosaic virus variant causing different diseases in <i>Glycine max</i> and <i>Nicotiana benthamiana</i> . <i>Archives of Virology</i> , 2017, 162, 549-553.                                | 2.1 | 10        |
| 59 | Key biological factors related to outcrossing-productivity of cytoplasmic-nuclear male-sterile lines in soybean [ <i>Glycine max</i> (L.) Merr.]. <i>Euphytica</i> , 2017, 213, 1.                                      | 1.2 | 11        |
| 60 | Optimization of <i>Agrobacterium</i> -Mediated Transformation in Soybean. <i>Frontiers in Plant Science</i> , 2017, 8, 246.   | 3.6 | 117       |
| 61 | Identification of Major Quantitative Trait Loci for Seed Oil Content in Soybeans by Combining Linkage and Genome-Wide Association Mapping. <i>Frontiers in Plant Science</i> , 2017, 8, 1222.                           | 3.6 | 101       |
| 62 | Genome-wide comparative analysis of DNA methylation between soybean cytoplasmic male-sterile line NJCMS5A and its maintainer NJCMS5B. <i>BMC Genomics</i> , 2017, 18, 596.  | 2.8 | 34        |
| 63 | Genome-wide characterization of the aldehyde dehydrogenase gene superfamily in soybean and its potential role in drought stress response. <i>BMC Genomics</i> , 2017, 18, 518.  | 2.8 | 59        |
| 64 | A high-throughput phenotyping procedure for evaluation of antixenosis against common cutworm at early seedling stage in soybean. <i>Plant Methods</i> , 2017, 13, 66.   | 4.3 | 17        |
| 65 | Genetic variation of world soybean maturity date and geographic distribution of maturity groups. <i>Breeding Science</i> , 2017, 67, 221-232.   | 1.9 | 43        |
| 66 | Evaluation of Reference Genes for Normalization of Gene Expression Using Quantitative RT-PCR under Aluminum, Cadmium, and Heat Stresses in Soybean. <i>PLoS ONE</i> , 2017, 12, e0168965.                               | 2.5 | 46        |
| 67 | Identification and Analysis of NaHCO <sub>3</sub> Stress Responsive Genes in Wild Soybean ( <i>Glycine soja</i> ) Roots by RNA-seq. <i>Frontiers in Plant Science</i> , 2016, 7, 1842.                                  | 3.6 | 31        |
| 68 | Identification of Two Duplicated Loci Controlling a Disease-like Rugose Leaf Phenotype in Soybean. <i>Crop Science</i> , 2016, 56, 1611-1618.   | 1.8 | 4         |
| 69 | Genome-wide Analysis of Phosphoenolpyruvate Carboxylase Gene Family and Their Response to Abiotic Stresses in Soybean. <i>Scientific Reports</i> , 2016, 6, 38448.  | 3.3 | 26        |
| 70 | Detecting the QTL-allele system of seed isoflavone content in Chinese soybean landrace population for optimal cross design and gene system exploration. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1557-1576. | 3.6 | 70        |
| 71 | Genome-Wide Identification of Soybean U-Box E3 Ubiquitin Ligases and Roles of GmPUB8 in Negative Regulation of Drought Stress Response in <i>Arabidopsis</i> . <i>Plant and Cell Physiology</i> , 2016, 57, 1189-1209.  | 3.1 | 101       |
| 72 | Soybean SPX1 is an important component of the response to phosphate deficiency for phosphorus homeostasis. <i>Plant Science</i> , 2016, 248, 82-91.   | 3.6 | 43        |

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|----|---|-----|-----------|
| 73 | Identification of miRNAs and their targets by high-throughput sequencing and degradome analysis in cytoplasmic male-sterile line NJCMS1A and its maintainer NJCMS1B of soybean. <i>BMC Genomics</i> , 2016, 17, 24.                   | 2.8 | 43        |
| 74 | Genome-wide analysis of MATE transporters and expression patterns of a subgroup of MATE genes in response to aluminum toxicity in soybean. <i>BMC Genomics</i> , 2016, 17, 223.   | 2.8 | 112       |
