

Qi Sun

List of Publications by Year in descending order

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53
papers

11,764
citations

186254

28
h-index

182417

51
g-index

56
all docs

56
docs citations

56
times ranked

14357
citing authors

#	ARTICLE	IF	CITATIONS
1	A Robust, Simple Genotyping-by-Sequencing (GBS) Approach for High Diversity Species. <i>PLoS ONE</i> , 2011, 6, e19379.	2.5	5,470
2	TASSEL-GBS: A High Capacity Genotyping by Sequencing Analysis Pipeline. <i>PLoS ONE</i> , 2014, 9, e90346.	2.5	1,511
3	Genetic Properties of the Maize Nested Association Mapping Population. <i>Science</i> , 2009, 325, 737-740.	12.6	959
4	Host genetic variation impacts microbiome composition across human body sites. <i>Genome Biology</i> , 2015, 16, 191.	8.8	612
5	Sorting Signals, N-Terminal Modifications and Abundance of the Chloroplast Proteome. <i>PLoS ONE</i> , 2008, 3, e1994.	2.5	583
6	PPDB, the Plant Proteomics Database at Cornell. <i>Nucleic Acids Research</i> , 2009, 37, D969-D974.	14.5	356
7	Comparative analyses of C4 and C3 photosynthesis in developing leaves of maize and rice. <i>Nature Biotechnology</i> , 2014, 32, 1158-1165.	17.5	228
8	Construction of the third-generation Zea mays haplotype map. <i>GigaScience</i> , 2018, 7, 1-12.	6.4	191
9	The Role of cis Regulatory Evolution in Maize Domestication. <i>PLoS Genetics</i> , 2014, 10, e1004745.	3.5	144
10	Heterozygous Mapping Strategy (HetMappS) for High Resolution Genotyping-By-Sequencing Markers: A Case Study in Grapevine. <i>PLoS ONE</i> , 2015, 10, e0134880.	2.5	120
11	Computational Analysis of AmpSeq Data for Targeted, High-Throughput Genotyping of Amplicons. <i>Frontiers in Plant Science</i> , 2019, 10, 599.	3.6	115
12	Transcriptomic Analyses Indicate That Maize Ligule Development Recapitulates Gene Expression Patterns That Occur during Lateral Organ Initiation. <i>Plant Cell</i> , 2015, 26, 4718-4732.	6.6	99
13	MASCP Gator: An Aggregation Portal for the Visualization of Arabidopsis Proteomics Data. <i>Plant Physiology</i> , 2011, 155, 259-270.	4.8	94
14	White shark genome reveals ancient elasmobranch adaptations associated with wound healing and the maintenance of genome stability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 4446-4455.	7.1	92
15	A next-generation marker genotyping platform (AmpSeq) in heterozygous crops: a case study for marker-assisted selection in grapevine. <i>Horticulture Research</i> , 2016, 3, 16002.	6.3	90
16	Genetic dissection of powdery mildew resistance in interspecific half-sib grapevine families using SNP-based maps. <i>Molecular Breeding</i> , 2017, 37, 1.	2.1	82
17	BrAPI: an application programming interface for plant breeding applications. <i>Bioinformatics</i> , 2019, 35, 4147-4155.	4.1	82
18	Developmental dynamics of Kranz cell transcriptional specificity in maize leaf reveals early onset of C4-related processes. <i>Journal of Experimental Botany</i> , 2014, 65, 3543-3555.	4.8	78

