

Qijian Song

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

71
papers

7,810
citations

31
h-index

78
g-index

78
ext. papers

10,015
ext. citations

5.5
avg, IF

5.38
L-index

#	Paper	IF	Citations
71	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	4.5	1
70	Genotype imputation for soybean nested association mapping population to improve precision of QTL detection.. <i>Theoretical and Applied Genetics</i> , 2022 , 1	6	1
69	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 , 1	6	0
68	Identification of Quantitative Disease Resistance Loci Toward Four Species in Soybean. <i>Frontiers in Plant Science</i> , 2021 , 12, 644746	6.2	1
67	Identification and characterization of novel QTL conferring internal detoxification of aluminium in soybean. <i>Journal of Experimental Botany</i> , 2021 , 72, 4993-5009	7	3
66	Genome-Wide Association Study Reveals Genomic Regions Associated with Fusarium Wilt Resistance in Common Bean. <i>Genes</i> , 2021 , 12,	4.2	3
65	Genome-Wide Association Study and Genomic Prediction for Soybean Cyst Nematode Resistance in USDA Common Bean () Core Collection. <i>Frontiers in Plant Science</i> , 2021 , 12, 624156	6.2	5
64	Genomic prediction using training population design in interspecific soybean populations. <i>Molecular Breeding</i> , 2021 , 41, 1	3.4	2
63	Genetic diversity and inter-gene pool introgression of Mesoamerican Diversity Panel in common beans. <i>Journal of Applied Genetics</i> , 2021 , 62, 585-600	2.5	
62	Genome-wide association study and genomic selection for yield and related traits in soybean. <i>PLoS ONE</i> , 2021 , 16, e0255761	3.7	3
61	Nested association mapping of important agronomic traits in three interspecific soybean populations. <i>Theoretical and Applied Genetics</i> , 2020 , 133, 1039-1054	6	6
60	Selection of GmSWEET39 for oil and protein improvement in soybean. <i>PLoS Genetics</i> , 2020 , 16, e1009114		11
59	Fine mapping of an anthracnose-resistance locus in Andean common bean cultivar Amendoim Cavalo. <i>PLoS ONE</i> , 2020 , 15, e0239763	3.7	5
58	Genetic Diversity, Population Structure, and Andean Introgression in Brazilian Common Bean Cultivars after Half a Century of Genetic Breeding. <i>Genes</i> , 2020 , 11,	4.2	12
57	Soybean BARCSoySNP6K: An assay for soybean genetics and breeding research. <i>Plant Journal</i> , 2020 , 104, 800-811	6.9	20
56	An evolutionary population structure model reveals pleiotropic effects of GmPDAT for traits related to seed size and oil content in soybean. <i>Journal of Experimental Botany</i> , 2020 , 71, 6988-7002	7	11
55	Genomic Selection for Yield and Seed Composition Traits Within an Applied Soybean Breeding Program. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 2253-2265	3.2	27

54	Haplotype analysis of a major and stable QTL underlying soybean (<i>Glycine max</i>) seed oil content reveals footprint of artificial selection. <i>Molecular Breeding</i> , 2019 , 39, 1	3.4	2
53	Genetic Diversity and Phylogenetic Relationships of Annual and Perennial Species. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 2325-2336	3.2	2
52	Different loci associated with root and foliar resistance to sudden death syndrome (<i>Fusarium virguliforme</i>) in soybean. <i>Theoretical and Applied Genetics</i> , 2019 , 132, 501-513	6	7
51	Pyramiding different aphid-resistance genes in elite soybean germplasm to combat dynamic aphid populations. <i>Molecular Breeding</i> , 2018 , 38, 1	3.4	13
50	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	14.4	67
49	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	11.6	31
48	Genetic Architecture of Soybean Yield and Agronomic Traits. <i>G3: Genes, Genomes, Genetics</i> , 2018 , 8, 3367-3375	3.375	44
47	Validation of the quantitative trait locus underlying soybean plant height using residual heterozygous lines and near-isogenic lines across multi-environments. <i>Euphytica</i> , 2017 , 213, 1	2.1	2
46	Genetics and mapping of a new anthracnose resistance locus in Andean common bean Paloma. <i>BMC Genomics</i> , 2017 , 18, 306	4.5	31
45	Fine Mapping of , a Historically Important Rust Resistance Locus in Common Bean. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 557-569	3.2	14
44	Fine mapping of the soybean aphid-resistance genes Rag6 and Rag3c from <i>Glycine soja</i> 85-32. <i>Theoretical and Applied Genetics</i> , 2017 , 130, 2601-2615	6	16
43	Registration of Wyandot [PI 567301B Soybean Recombinant Inbred Line Population. <i>Journal of Plant Registrations</i> , 2017 , 11, 324-327	0.7	3
42	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	4.5	37
41	Mapping novel aphid resistance QTL from wild soybean, <i>Glycine soja</i> 85-32. <i>Theoretical and Applied Genetics</i> , 2017 , 130, 1941-1952	6	23
40	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	6	81
39	Genome-wide detection of genetic loci associated with soybean aphid resistance in soybean germplasm PI 603712. <i>Euphytica</i> , 2017 , 213, 1	2.1	8
38	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	4.5	30
37	Genome-wide Association Analysis for Drought Tolerance and Associated Traits in Common Bean. <i>Plant Genome</i> , 2017 , 10, plantgenome2015.12.0122	4.4	42

