

# Qijian Song

## List of Publications by Year in descending order

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76  
papers

11,664  
citations

94433

37  
h-index

76900

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.	27.8	3,854
2	A genome-wide association study of seed protein and oil content in soybean. <i>BMC Genomics</i> , 2014, 15, 1.	2.8	1,312
3	A reference genome for common bean and genome-wide analysis of dual domestications. <i>Nature Genetics</i> , 2014, 46, 707-713.	21.4	1,159
4	Development and Evaluation of SoySNP50K, a High-Density Genotyping Array for Soybean. <i>PLoS ONE</i> , 2013, 8, e54985.	2.5	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.	2.8	299
6	A Soybean Transcript Map: Gene Distribution, Haplotype and Single-Nucleotide Polymorphism Analysis. <i>Genetics</i> , 2007, 176, 685-696.	2.9	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.	1.8	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.	1.8	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.	2.8	242
10	Fingerprinting Soybean Germplasm and Its Utility in Genomic Research. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1999-2006.	1.8	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.	2.8	174
12	Genome-wide association mapping of quantitative resistance to sudden death syndrome in soybean. <i>BMC Genomics</i> , 2014, 15, 809.	2.8	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.	3.6	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.	3.6	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.	1.8	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.	1.8	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.	2.8	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.	4.8	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.	2.8	136
20	Genomic consequences of selection and genome-wide association mapping in soybean. <i>BMC Genomics</i> , 2015, 16, 671.	2.8	121
21	Genetic Characterization of the Soybean Nested Association Mapping Population. <i>Plant Genome</i> , 2017, 10, plantgenome2016.10.0109.	2.8	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.	8.3	111
23	Genetic Architecture of Soybean Yield and Agronomic Traits. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3367-3375.	1.8	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.	1.8	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.	3.6	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.	2.8	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.	3.6	79
28	Genome-Wide Association Analysis for Drought Tolerance and Associated Traits in Common Bean. <i>Plant Genome</i> , 2017, 10, plantgenome2015.12.0122.	2.8	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.	1.8	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.	3.3	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.	8.3	60
32	Soybean BARCSoySNP6K: An assay for soybean genetics and breeding research. <i>Plant Journal</i> , 2020, 104, 800-811.	5.7	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.	2.8	58
34	Selection of GmSWEET39 for oil and protein improvement in soybean. <i>PLoS Genetics</i> , 2020, 16, e1009114.	3.5	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.	2.8	46
36	Genetics and mapping of a new anthracnose resistance locus in Andean common bean Paloma. <i>BMC Genomics</i> , 2017, 18, 306.	2.8	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.	1.8	42
38	POWR1 is a domestication gene pleiotropically regulating seed quality and yield in soybean. <i>Nature Communications</i> , 2022, 13, .	12.8	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.	1.8	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.	4.8	35
41	Genetic dissection of heterosis using epistatic association mapping in a partial NCII mating design. <i>Scientific Reports</i> , 2016, 5, 18376.	3.3	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.	1.8	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.	3.6	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.	3.6	28
45	Genome-wide association study and genomic selection for yield and related traits in soybean. <i>PLoS ONE</i> , 2021, 16, e0255761.	2.5	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.	1.8	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.	2.1	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.	2.4	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.	3.6	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.	2.1	15
52	Genome-Wide Association Study Reveals Genomic Regions Associated with Fusarium Wilt Resistance in Common Bean. <i>Genes</i> , 2021, 12, 765.	2.4	15
53	Fine mapping of an anthracnose-resistance locus in Andean common bean cultivar Amendoim Cavalo. <i>PLoS ONE</i> , 2020, 15, e0239763.	2.5	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 rgBT /Overlock 10 T	3.6	12
56	Nested association mapping of important agronomic traits in three interspecific soybean populations. Theoretical and Applied Genetics, 2020, 133, 1039-1054.	3.6	12
57	Identification and characterization of novel QTL conferring internal detoxification of aluminium in soybean. Journal of Experimental Botany, 2021, 72, 4993-5009.	4.8	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.	2.8	11
59	Genome-wide detection of genetic loci associated with soybean aphid resistance in soybean germplasm PI 603712. Euphytica, 2017, 213, 1.	1.2	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.	3.5	10
61	Identification of Candidate Genes and Genomic Selection for Seed Protein in Soybean Breeding Pipeline. Frontiers in Plant Science, 0, 13, .	3.6	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.	1.7	7
63	Genetic Diversity and Phylogenetic Relationships of Annual and Perennial Glycine Species. G3: Genes, Genomes, Genetics, 2019, 9, 2325-2336.	1.8	7
64	Genomic prediction using training population design in interspecific soybean populations. Molecular Breeding, 2021, 41, 1.	2.1	7
65	Identification of Quantitative Disease Resistance Loci Toward Four Pythium Species in Soybean. Frontiers in Plant Science, 2021, 12, 644746.	3.6	7
66	Impact of multiple selective breeding programs on genetic diversity in soybean germplasm. Theoretical and Applied Genetics, 2022, 135, 1591-1602.	3.6	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.	3.6	7
68	Registration of Wyandot " PI 567301B Soybean Recombinant Inbred Line Population. Journal of Plant Registrations, 2017, 11, 324-327.	0.5	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.	2.1	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.	1.7	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.	1.2	3
72	Genetic Mapping for Agronomic Traits in IAPAR 81/LP97-28 Population of Common Bean (Phaseolus) Tj ETQq0 0 0 rgBT /Overlock 10 T	3.5	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.	3.6	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.	1.7	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.	1.9	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.	1.7	0