

# Qijian Song

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/49597/publications.pdf>

Version: 2024-02-01

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	Impact of multiple selective breeding programs on genetic diversity in soybean germplasm. <i>Theoretical and Applied Genetics</i> , 2022, 135, 1591-1602.	3.6	7
2	Development of a versatile resource for post-genomic research through consolidating and characterizing 1500 diverse wild and cultivated soybean genomes. <i>BMC Genomics</i> , 2022, 23, 250.	2.8	11
3	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
4	Epistatic interaction between Rhg1-a and Rhg2 in PI 90763 confers resistance to virulent soybean cyst nematode populations. <i>Theoretical and Applied Genetics</i> , 2022, 135, 2025-2039.	3.6	7
5	POWR1 is a domestication gene pleiotropically regulating seed quality and yield in soybean. <i>Nature Communications</i> , 2022, 13, .	12.8	39
6	Genomic prediction using training population design in interspecific soybean populations. <i>Molecular Breeding</i> , 2021, 41, 1.	2.1	7
7	Identification of Quantitative Disease Resistance Loci Toward Four Pythium Species in Soybean. <i>Frontiers in Plant Science</i> , 2021, 12, 644746.	3.6	7
8	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
9	Genome-Wide Association Study Reveals Genomic Regions Associated with Fusarium Wilt Resistance in Common Bean. <i>Genes</i> , 2021, 12, 765.	2.4	15
10	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
11	Genetic Mapping for Agronomic Traits in IAPAR 81/LP97-28 Population of Common Bean ( <i>Phaseolus</i> ) Tj ETQq1 1 0.784314 rgBT /Over to	3.5	9
12	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
13	Genome-wide association study and genomic selection for yield and related traits in soybean. <i>PLoS ONE</i> , 2021, 16, e0255761.	2.5	28
14	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
15	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
16	Soybean BARCSoySNP6K: An assay for soybean genetics and breeding research. <i>Plant Journal</i> , 2020, 104, 800-811.	5.7	60
17	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
18	Nested association mapping of important agronomic traits in three interspecific soybean populations. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1039-1054.	3.6	12

#	ARTICLE	IF	CITATIONS
19	Selection of GmSWEET39 for oil and protein improvement in soybean. PLoS Genetics, 2020, 16, e1009114.	3.5	54
20	Fine mapping of an anthracnose-resistance locus in Andean common bean cultivar Amendoim Cavalo. PLoS ONE, 2020, 15, e0239763.	2.5	14
21	Genomic Selection for Yield and Seed Composition Traits Within an Applied Soybean Breeding Program. G3: Genes, Genomes, Genetics, 2019, 9, 2253-2265.	1.8	63
22	Haplotype analysis of a major and stable QTL underlying soybean ( <i>Glycine max</i> ) seed oil content reveals footprint of artificial selection. Molecular Breeding, 2019, 39, 1.	2.1	5
23	Genetic Diversity and Phylogenetic Relationships of Annual and Perennial <i>Glycine</i> Species. G3: Genes, Genomes, Genetics, 2019, 9, 2325-2336.	1.8	7
24	Different loci associated with root and foliar resistance to sudden death syndrome (Fusarium) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 542	3.6	12
25	Pyramiding different aphid-resistance genes in elite soybean germplasm to combat dynamic aphid populations. Molecular Breeding, 2018, 38, 1.	2.1	15
26	Genome-wide Scan for Seed Composition Provides Insights into Soybean Quality Improvement and the Impacts of Domestication and Breeding. Molecular Plant, 2018, 11, 460-472.	8.3	111
27	Integrating GWAS and gene expression data for functional characterization of resistance to white mould in soya bean. Plant Biotechnology Journal, 2018, 16, 1825-1835.	8.3	60
28	Genetic Architecture of Soybean Yield and Agronomic Traits. G3: Genes, Genomes, Genetics, 2018, 8, 3367-3375.	1.8	98
29	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
30	Genetics and mapping of a new anthracnose resistance locus in Andean common bean Paloma. BMC Genomics, 2017, 18, 306.	2.8	46
31	Fine Mapping of <i>Ur-3</i> , a Historically Important Rust Resistance Locus in Common Bean. G3: Genes, Genomes, Genetics, 2017, 7, 557-569.	1.8	33
32	Fine mapping of the soybean aphid-resistance genes Rag6 and Rag3c from <i>Glycine soja</i> 85-32. Theoretical and Applied Genetics, 2017, 130, 2601-2615.	3.6	28
33	Mapping novel aphid resistance QTL from wild soybean, <i>Glycine soja</i> 85-32. Theoretical and Applied Genetics, 2017, 130, 1941-1952.	3.6	28
34	Molecular mapping and genomics of soybean seed protein: a review and perspective for the future. Theoretical and Applied Genetics, 2017, 130, 1975-1991.	3.6	160
35	Genome-wide detection of genetic loci associated with soybean aphid resistance in soybean germplasm PI 603712. Euphytica, 2017, 213, 1.	1.2	10
36	Association mapping of loci controlling genetic and environmental interaction of soybean flowering time under various photo-thermal conditions. BMC Genomics, 2017, 18, 415.	2.8	58