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19	Analysis of Curated and Predicted Plastid Subproteomes of Arabidopsis. Subcellular Compartmentalization Leads to Distinctive Proteome Properties. <i>Plant Physiology</i> , 2004, 135, 723-734.	4.8	73
20	Identification of Photosynthesis-Associated C4 Candidate Genes through Comparative Leaf Gradient Transcriptome in Multiple Lineages of C3 and C4 Species. <i>PLoS ONE</i> , 2015, 10, e0140629.	2.5	63
21	Gene Discovery Using Mutagen-Induced Polymorphisms and Deep Sequencing: Application to Plant Disease Resistance. <i>Genetics</i> , 2012, 192, 139-146.	2.9	59
22	The genetic architecture of teosinte catalyzed and constrained maize domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 5643-5652.	7.1	59
23	Haplotyping the <i>Vitis</i> collinear core genome with rhAmpSeq improves marker transferability in a diverse genus. <i>Nature Communications</i> , 2020, 11, 413.	12.8	52
24	HOS15 and HDA9 negatively regulate immunity through histone deacetylation of intracellular immune receptor NLR genes in Arabidopsis. <i>New Phytologist</i> , 2020, 226, 507-522.	7.3	48
25	Transcriptome response of cassava leaves under natural shade. <i>Scientific Reports</i> , 2016, 6, 31673.	3.3	43
26	Next Generation Mapping of Enological Traits in an F2 Interspecific Grapevine Hybrid Family. <i>PLoS ONE</i> , 2016, 11, e0149560.	2.5	40
27	The Arabidopsis Chromatin-Remodeling Factor CHR5 Regulates Plant Immune Responses and Nucleosome Occupancy. <i>Plant and Cell Physiology</i> , 2017, 58, 2202-2216.	3.1	40
28	Genotyping-by-sequencing of Brassica oleracea vegetables reveals unique phylogenetic patterns, population structure and domestication footprints. <i>Horticulture Research</i> , 2018, 5, 38.	6.3	37
29	Workflow for Large Scale Detection and Validation of Peptide Modifications by RPLC-LTQ-Orbitrap: Application to the <i>Arabidopsis thaliana</i> Leaf Proteome and an Online Modified Peptide Library. <i>Analytical Chemistry</i> , 2009, 81, 8015-8024.	6.5	36
30	The Arabidopsis PeptideAtlas: Harnessing worldwide proteomics data to create a comprehensive community proteomics resource. <i>Plant Cell</i> , 2021, 33, 3421-3453.	6.6	36
31	Multiple independent recombinations led to hermaphroditism in grapevine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	32
32	The Plastid and Mitochondrial Peptidase Network in <i>Arabidopsis thaliana</i> : A Foundation for Testing Genetic Interactions and Functions in Organellar Proteostasis. <i>Plant Cell</i> , 2017, 29, 2687-2710.	6.6	31
33	Developmental and Subcellular Organization of Single-Cell C4Photosynthesis in <i>Bienertia sinuspersici</i> Determined by Large-Scale Proteomics and cDNA Assembly from 454 DNA Sequencing. <i>Journal of Proteome Research</i> , 2015, 14, 2090-2108.	3.7	30
34	Lessons from a Phenotyping Center Revealed by the Genome-Guided Mapping of Powdery Mildew Resistance Loci. <i>Phytopathology</i> , 2016, 106, 1159-1169.	2.2	27
35	The genetic architecture of the maize progenitor, teosinte, and how it was altered during maize domestication. <i>PLoS Genetics</i> , 2020, 16, e1008791.	3.5	27
36	Gene Evolutionary Trajectories and GC Patterns Driven by Recombination in <i>Zea mays</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1433.	3.6	16

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37	Natural variations of growth thermo-responsiveness determined by SAUR26/27/28 proteins in <i>Arabidopsis thaliana</i> . <i>New Phytologist</i> , 2019, 224, 291-305.	7.3	16
38	Interaction of Arabidopsis Trihelix-Domain Transcription Factors VFP3 and VFP5 with Agrobacterium Virulence Protein VirF. <i>PLoS ONE</i> , 2015, 10, e0142128.	2.5	13
39	A Role of Cytokinin Transporter in <i>Arabidopsis</i> Immunity. <i>Molecular Plant-Microbe Interactions</i> , 2017, 30, 325-333.	2.6	12
40	An integrative AmpSeq platform for highly multiplexed marker-assisted pyramiding of grapevine powdery mildew resistance loci. <i>Molecular Breeding</i> , 2017, 37, 1.	2.1	12
41	Characterization of maize leaf pyruvate orthophosphate dikinase using high throughput sequencing. <i>Journal of Integrative Plant Biology</i> , 2018, 60, 670-690.	8.5	12
42	Cardiac Pathology and Genomics of Sudden Death in Racehorses From New York and Maryland Racetracks. <i>Veterinary Pathology</i> , 2019, 56, 576-585.	1.7	9
43	Berry Anthocyanin, Acid, and Volatile Trait Analyses in a Grapevine-Interspecific F2 Population Using an Integrated GBS and rhAmpSeq Genetic Map. <i>Plants</i> , 2022, 11, 696.	3.5	5
44	Domestication reshaped the genetic basis of inbreeding depression in a maize landrace compared to its wild relative, teosinte. <i>PLoS Genetics</i> , 2021, 17, e1009797.	3.5	5
45	Mapping and Cloning of Chemical Induced Mutations by Whole-Genome Sequencing of Bulked Segregants. <i>Methods in Molecular Biology</i> , 2017, 1578, 285-289.	0.9	4
46	Evolutionary Genomic and Bacterial Genome-Wide Association Study of <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> and Dairy Cattle Johne's Disease Phenotypes. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	3.1	4
47	Genome-wide analysis of deletions in maize population reveals abundant genetic diversity and functional impact. <i>Theoretical and Applied Genetics</i> , 2021, 135, 273.	3.6	4
48	Candidate resistance genes to foliar phylloxera identified at <i>Rdv3</i> of hybrid grape. <i>Horticulture Research</i> , 2022, 9, .	6.3	3
49	Mitochondrial genome of an Atlantic white shark (<i>Carcharodon carcharias</i>). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 717-719.	0.4	2
50	Mapping Recombination Initiation Sites Using Chromatin Immunoprecipitation. <i>Methods in Molecular Biology</i> , 2016, 1429, 177-188.	0.9	2
51	Toward the elucidation of cytoplasmic diversity in North American grape breeding programs. <i>Molecular Breeding</i> , 2016, 36, 1.	2.1	1
52	A conserved genetic architecture among populations of the maize progenitor, teosinte, was radically altered by domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	1
53	STENCIL: A web templating engine for visualizing and sharing life science datasets. <i>PLoS Computational Biology</i> , 2022, 18, e1009859.	3.2	0