| 75 | Differential proteomics analysis to identify proteins and pathways associated with male sterility of soybean using iTRAQ-based strategy. <i>Journal of Proteomics</i> , 2016, 138, 72-82.   | 2.4 | 61        |
| 76 | Fine mapping of the genetic locus <i>L1</i> conferring black pods using a chromosome segment substitution line population of soybean. <i>Plant Breeding</i> , 2015, 134, 437-445.   | 1.9 | 23        |
| 77 | Comparative Transcriptome Analysis between the Cytoplasmic Male Sterile Line NJCMS1A and Its Maintainer NJCMS1B in Soybean ( <i>Glycine max</i> (L.) Merr.). <i>PLoS ONE</i> , 2015, 10, e0126771.                                    | 2.5 | 53        |
| 78 | Establishment of a 100-seed weight quantitative trait locus "allele matrix of the germplasm population for optimal recombination design in soybean breeding programmes. <i>Journal of Experimental Botany</i> , 2015, 66, 6311-6325.  | 4.8 | 91        |
| 79 | An environmental differential association analysis of antibiosis to common cutworm in a Chinese soybean germplasm population and optimization of the cross design. <i>Molecular Breeding</i> , 2015, 35, 1.                           | 2.1 | 7         |
| 80 | Composite Interval Mapping Based on Lattice Design for Error Control May Increase Power of Quantitative Trait Locus Detection. <i>PLoS ONE</i> , 2015, 10, e0130125.  | 2.5 | 3         |
| 81 | QTL mapping for the number of branches and pods using wild chromosome segment substitution lines in soybean [ <i>Glycine max</i> (L.) Merr.]. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2014, 12, S172-S177. | 0.8 | 15        |
| 82 | Identification of QTL/segments related to seed-quality traits in <i>G. soja</i> using chromosome segment substitution lines. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2014, 12, S65-S69.                    | 0.8 | 7         |
| 83 | Constitution of resistance to common cutworm in terms of antibiosis and antixenosis in soybean RIL populations. <i>Euphytica</i> , 2014, 196, 137-154.  | 1.2 | 21        |
| 84 | Exploration of presence/absence variation and corresponding polymorphic markers in soybean genome. <i>Journal of Integrative Plant Biology</i> , 2014, 56, 1009-1019.   | 8.5 | 21        |
| 85 | Genome-Wide Identification and Characterization of RBR Ubiquitin Ligase Genes in Soybean. <i>PLoS ONE</i> , 2014, 9, e87282.  | 2.5 | 4         |
| 86 | Overexpression of a Soybean Ariadne-Like Ubiquitin Ligase Gene <i>GmARI1</i> Enhances Aluminum Tolerance in <i>Arabidopsis</i> . <i>PLoS ONE</i> , 2014, 9, e111120.  | 2.5 | 22        |
| 87 | Association mapping combined with linkage analysis for aluminum tolerance among soybean cultivars released in Yellow and Changjiang River Valleys in China. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1659-1675.           | 3.6 | 59        |
| 88 | Development of a chromosome segment substitution line population with wild soybean ( <i>Glycine soja</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T   | 1.2 | 36        |
| 89 | Identification of QTLs for growth period traits in soybean using association analysis and linkage mapping. <i>Plant Breeding</i> , 2013, 132, 317-323.  | 1.9 | 11        |
| 90 | The Mitochondrial Genome of Soybean Reveals Complex Genome Structures and Gene Evolution at Intercellular and Phylogenetic Levels. <i>PLoS ONE</i> , 2013, 8, e56502.   | 2.5 | 67        |

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| 91  | Genome-wide genetic dissection of germplasm resources and implications for breeding by design in soybean. <i>Breeding Science</i> , 2012, 61, 495-510.  | 1.9 | 42        |