#	ARTICLE	IF	CITATIONS
37	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
38	Genetic Characterization of the Soybean Nested Association Mapping Population. <i>Plant Genome</i> , 2017, 10, plantgenome2016.10.0109.	2.8	114
39	Registration of Wyandot – PI 567301B Soybean Recombinant Inbred Line Population. <i>Journal of Plant Registrations</i> , 2017, 11, 324-327.	0.5	5
40	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
41	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
42	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
43	Genetic dissection of heterosis using epistatic association mapping in a partial NCII mating design. <i>Scientific Reports</i> , 2016, 5, 18376.	3.3	34
44	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
45	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
46	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
47	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
48	Genomic consequences of selection and genome-wide association mapping in soybean. <i>BMC Genomics</i> , 2015, 16, 671.	2.8	121
49	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
50	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
51	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
52	Fingerprinting Soybean Germplasm and Its Utility in Genomic Research. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1999-2006.	1.8	212
53	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
54	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

#	ARTICLE	IF	CITATIONS
55	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
56	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
57	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
58	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
59	Distinct Copy Number, Coding Sequence, and Locus Methylation Patterns Underlie Rhg1-Mediated Soybean Resistance to Soybean Cyst Nematode $\ddot{A}$ . <i>Plant Physiology</i> , 2014, 165, 630-647.	4.8	136
60	A Roadmap for Functional Structural Variants in the Soybean Genome. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1307-1318.	1.8	42
61	Genome-wide association mapping of quantitative resistance to sudden death syndrome in soybean. <i>BMC Genomics</i> , 2014, 15, 809.	2.8	164
62	A genome-wide association study of seed protein and oil content in soybean. <i>BMC Genomics</i> , 2014, 15, 1.	2.8	1,312
63	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
64	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
65	Development and Evaluation of SoySNP50K, a High-Density Genotyping Array for Soybean. <i>PLoS ONE</i> , 2013, 8, e54985.	2.5	490
66	Alternative splicing and genetic diversity of the white collar-1 (wc-1) gene in cereal <i>Phaeosphaeria</i> pathogens. <i>European Journal of Plant Pathology</i> , 2010, 127, 351-363.	1.7	3
67	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
68	Genome sequence of the palaeopolyploid soybean. <i>Nature</i> , 2010, 463, 178-183.	27.8	3,854
69	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
70	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
71	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
72	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

#	ARTICLE	IF	CITATIONS
73	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
74	Genetic linkage map of <i>Phaeosphaeria nodorum</i> , the causal agent of stagonospora nodorum blotch disease of wheat. <i>European Journal of Plant Pathology</i> , 2009, 124, 681-690.	1.7	7
75	A Soybean Transcript Map: Gene Distribution, Haplotype and Single-Nucleotide Polymorphism Analysis. <i>Genetics</i> , 2007, 176, 685-696.	2.9	285
76	Identification of Candidate Genes and Genomic Selection for Seed Protein in Soybean Breeding Pipeline. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	9