

Sanzhen Liu

List of Publications by Year in descending order

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64
papers

7,192
citations

172457
29
h-index

110387
64
g-index

79
all docs

79
docs citations

79
times ranked

9472
citing authors

#	ARTICLE	IF	CITATIONS
1	A conserved hypothetical gene is required but not sufficient for Ptr ToxC production in <i>Pyrenophora tritici-repentis</i> . <i>Molecular Plant-Microbe Interactions</i> , 2022, , .	2.6	11
2	Cloning of the broadly effective wheat leaf rust resistance gene Lr42 transferred from <i>Aegilops tauschii</i> . <i>Nature Communications</i> , 2022, 13, .	12.8	29
3	Multiple origins of Indian dwarf wheat by mutations targeting the TREE domain of a GSK3-like kinase for drought tolerance, phosphate uptake, and grain quality. <i>Theoretical and Applied Genetics</i> , 2021, 134, 633-645.	3.6	12
4	Ectopic Expression of a Heterologous Glutaredoxin Enhances Drought Tolerance and Grain Yield in Field Grown Maize. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5331.	4.1	8
5	Identification of biological pathway and process regulators using sparse partial least squares and triple-gene mutual interaction. <i>Scientific Reports</i> , 2021, 11, 13174.	3.3	2
6	Chromosome-level genome assembly of a regenerable maize inbred line A188. <i>Genome Biology</i> , 2021, 22, 175.	8.8	32
7	A genome-wide genetic linkage map and reference quality genome sequence for a new race in the wheat pathogen <i>Pyrenophora tritici-repentis</i> . <i>Fungal Genetics and Biology</i> , 2021, 152, 103571.	2.1	8
8	HB-PLS: A statistical method for identifying biological process or pathway regulators by integrating Huber loss and Berhu penalty with partial least squares regression. <i>Forestry Research</i> , 2021, 1, 0-0.	1.1	1
9	Multi-Omics Analyses Reveal Systemic Insights into Maize Vivipary. <i>Plants</i> , 2021, 10, 2437.	3.5	2
10	Factorial estimating assembly base errors using k-mer abundance difference (KAD) between short reads and genome assembled sequences. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa075.	3.2	8
11	Characterization, Genetic Analyses, and Identification of QTLs Conferring Metabolic Resistance to a 4-Hydroxyphenylpyruvate Dioxygenase Inhibitor in Sorghum (<i>Sorghum bicolor</i>). <i>Frontiers in Plant Science</i> , 2020, 11, 596581.	3.6	11
12	Xa1 Allelic R Genes Activate Rice Blight Resistance Suppressed by Interfering TAL Effectors. <i>Plant Communications</i> , 2020, 1, 100087.	7.7	52
13	A rare single nucleotide variant in <i>Pm5e</i> confers powdery mildew resistance in common wheat. <i>New Phytologist</i> , 2020, 228, 1011-1026.	7.3	92
14	Increased Power and Accuracy of Causal Locus Identification in Time Series Genome-wide Association in Sorghum. <i>Plant Physiology</i> , 2020, 183, 1898-1909.	4.8	39
15	Genomic Acquisitions in Emerging Populations of <i>Xanthomonas vasicola</i> pv. <i>vasculorum</i> Infecting Corn in the United States and Argentina. <i>Phytopathology</i> , 2020, 110, 1161-1173.	2.2	16
16	Early Drought-Responsive Genes Are Variable and Relevant to Drought Tolerance. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1657-1670.	1.8	13
17	Co-expression analysis aids in the identification of genes in the cuticular wax pathway in maize. <i>Plant Journal</i> , 2019, 97, 530-542.	5.7	34
18	Cellular Dynamics and Genomic Identity of Centromeres in Cereal Blast Fungus. <i>MBio</i> , 2019, 10, .	4.1	18

