

# Qi Sun

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/545671/publications.pdf>

Version: 2024-02-01

53  
papers

11,764  
citations

212478

28  
h-index

206121

51  
g-index

56  
all docs

56  
docs citations

56  
times ranked

15965  
citing authors

#	ARTICLE	IF	CITATIONS
1	STENCIL: A web templating engine for visualizing and sharing life science datasets. <i>PLoS Computational Biology</i> , 2022, 18, e1009859.	1.5	0
2	Candidate resistance genes to foliar phylloxera identified at <i>Rdv3</i> of hybrid grape. <i>Horticulture Research</i> , 2022, 9, .	2.9	3
3	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.	1.6	5
4	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, .	1.4	4
5	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, .	3.3	32
6	The Arabidopsis PeptideAtlas: Harnessing worldwide proteomics data to create a comprehensive community proteomics resource. <i>Plant Cell</i> , 2021, 33, 3421-3453.	3.1	36
7	Genome-wide analysis of deletions in maize population reveals abundant genetic diversity and functional impact. <i>Theoretical and Applied Genetics</i> , 2021, 135, 273.	1.8	4
8	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, .	3.3	1
9	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.	1.5	5
10	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.	3.5	48
11	The genetic architecture of the maize progenitor, teosinte, and how it was altered during maize domestication. <i>PLoS Genetics</i> , 2020, 16, e1008791.	1.5	27
12	Haplotyping the <i>Vitis</i> collinear core genome with rhAmpSeq improves marker transferability in a diverse genus. <i>Nature Communications</i> , 2020, 11, 413.	5.8	52
13	BrAPI—an application programming interface for plant breeding applications. <i>Bioinformatics</i> , 2019, 35, 4147-4155.	1.8	82
14	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.	3.5	16
15	Computational Analysis of AmpSeq Data for Targeted, High-Throughput Genotyping of Amplicons. <i>Frontiers in Plant Science</i> , 2019, 10, 599.	1.7	115
16	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.	3.3	59
17	Cardiac Pathology and Genomics of Sudden Death in Racehorses From New York and Maryland Racetracks. <i>Veterinary Pathology</i> , 2019, 56, 576-585.	0.8	9
18	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.	3.3	92

#	ARTICLE	IF	CITATIONS
19	Characterization of maize leaf pyruvate orthophosphate dikinase using high throughput sequencing. <i>Journal of Integrative Plant Biology</i> , 2018, 60, 670-690.	4.1	12
20	Construction of the third-generation <i>Zea mays</i> haplotype map. <i>GigaScience</i> , 2018, 7, 1-12.	3.3	191
21	Genotyping-by-sequencing of <i>Brassica oleracea</i> vegetables reveals unique phylogenetic patterns, population structure and domestication footprints. <i>Horticulture Research</i> , 2018, 5, 38.	2.9	37
22	Genetic dissection of powdery mildew resistance in interspecific half-sib grapevine families using SNP-based maps. <i>Molecular Breeding</i> , 2017, 37, 1.	1.0	82
23	Mapping and Cloning of Chemical Induced Mutations by Whole-Genome Sequencing of Bulk Segregants. <i>Methods in Molecular Biology</i> , 2017, 1578, 285-289.	0.4	4
24	A Role of Cytokinin Transporter in <i>Arabidopsis</i> Immunity. <i>Molecular Plant-Microbe Interactions</i> , 2017, 30, 325-333.	1.4	12
25	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.	3.1	31
26	An integrative AmpSeq platform for highly multiplexed marker-assisted pyramiding of grapevine powdery mildew resistance loci. <i>Molecular Breeding</i> , 2017, 37, 1.	1.0	12
27	The <i>Arabidopsis</i> Chromatin-Remodeling Factor CHR5 Regulates Plant Immune Responses and Nucleosome Occupancy. <i>Plant and Cell Physiology</i> , 2017, 58, 2202-2216.	1.5	40
28	Next Generation Mapping of Enological Traits in an F2 Interspecific Grapevine Hybrid Family. <i>PLoS ONE</i> , 2016, 11, e0149560.	1.1	40
29	Gene Evolutionary Trajectories and GC Patterns Driven by Recombination in <i>Zea mays</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1433.	1.7	16
30	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.	2.9	90
31	Mitochondrial genome of an Atlantic white shark ( <i>Carcharodon carcharias</i> ). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 717-719.	0.2	2
32	Mapping Recombination Initiation Sites Using Chromatin Immunoprecipitation. <i>Methods in Molecular Biology</i> , 2016, 1429, 177-188.	0.4	2
33	Toward the elucidation of cytoplasmic diversity in North American grape breeding programs. <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	1
34	Lessons from a Phenotyping Center Revealed by the Genome-Guided Mapping of Powdery Mildew Resistance Loci. <i>Phytopathology</i> , 2016, 106, 1159-1169.	1.1	27
35	Transcriptome response of cassava leaves under natural shade. <i>Scientific Reports</i> , 2016, 6, 31673.	1.6	43
36	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.	1.1	63