36	Genetic Characterization of the Soybean Nested Association Mapping Population. <i>Plant Genome</i> , 2017 , 10, plantgenome2016.10.0109	4.4	67
35	Construction of high resolution genetic linkage maps to improve the soybean genome sequence assembly Glyma1.01. <i>BMC Genomics</i> , 2016 , 17, 33	4.5	73
34	Draft genome sequence of Diaporthe aspalathi isolate MS-SSC91, a fungus causing stem canker in soybean. <i>Genomics Data</i> , 2016 , 7, 262-3		10
33	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, 117-30	6	102
32	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	4.4	86
31	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	4.5	34
30	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	1.4	2
29	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	4.9	48
28	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, 2285-90	3.2	95
27	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	6	72
26	Genomic consequences of selection and genome-wide association mapping in soybean. <i>BMC Genomics</i> , 2015 , 16, 671	4.5	44
25	Draft Genome Sequence of <i>Phomopsis longicolla</i> Type Strain TWH P74, a Fungus Causing <i>Phomopsis</i> Seed Decay in Soybean. <i>Genome Announcements</i> , 2015 , 3,		7
24	A Population Structure and Genome-Wide Association Analysis on the USDA Soybean Germplasm Collection. <i>Plant Genome</i> , 2015 , 8, eplantgenome2015.04.0024	4.4	96
23	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	4.5	148
22	Fingerprinting Soybean Germplasm and Its Utility in Genomic Research. <i>G3: Genes, Genomes, Genetics</i> , 2015 , 5, 1999-2006	3.2	138
21	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, 2391-403	3.2	32
20	A high-resolution genetic linkage map of soybean based on 357 recombinant inbred lines genotyped with BARCSoySNP6K. <i>Molecular Breeding</i> , 2015 , 35, 1	3.4	22
19	Genetic dissection of heterosis using epistatic association mapping in a partial NCII mating design. <i>Scientific Reports</i> , 2015 , 5, 18376	4.9	16

18	A reference genome for common bean and genome-wide analysis of dual domestications. <i>Nature Genetics</i> , 2014 , 46, 707-13	36.3	772
17	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, 2283-94	3.2	54
16	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	6.2	54
15	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	6.6	90
14	A roadmap for functional structural variants in the soybean genome. <i>G3: Genes, Genomes, Genetics</i> , 2014 , 4, 1307-18	3.2	31
13	Genome-wide association mapping of quantitative resistance to sudden death syndrome in soybean. <i>BMC Genomics</i> , 2014 , 15, 809	4.5	106
12	A genome-wide association study of seed protein and oil content in soybean. <i>BMC Genomics</i> , 2014 , 15, 1	4.5	653
11	Development and evaluation of SoySNP50K, a high-density genotyping array for soybean. <i>PLoS ONE</i> , 2013 , 8, e54985	3.7	344
10	Genome sequence of the palaeopolyploid soybean. <i>Nature</i> , 2010 , 463, 178-83	50.4	2997
9	Abundance of SSR Motifs and Development of Candidate Polymorphic SSR Markers (BARCSOYSSR_1.0) in Soybean. <i>Crop Science</i> , 2010 , 50, 1950-1960	2.4	220
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	2.4	215
7	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	1.6	
6	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	2.1	1
5	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	4.5	219
4	Bulked Segregant Analysis Using the GoldenGate Assay to Locate the Rpp3 Locus that Confers Resistance to Soybean Rust in Soybean. <i>Crop Science</i> , 2009 , 49, 265-271	2.4	115
3	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	2.1	4
2	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	2.4	19
1	A soybean transcript map: gene distribution, haplotype and single-nucleotide polymorphism analysis. <i>Genetics</i> , 2007 , 176, 685-96	4	258

