

Qijian Song

List of Publications by Year in descending order

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76
papers

11,664
citations

94381

37
h-index

76872

74
g-index

78
all docs

78
docs citations

78
times ranked

9762
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Genome sequence of the palaeopolyploid soybean. <i>Nature</i> , 2010, 463, 178-183. | 13.7 | 3,854 |
| 2 | A genome-wide association study of seed protein and oil content in soybean. <i>BMC Genomics</i> , 2014, 15, 1. | 1.2 | 1,312 |
| 3 | A reference genome for common bean and genome-wide analysis of dual domestications. <i>Nature Genetics</i> , 2014, 46, 707-713. | 9.4 | 1,159 |
| 4 | Development and Evaluation of SoySNP50K, a High-Density Genotyping Array for Soybean. <i>PLoS ONE</i> , 2013, 8, e54985. | 1.1 | 490 |
| 5 | Genome-wide association study for flowering time, maturity dates and plant height in early maturing soybean (<i>Glycine max</i>) germplasm. <i>BMC Genomics</i> , 2015, 16, 217. | 1.2 | 299 |
| 6 | A Soybean Transcript Map: Gene Distribution, Haplotype and Single-Nucleotide Polymorphism Analysis. <i>Genetics</i> , 2007, 176, 685-696. | 1.2 | 285 |
| 7 | Abundance of SSR Motifs and Development of Candidate Polymorphic SSR Markers (BARCSOYSSR_1.0) in Soybean. <i>Crop Science</i> , 2010, 50, 1950-1960. | 0.8 | 282 |
| 8 | 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. | 0.8 | 247 |
| 9 | 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. | 1.2 | 242 |
| 10 | Fingerprinting Soybean Germplasm and Its Utility in Genomic Research. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1999-2006. | 0.8 | 212 |
| 11 | A Population Structure and Genome-Wide Association Analysis on the USDA Soybean Germplasm Collection. <i>Plant Genome</i> , 2015, 8, eplantgenome2015.04.0024. | 1.6 | 174 |
| 12 | Genome-wide association mapping of quantitative resistance to sudden death syndrome in soybean. <i>BMC Genomics</i> , 2014, 15, 809. | 1.2 | 164 |
| 13 | Genome-wide association study, genomic prediction and marker-assisted selection for seed weight in soybean (<i>Glycine max</i>). <i>Theoretical and Applied Genetics</i> , 2016, 129, 117-130. | 1.8 | 160 |
| 14 | 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 |
| 15 | 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, 2285-2290. | 0.8 | 147 |
| 16 | Bulked Segregant Analysis Using the GoldenGate Assay to Locate the <i>Rpp3</i> Locus that Confers Resistance to Soybean Rust in Soybean. <i>Crop Science</i> , 2009, 49, 265-271. | 0.8 | 138 |
| 17 | Construction of high resolution genetic linkage maps to improve the soybean genome sequence assembly Glyma1.01. <i>BMC Genomics</i> , 2016, 17, 33. | 1.2 | 137 |
| 18 | Distinct Copy Number, Coding Sequence, and Locus Methylation Patterns Underlie Rhg1-Mediated Soybean Resistance to Soybean Cyst Nematode. <i>Plant Physiology</i> , 2014, 165, 630-647. | 2.3 | 136 |

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|----|--|-----|-----------|
| 19 | Genome-Wide Association Study Identifies Candidate Loci Underlying Agronomic Traits in a Middle American Diversity Panel of Common Bean. <i>Plant Genome</i> , 2016, 9, plantgenome2016.02.0012. | 1.6 | 136 |
| 20 | Genomic consequences of selection and genome-wide association mapping in soybean. <i>BMC Genomics</i> , 2015, 16, 671. | 1.2 | 121 |
| 21 | Genetic Characterization of the Soybean Nested Association Mapping Population. <i>Plant Genome</i> , 2017, 10, plantgenome2016.10.0109. | 1.6 | 114 |
| 22 | Genome-wide Scan for Seed Composition Provides Insights into Soybean Quality Improvement and the Impacts of Domestication and Breeding. <i>Molecular Plant</i> , 2018, 11, 460-472. | 3.9 | 111 |
| 23 | Genetic Architecture of Soybean Yield and Agronomic Traits. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3367-3375. | 0.8 | 98 |
| 24 | The Genetic Architecture of Seed Composition in Soybean Is Refined by Genome-Wide Association Scans Across Multiple Populations. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 2283-2294. | 0.8 | 93 |
| 25 | Genome-wide association study (GWAS) of carbon isotope ratio ($\delta^{13}C$) in diverse soybean [<i>Glycine max</i> (L.) Merr.] genotypes. <i>Theoretical and Applied Genetics</i> , 2015, 128, 73-91. | 1.8 | 89 |
| 26 | Identification of QTL with large effect on seed weight in a selective population of soybean with genome-wide association and fixation index analyses. <i>BMC Genomics</i> , 2017, 18, 529. | 1.2 | 87 |
| 27 | Developing market class specific InDel markers from next generation sequence data in <i>Phaseolus vulgaris</i> L. <i>Frontiers in Plant Science</i> , 2014, 5, 185. | 1.7 | 79 |
| 28 | Genome-Wide Association Analysis for Drought Tolerance and Associated Traits in Common Bean. <i>Plant Genome</i> , 2017, 10, plantgenome2015.12.0122. | 1.6 | 74 |
| 29 | Genomic Selection for Yield and Seed Composition Traits Within an Applied Soybean Breeding Program. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2253-2265. | 0.8 | 63 |
| 30 | Identification of domestication-related loci associated with flowering time and seed size in soybean with the RAD-seq genotyping method. <i>Scientific Reports</i> , 2015, 5, 9350. | 1.6 | 62 |
| 31 | Integrating GWAS and gene expression data for functional characterization of resistance to white mould in soya bean. <i>Plant Biotechnology Journal</i> , 2018, 16, 1825-1835. | 4.1 | 60 |
| 32 | Soybean BARCSoySNP6K: An assay for soybean genetics and breeding research. <i>Plant Journal</i> , 2020, 104, 800-811. | 2.8 | 60 |
| 33 | Association mapping of loci controlling genetic and environmental interaction of soybean flowering time under various photo-thermal conditions. <i>BMC Genomics</i> , 2017, 18, 415. | 1.2 | 58 |
| 34 | Selection of GmSWEET39 for oil and protein improvement in soybean. <i>PLoS Genetics</i> , 2020, 16, e1009114. | 1.5 | 54 |
| 35 | Genome-wide association mapping of partial resistance to <i>Phytophthora sojae</i> in soybean plant introductions from the Republic of Korea. <i>BMC Genomics</i> , 2016, 17, 607. | 1.2 | 46 |
| 36 | Genetics and mapping of a new anthracnose resistance locus in Andean common bean Paloma. <i>BMC Genomics</i> , 2017, 18, 306. | 1.2 | 46 |