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19	Effector gene reshuffling involves dispensable mini-chromosomes in the wheat blast fungus. <i>PLoS Genetics</i> , 2019, 15, e1008272.	3.5	103
20	<i>Xanthomonas translucens</i> commandeers the host rate-limiting step in ABA biosynthesis for disease susceptibility. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 20938-20946.	7.1	58
21	Temporal Small RNA Expression Profiling under Drought Reveals a Potential Regulatory Role of Small Nucleolar RNAs in the Drought Responses of Maize. <i>Plant Genome</i> , 2019, 12, 180058.	2.8	17
22	Maize glossy6 is involved in cuticular wax deposition and drought tolerance. <i>Journal of Experimental Botany</i> , 2019, 70, 3089-3099.	4.8	62
23	Genetic mapping of a major gene in triticale conferring resistance to bacterial leaf streak. <i>Theoretical and Applied Genetics</i> , 2018, 131, 649-658.	3.6	23
24	JRmGRN: joint reconstruction of multiple gene regulatory networks with common hub genes using data from multiple tissues or conditions. <i>Bioinformatics</i> , 2018, 34, 3470-3478.	4.1	19
25	TILL-D: An <i>Aegilops tauschii</i> TILLING Resource for Wheat Improvement. <i>Frontiers in Plant Science</i> , 2018, 9, 1665.	3.6	26
26	FERONIA Receptor Kinase Contributes to Plant Immunity by Suppressing Jasmonic Acid Signaling in <i>Arabidopsis thaliana</i> . <i>Current Biology</i> , 2018, 28, 3316-3324.e6.	3.9	154
27	Intragenic Meiotic Crossovers Generate Novel Alleles with Transgressive Expression Levels. <i>Molecular Biology and Evolution</i> , 2018, 35, 2762-2772.	8.9	4
28	Analysis of Extreme Phenotype Bulk Copy Number Variation (XP-CNV) Identified the Association of <i>rp1</i> with Resistance to Goss's Wilt of Maize. <i>Frontiers in Plant Science</i> , 2018, 9, 110.	3.6	23
29	Homologues of <i>CsLOB1</i> in citrus function as disease susceptibility genes in citrus canker. <i>Molecular Plant Pathology</i> , 2017, 18, 798-810.	4.2	38
30	A Dimorphic and Virulence-Enhancing Endosymbiont Bacterium Discovered in <i>Rhizoctonia solani</i> . <i>Phytobiomes Journal</i> , 2017, 1, 14-23.	2.7	24
31	Identification of Brassinosteroid Target Genes by Chromatin Immunoprecipitation Followed by High-Throughput Sequencing (ChIP-seq) and RNA-Sequencing. <i>Methods in Molecular Biology</i> , 2017, 1564, 63-79.	0.9	10
32	RD26 mediates crosstalk between drought and brassinosteroid signalling pathways. <i>Nature Communications</i> , 2017, 8, 14573.	12.8	202
33	Unbiased K-mer Analysis Reveals Changes in Copy Number of Highly Repetitive Sequences During Maize Domestication and Improvement. <i>Scientific Reports</i> , 2017, 7, 42444.	3.3	16
34	tGBS® genotyping-by-sequencing enables reliable genotyping of heterozygous loci. <i>Nucleic Acids Research</i> , 2017, 45, e178-e178.	14.5	115
35	A Comprehensive Analysis of Alternative Splicing in Paleopolyploid Maize. <i>Frontiers in Plant Science</i> , 2017, 8, 694.	3.6	109
36	Complete Genome Sequencing and Targeted Mutagenesis Reveal Virulence Contributions of <i>Tal2</i> and <i>Tal4b</i> of <i>Xanthomonas translucens</i> pv. <i>undulosa</i> ICMP11055 in Bacterial Leaf Streak of Wheat. <i>Frontiers in Microbiology</i> , 2017, 8, 1488.	3.5	37