| 92  | Association analysis of vegetable soybean quality traits with SSR markers. <i>Plant Breeding</i> , 2011, 130, 444-449.  | 1.9 | 29        |
| 93  | A study on relative importance of additive, epistasis and unmapped QTL for Aluminium tolerance at seedling stage in soybean. <i>Plant Breeding</i> , 2011, 130, 551-562.  | 1.9 | 35        |
| 94  | Proteomics study of changes in soybean lines resistant and sensitive to <i>Phytophthora sojae</i> . <i>Proteome Science</i> , 2011, 9, 52.  | 1.7 | 41        |
| 95  | Identification of phosphorus starvation tolerant soybean ( <i>Glycine max</i> ) germplasms. <i>Frontiers of Agriculture in China</i> , 2010, 4, 272-279.  | 0.2 | 7         |
| 96  | Genetic analysis of tolerance to aluminum toxin at seedling stage in soybean based on major gene plus polygene mixed inheritance model. <i>Frontiers of Agriculture in China</i> , 2010, 4, 265-271.  | 0.2 | 0         |
| 97  | Genetic bases of improved soybean cultivars released from 1923 to 2005 in China—A historical review. <i>Frontiers of Agriculture in China</i> , 2010, 4, 383-393.   | 0.2 | 4         |
| 98  | Polymorphisms of soybean isoflavone synthase and flavanone 3-hydroxylase genes are associated with soybean mosaic virus resistance. <i>Molecular Breeding</i> , 2010, 25, 13-24.  | 2.1 | 20        |
| 99  | Detection of quantitative trait loci for phosphorus deficiency tolerance at soybean seedling stage. <i>Euphytica</i> , 2009, 167, 313-322.  | 1.2 | 87        |
| 100 | Methodologies for segregation analysis and QTL mapping in plants. <i>Genetica</i> , 2009, 136, 311-318.   | 1.1 | 14        |
| 101 | Somatic embryogenesis and plant regeneration in Chinese soybean ( <i>Glycine max</i> (L.) Merr.)—impacts of mannitol, abscisic acid, and explant age. <i>In Vitro Cellular and Developmental Biology - Plant</i> , 2009, 45, 180-188.           | 2.1 | 13        |
| 102 | Genetic diversity and peculiarity of annual wild soybean ( <i>G. soja</i> Sieb. et Zucc.) from various eco-regions in China. <i>Theoretical and Applied Genetics</i> , 2009, 119, 371-381.  | 3.6 | 92        |
| 103 | Characterization of O-Acetylserine(Thiol)Lyase-Encoding Genes Reveals Their Distinct but Cooperative Expression in Cysteine Synthesis of Soybean [ <i>Glycine max</i> (L.) Merr.]. <i>Plant Molecular Biology Reporter</i> , 2008, 26, 277-291. | 1.8 | 14        |
| 104 | Molecular cloning and characterization of a LEAFY-like gene highly expressed in developing soybean seeds. <i>Seed Science Research</i> , 2007, 17, 297-302.   | 1.7 | 17        |
| 105 | A Study on Subunit Groups of Soybean Protein Extracts under SDS—PAGE. <i>JAOCS, Journal of the American Oil Chemists' Society</i> , 2007, 84, 793-801.  | 1.9 | 40        |
| 106 | A comparative study on segregation analysis and QTL mapping of quantitative traits in plants—with a case in soybean. <i>Frontiers of Agriculture in China</i> , 2007, 1, 1-7.   | 0.2 | 114       |
| 107 | Identification, inheritance and QTL mapping of root traits related to tolerance to rhizo-spheric stresses in soybean ( <i>G. max</i> (L.) Merr.). <i>Frontiers of Agriculture in China</i> , 2007, 1, 119-128.                                  | 0.2 | 22        |
| 108 | Development of a cytoplasmic-nuclear male-sterile line of soybean. <i>Euphytica</i> , 2002, 124, 85-91.   | 1.2 | 27        |

| #   | ARTICLE   | IF  | CITATIONS |
|-----|---|-----|-----------|
| 109 | Germplasm Sources, Genetic Richness, and Population Differentiation of Modern Chinese Soybean Cultivars Based on Pedigree Integrated With Genomic-Marker Analysis. <i>Frontiers in Plant Science</i> , 0, 13, . | 3.6 | 0         |