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|----|--|-----|-----------|
| 37 | A Roadmap for Functional Structural Variants in the Soybean Genome. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1307-1318. | 0.8 | 42 |
| 38 | POWR1 is a domestication gene pleiotropically regulating seed quality and yield in soybean. <i>Nature Communications</i> , 2022, 13, . | 5.8 | 39 |
| 39 | Genome-Wide Association Study of Ureide Concentration in Diverse Maturity Group IV Soybean [<i>Glycine max</i> (L.) Merr.] Accessions. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2391-2403. | 0.8 | 38 |
| 40 | An evolutionary population structure model reveals pleiotropic effects of <i>GmPDAT</i> for traits related to seed size and oil content in soybean. <i>Journal of Experimental Botany</i> , 2020, 71, 6988-7002. | 2.4 | 35 |
| 41 | Genetic dissection of heterosis using epistatic association mapping in a partial NCII mating design. <i>Scientific Reports</i> , 2016, 5, 18376. | 1.6 | 34 |
| 42 | Fine Mapping of <i>Ur-3</i> , a Historically Important Rust Resistance Locus in Common Bean. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 557-569. | 0.8 | 33 |
| 43 | Fine mapping of the soybean aphid-resistance genes <i>Rag6</i> and <i>Rag3c</i> from <i>Glycine soja</i> 85-32. <i>Theoretical and Applied Genetics</i> , 2017, 130, 2601-2615. | 1.8 | 28 |
| 44 | Mapping novel aphid resistance QTL from wild soybean, <i>Glycine soja</i> 85-32. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1941-1952. | 1.8 | 28 |
| 45 | Genome-wide association study and genomic selection for yield and related traits in soybean. <i>PLoS ONE</i> , 2021, 16, e0255761. | 1.1 | 28 |
| 46 | Population Structure and Genetic Diversity of the Trinitario Cacao (<i>Theobroma cacao</i> L.) from Trinidad and Tobago. <i>Crop Science</i> , 2009, 49, 564-572. | 0.8 | 27 |
| 47 | A high-resolution genetic linkage map of soybean based on 357 recombinant inbred lines genotyped with BARCSoySNP6K. <i>Molecular Breeding</i> , 2015, 35, 1. | 1.0 | 24 |
| 48 | Genetic Diversity, Population Structure, and Andean Introgression in Brazilian Common Bean Cultivars after Half a Century of Genetic Breeding. <i>Genes</i> , 2020, 11, 1298. | 1.0 | 20 |
| 49 | Genome-Wide Association Study and Genomic Prediction for Soybean Cyst Nematode Resistance in USDA Common Bean (<i>Phaseolus vulgaris</i>) Core Collection. <i>Frontiers in Plant Science</i> , 2021, 12, 624156. | 1.7 | 20 |
| 50 | Draft genome sequence of <i>Diaporthe aspalathi</i> isolate MS-SSC91, a fungus causing stem canker in soybean. <i>Genomics Data</i> , 2016, 7, 262-263. | 1.3 | 18 |
| 51 | Pyramiding different aphid-resistance genes in elite soybean germplasm to combat dynamic aphid populations. <i>Molecular Breeding</i> , 2018, 38, 1. | 1.0 | 15 |
| 52 | Genome-Wide Association Study Reveals Genomic Regions Associated with Fusarium Wilt Resistance in Common Bean. <i>Genes</i> , 2021, 12, 765. | 1.0 | 15 |
| 53 | Fine mapping of an anthracnose-resistance locus in Andean common bean cultivar Amendoim Cavalo. <i>PLoS ONE</i> , 2020, 15, e0239763. | 1.1 | 14 |
| 54 | Draft Genome Sequence of <i>Phomopsis longicolla</i> Type Strain TWH P74, a Fungus Causing Phomopsis Seed Decay in Soybean. <i>Genome Announcements</i> , 2015, 3, . | 0.8 | 12 |

