

Zhixi Tian

List of Publications by Year in descending order

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68
papers

11,291
citations

94433

37
h-index

98798

67
g-index

69
all docs

69
docs citations

69
times ranked

9925
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequence of the palaeopolyploid soybean. <i>Nature</i> , 2010, 463, 178-183.	27.8	3,854
2	Resequencing 302 wild and cultivated accessions identifies genes related to domestication and improvement in soybean. <i>Nature Biotechnology</i> , 2015, 33, 408-414.	17.5	1,023
3	Pan-Genome of Wild and Cultivated Soybeans. <i>Cell</i> , 2020, 182, 162-176.e13.	28.9	508
4	Allelic diversities in rice starch biosynthesis lead to a diverse array of rice eating and cooking qualities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 21760-21765.	7.1	469
5	Genome-wide association studies dissect the genetic networks underlying agronomical traits in soybean. <i>Genome Biology</i> , 2017, 18, 161.	8.8	363
6	Natural variation at the soybean J locus improves adaptation to the tropics and enhances yield. <i>Nature Genetics</i> , 2017, 49, 773-779.	21.4	341
7	Artificial selection for determinate growth habit in soybean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 8563-8568.	7.1	330
8	Rational design of high-yield and superior-quality rice. <i>Nature Plants</i> , 2017, 3, 17031.	9.3	293
9	Global Dissection of Alternative Splicing in Paleopolyploid Soybean. <i>Plant Cell</i> , 2014, 26, 996-1008.	6.6	273
10	A route to de novo domestication of wild allotetraploid rice. <i>Cell</i> , 2021, 184, 1156-1170.e14.	28.9	259
11	Stepwise selection on homeologous PRR genes controlling flowering and maturity during soybean domestication. <i>Nature Genetics</i> , 2020, 52, 428-436.	21.4	229
12	Genome-wide association study of 12 agronomic traits in peach. <i>Nature Communications</i> , 2016, 7, 13246.	12.8	202
13	Do genetic recombination and gene density shape the pattern of DNA elimination in rice long terminal repeat retrotransposons?. <i>Genome Research</i> , 2009, 19, 2221-2230.	5.5	169
14	Parallel selection on a dormancy gene during domestication of crops from multiple families. <i>Nature Genetics</i> , 2018, 50, 1435-1441.	21.4	168
15	Control of Grain Size and Weight by the OsMKKK10-OsMKK4-OsMAPK6 Signaling Pathway in Rice. <i>Molecular Plant</i> , 2018, 11, 860-873.	8.3	168
16	Toward a "Green Revolution" for Soybean. <i>Molecular Plant</i> , 2020, 13, 688-697.	8.3	162
17	Evolutionary conservation, diversity and specificity of LTR retrotransposons in flowering plants: insights from genome-wide analysis and multi-specific comparison. <i>Plant Journal</i> , 2010, 63, 584-598.	5.7	153
18	<i>DT2</i> Is a Gain-of-Function MADS-Domain Factor Gene That Specifies Semideterminacy in Soybean. <i>Plant Cell</i> , 2014, 26, 2831-2842.	6.6	136