#	ARTICLE	IF	CITATIONS
37	Interaction of Arabidopsis Trihelix-Domain Transcription Factors VFP3 and VFP5 with Agrobacterium Virulence Protein VirF. PLoS ONE, 2015, 10, e0142128.	1.1	13
38	Developmental and Subcellular Organization of Single-Cell C4Photosynthesis in Bienertia sinuspersici Determined by Large-Scale Proteomics and cDNA Assembly from 454 DNA Sequencing. Journal of Proteome Research, 2015, 14, 2090-2108.	1.8	30
39	Host genetic variation impacts microbiome composition across human body sites. Genome Biology, 2015, 16, 191.	3.8	612
40	Transcriptomic Analyses Indicate That Maize Ligule Development Recapitulates Gene Expression Patterns That Occur during Lateral Organ Initiation. Plant Cell, 2015, 26, 4718-4732.	3.1	99
41	Heterozygous Mapping Strategy (HetMappS) for High Resolution Genotyping-By-Sequencing Markers: A Case Study in Grapevine. PLoS ONE, 2015, 10, e0134880.	1.1	120
42	The Role of cis Regulatory Evolution in Maize Domestication. PLoS Genetics, 2014, 10, e1004745.	1.5	144
43	TASSEL-GBS: A High Capacity Genotyping by Sequencing Analysis Pipeline. PLoS ONE, 2014, 9, e90346.	1.1	1,511
44	Developmental dynamics of Kranz cell transcriptional specificity in maize leaf reveals early onset of C4-related processes. Journal of Experimental Botany, 2014, 65, 3543-3555.	2.4	78
45	Comparative analyses of C4 and C3 photosynthesis in developing leaves of maize and rice. Nature Biotechnology, 2014, 32, 1158-1165.	9.4	228
46	Gene Discovery Using Mutagen-Induced Polymorphisms and Deep Sequencing: Application to Plant Disease Resistance. Genetics, 2012, 192, 139-146.	1.2	59
47	A Robust, Simple Genotyping-by-Sequencing (GBS) Approach for High Diversity Species. PLoS ONE, 2011, 6, e19379.	1.1	5,470
48	MASCP Gator: An Aggregation Portal for the Visualization of Arabidopsis Proteomics Data. Plant Physiology, 2011, 155, 259-270.	2.3	94
49	Workflow for Large Scale Detection and Validation of Peptide Modifications by RPLC-LTQ-Orbitrap: Application to the Arabidopsis thaliana Leaf Proteome and an Online Modified Peptide Library. Analytical Chemistry, 2009, 81, 8015-8024.	3.2	36
50	PPDB, the Plant Proteomics Database at Cornell. Nucleic Acids Research, 2009, 37, D969-D974.	6.5	356
51	Genetic Properties of the Maize Nested Association Mapping Population. Science, 2009, 325, 737-740.	6.0	959
52	Sorting Signals, N-Terminal Modifications and Abundance of the Chloroplast Proteome. PLoS ONE, 2008, 3, e1994.	1.1	583
53	Analysis of Curated and Predicted Plastid Subproteomes of Arabidopsis. Subcellular Compartmentalization Leads to Distinctive Proteome Properties. Plant Physiology, 2004, 135, 723-734.	2.3	73