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37	Substantial contribution of genetic variation in the expression of transcription factors to phenotypic variation revealed by eRD-GWAS. <i>Genome Biology</i> , 2017, 18, 192.	8.8	56
38	Genes Expressed Differentially in Hessian Fly Larvae Feeding in Resistant and Susceptible Plants. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1324.	4.1	7
39	Massive Shift in Gene Expression during Transitions between Developmental Stages of the Gall Midge, <i>Mayetiola Destructor</i> . <i>PLoS ONE</i> , 2016, 11, e0155616.	2.5	8
40	Characterization of maize roothairless6 which encodes a D-type cellulose synthase and controls the switch from bulge formation to tip growth. <i>Scientific Reports</i> , 2016, 6, 34395.	3.3	31
41	Long read and single molecule DNA sequencing simplifies genome assembly and TAL effector gene analysis of <i>Xanthomonas translucens</i> . <i>BMC Genomics</i> , 2016, 17, 21.	2.8	97
42	Emergence of a New Population of <i>Rathayibacter toxicus</i> : An Ecologically Complex, Geographically Isolated Bacterium. <i>PLoS ONE</i> , 2016, 11, e0156182.	2.5	19
43	Gene targeting by the <i>TAL</i> effector PthXo2 reveals cryptic resistance gene for bacterial blight of rice. <i>Plant Journal</i> , 2015, 82, 632-643.	5.7	409
44	The maize <i>brown midrib4</i> (<i>bm4</i>) gene encodes a functional folylpolyglutamate synthase. <i>Plant Journal</i> , 2015, 81, 493-504.	5.7	42
45	Genome-wide analysis of regulation of gene expression and H3K9me2 distribution by JIL-1 kinase mediated histone H3S10 phosphorylation in <i>Drosophila</i> . <i>Nucleic Acids Research</i> , 2014, 42, 5456-5467.	14.5	21
46	The Aux/IAA gene <i>rum1</i> involved in seminal and lateral root formation controls vascular patterning in maize (<i>Zea mays</i> L.) primary roots. <i>Journal of Experimental Botany</i> , 2014, 65, 4919-4930.	4.8	69
47	The maize <i>brown midrib2</i> (<i>bm2</i>) gene encodes a methylenetetrahydrofolate reductase that contributes to lignin accumulation. <i>Plant Journal</i> , 2014, 77, 380-392.	5.7	94
48	<i>Roothairless5</i> , which functions in maize (<i>Zea mays</i> L.) root hair initiation and elongation encodes a monocot-specific <i>NADPH</i> oxidase. <i>Plant Journal</i> , 2014, 79, 729-740.	5.7	118
49	Histone Lysine Methyltransferase SDG8 Is Involved in Brassinosteroid-Regulated Gene Expression in <i>Arabidopsis thaliana</i> . <i>Molecular Plant</i> , 2014, 7, 1303-1315.	8.3	64
50	Mendelian and Non-Mendelian Regulation of Gene Expression in Maize. <i>PLoS Genetics</i> , 2013, 9, e1003202.	3.5	84
51	The Maize <i>glossy13</i> Gene, Cloned via BSR-Seq and Seq-Walking Encodes a Putative ABC Transporter Required for the Normal Accumulation of Epicuticular Waxes. <i>PLoS ONE</i> , 2013, 8, e82333.	2.5	75
52	Digestion–Ligation–Amplification (DLA): A Simple Genome Walking Method to Amplify Unknown Sequences Flanking Mutator (Mu) Transposons and Thereby Facilitate Gene Cloning. <i>Methods in Molecular Biology</i> , 2013, 1057, 167-176.	0.9	2
53	Changes in genome content generated via segregation of non-allelic homologs. <i>Plant Journal</i> , 2012, 72, 390-399.	5.7	24
54	Gene Mapping via Bulk Segregant RNA-Seq (BSR-Seq). <i>PLoS ONE</i> , 2012, 7, e36406.	2.5	297

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55	B73-Mo17 Near-Isogenic Lines Demonstrate Dispersed Structural Variation in Maize. <i>Plant Physiology</i> , 2011, 156, 1679-1690.	4.8	76
56	Heritable Epigenetic Variation among Maize Inbreds. <i>PLoS Genetics</i> , 2011, 7, e1002372.	3.5	150
57	High-Throughput Genetic Mapping of Mutants via Quantitative Single Nucleotide Polymorphism Typing. <i>Genetics</i> , 2010, 184, 19-26.	2.9	66
58	DLA-Based Strategies for Cloning Insertion Mutants: Cloning the <i>gl4</i> Locus of Maize Using <i>Mu</i> Transposon Tagged Alleles. <i>Genetics</i> , 2009, 183, 1215-1225.	2.9	38
59	The B73 Maize Genome: Complexity, Diversity, and Dynamics. <i>Science</i> , 2009, 326, 1112-1115.	12.6	3,612
60	Mu Transposon Insertion Sites and Meiotic Recombination Events Co-Localize with Epigenetic Marks for Open Chromatin across the Maize Genome. <i>PLoS Genetics</i> , 2009, 5, e1000733.	3.5	196
61	Study on the Dynamic Behavior of a DNA Microarray. <i>Journal of Nanoscience and Nanotechnology</i> , 2005, 5, 1249-1255.	0.9	11
62	Analysis of the factors affecting the accuracy of detection for single base alterations by oligonucleotide microarray. <i>Experimental and Molecular Medicine</i> , 2005, 37, 71-77.	7.7	8
63	Systematic comparison of the fidelity of aRNA, mRNA and T-RNA on gene expression profiling using cDNA microarray. <i>Journal of Biotechnology</i> , 2004, 107, 19-28.	3.8	51
64	Comparison of Hybridization Behavior between Double and Single Strand of Targets and the Application of Asymmetric PCR Targets in cDNA Microarray. <i>BMB Reports</i> , 2004, 37, 439-444.	2.4	8