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|----|--|-----|-----------|
| 55 | Different loci associated with root and foliar resistance to sudden death syndrome (Fusarium) Tj ETQq1 1 0.784314 1.8 BT /Overlock 10 T | 1.8 | 12 |
| 56 | Nested association mapping of important agronomic traits in three interspecific soybean populations. Theoretical and Applied Genetics, 2020, 133, 1039-1054. | 1.8 | 12 |
| 57 | Identification and characterization of novel QTL conferring internal detoxification of aluminium in soybean. Journal of Experimental Botany, 2021, 72, 4993-5009. | 2.4 | 12 |
| 58 | Development of a versatile resource for post-genomic research through consolidating and characterizing 1500 diverse wild and cultivated soybean genomes. BMC Genomics, 2022, 23, 250. | 1.2 | 11 |
| 59 | Genome-wide detection of genetic loci associated with soybean aphid resistance in soybean germplasm PI 603712. Euphytica, 2017, 213, 1. | 0.6 | 10 |
| 60 | The Soybean High Density "Forrest"™ by "Williams 82"™ SNP-Based Genetic Linkage Map Identifies QTL and Candidate Genes for Seed Isoflavone Content. Plants, 2021, 10, 2029. | 1.6 | 10 |
| 61 | Identification of Candidate Genes and Genomic Selection for Seed Protein in Soybean Breeding Pipeline. Frontiers in Plant Science, 0, 13, . | 1.7 | 9 |
| 62 | Genetic linkage map of Phaeosphaeria nodorum, the causal agent of stagonospora nodorum blotch disease of wheat. European Journal of Plant Pathology, 2009, 124, 681-690. | 0.8 | 7 |
| 63 | Genetic Diversity and Phylogenetic Relationships of Annual and Perennial Glycine Species. G3: Genes, Genomes, Genetics, 2019, 9, 2325-2336. | 0.8 | 7 |
| 64 | Genomic prediction using training population design in interspecific soybean populations. Molecular Breeding, 2021, 41, 1. | 1.0 | 7 |
| 65 | Identification of Quantitative Disease Resistance Loci Toward Four Pythium Species in Soybean. Frontiers in Plant Science, 2021, 12, 644746. | 1.7 | 7 |
| 66 | Impact of multiple selective breeding programs on genetic diversity in soybean germplasm. Theoretical and Applied Genetics, 2022, 135, 1591-1602. | 1.8 | 7 |
| 67 | Epistatic interaction between Rhg1-a and Rhg2 in PI 90763 confers resistance to virulent soybean cyst nematode populations. Theoretical and Applied Genetics, 2022, 135, 2025-2039. | 1.8 | 7 |
| 68 | Registration of Wyandot " PI 567301B Soybean Recombinant Inbred Line Population. Journal of Plant Registrations, 2017, 11, 324-327. | 0.4 | 5 |
| 69 | Haplotype analysis of a major and stable QTL underlying soybean (Glycine max) seed oil content reveals footprint of artificial selection. Molecular Breeding, 2019, 39, 1. | 1.0 | 5 |
| 70 | Alternative splicing and genetic diversity of the white collar-1 (wc-1) gene in cereal Phaeosphaeria pathogens. European Journal of Plant Pathology, 2010, 127, 351-363. | 0.8 | 3 |
| 71 | Validation of the quantitative trait locus underlying soybean plant height using residual heterozygous lines and near-isogenic lines across multi-environments. Euphytica, 2017, 213, 1. | 0.6 | 3 |
| 72 | Genetic Mapping for Agronomic Traits in IAPAR 81/LP97-28 Population of Common Bean (Phaseolus) Tj ETQq0 0 0 1.6 BT /Overlock 10 T | 1.6 | 3 |

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|----|---|-----|-----------|
| 73 | Genotype imputation for soybean nested association mapping population to improve precision of QTL detection. <i>Theoretical and Applied Genetics</i> , 2022, 135, 1797-1810. | 1.8 | 3 |
| 74 | Identifying and Validating a Quantitative Trait Locus on Chromosome 14 Underlying Stearic Acid in a Soybean Landrace. <i>Journal of Crop Improvement</i> , 2016, 30, 152-164. | 0.9 | 2 |
| 75 | Genetic diversity and inter-gene pool introgression of Mesoamerican Diversity Panel in common beans. <i>Journal of Applied Genetics</i> , 2021, 62, 585-600. | 1.0 | 1 |
| 76 | Determination of Seed Storage Proteins and Total Isoflavones in Wild and Cultivated Soybeans. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2010, 19, 115-118. | 0.9 | 0 |