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19	An R2R3-type MYB transcription factor, GmMYB29, regulates isoflavone biosynthesis in soybean. <i>PLoS Genetics</i> , 2017, 13, e1006770.	3.5	128
20	Simultaneous changes in seed size, oil content and protein content driven by selection of <i>SWEET</i> homologues during soybean domestication. <i>National Science Review</i> , 2020, 7, 1776-1786.	9.5	128
21	SoyTEdb: a comprehensive database of transposable elements in the soybean genome. <i>BMC Genomics</i> , 2010, 11, 113.	2.8	122
22	De novo assembly of a Chinese soybean genome. <i>Science China Life Sciences</i> , 2018, 61, 871-884.	4.9	122
23	Functional Evolution of Phosphatidylethanolamine Binding Proteins in Soybean and Arabidopsis. <i>Plant Cell</i> , 2015, 27, 323-336.	6.6	113
24	Designing future crops: challenges and strategies for sustainable agriculture. <i>Plant Journal</i> , 2021, 105, 1165-1178.	5.7	110
25	Genome sequencing of adzuki bean (<i>Vigna angularis</i>) provides insight into high starch and low fat accumulation and domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13213-13218.	7.1	104
26	A soybean quantitative trait locus that promotes flowering under long days is identified as <i>FT5a</i> , a <i>FLOWERING LOCUS T</i> ortholog. <i>Journal of Experimental Botany</i> , 2016, 67, 5247-5258.	4.8	83
27	The Genomics of <i>Oryza</i> Species Provides Insights into Rice Domestication and Heterosis. <i>Annual Review of Plant Biology</i> , 2019, 70, 639-665.	18.7	80
28	Pericentromeric Effects Shape the Patterns of Divergence, Retention, and Expression of Duplicated Genes in the Paleopolyploid Soybean. <i>Plant Cell</i> , 2012, 24, 21-32.	6.6	79
29	Progress in soybean functional genomics over the past decade. <i>Plant Biotechnology Journal</i> , 2022, 20, 256-282.	8.3	76
30	Elevation of soybean seed oil content through selection for seed coat shininess. <i>Nature Plants</i> , 2018, 4, 30-35.	9.3	75
31	<i>De novo</i> assembly of a wild pear (<i>Pyrus betuleafolia</i>) genome. <i>Plant Biotechnology Journal</i> , 2020, 18, 581-595.	8.3	72
32	Concerted evolution of <i>D1</i> and <i>D2</i> to regulate chlorophyll degradation in soybean. <i>Plant Journal</i> , 2014, 77, 700-712.	5.7	69
33	Update soybean Zhonghuang 13 genome to a golden reference. <i>Science China Life Sciences</i> , 2019, 62, 1257-1260.	4.9	65
34	DNA methylation footprints during soybean domestication and improvement. <i>Genome Biology</i> , 2018, 19, 128.	8.8	61
35	Genome-Wide Characterization of Nonreference Transposons Reveals Evolutionary Propensities of Transposons in Soybean. <i>Plant Cell</i> , 2012, 24, 4422-4436.	6.6	51
36	Adaptation of <i>Arabidopsis thaliana</i> to the Yangtze River basin. <i>Genome Biology</i> , 2017, 18, 239.	8.8	44

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37	Natural allelic variation of <i>GmSTO5</i> controlling seed size and quality in soybean. <i>Plant Biotechnology Journal</i> , 2022, 20, 1807-1818.	8.3	44
38	Bifurcation and Enhancement of Autonomous-Nonautonomous Retrotransposon Partnership through LTR Swapping in Soybean. <i>Plant Cell</i> , 2010, 22, 48-61.	6.6	42
39	Decrease of gene expression diversity during domestication of animals and plants. <i>BMC Evolutionary Biology</i> , 2019, 19, 19.	3.2	42
40	Identification of QTNs Controlling Seed Protein Content in Soybean Using Multi-Locus Genome-Wide Association Studies. <i>Frontiers in Plant Science</i> , 2018, 9, 1690.	3.6	40
41	Global investigation of the evolution of <i>MIRNA</i> genes and <i>microRNA</i> targets during soybean domestication. <i>Plant Journal</i> , 2016, 85, 396-409.	5.7	36
42	Protomer Roles in Chloroplast Chaperonin Assembly and Function. <i>Molecular Plant</i> , 2015, 8, 1478-1492.	8.3	33
43	Genomics progress will facilitate molecular breeding in soybean. <i>Science China Life Sciences</i> , 2015, 58, 813-815.	4.9	28
44	Cloning of Ln Gene Through Combined Approach of Map-based Cloning and Association Study in Soybean. <i>Journal of Genetics and Genomics</i> , 2013, 40, 93-96.	3.9	27
45	Identification of QTNs Controlling 100-Seed Weight in Soybean Using Multilocus Genome-Wide Association Studies. <i>Frontiers in Genetics</i> , 2020, 11, 689.	2.3	26
46	Omics-based interdisciplinarity is accelerating plant breeding. <i>Current Opinion in Plant Biology</i> , 2022, 66, 102167.	7.1	26
47	Downregulation of a gibberellin 3 β -hydroxylase enhances photosynthesis and increases seed yield in soybean. <i>New Phytologist</i> , 2022, 235, 502-517.	7.3	26
48	A Pd1 \rightarrow Ps \rightarrow P1 Feedback Loop Controls Pubescence Density in Soybean. <i>Molecular Plant</i> , 2020, 13, 1768-1783.	8.3	22
49	Development of gene-tagged molecular markers for starch synthesis-related genes in rice. <i>Science Bulletin</i> , 2010, 55, 3768-3777.	1.7	20
50	Functional conservation and divergence of <i>GmCHLI</i> genes in polyploid soybean. <i>Plant Journal</i> , 2016, 88, 584-596.	5.7	20
51	Linkage Analysis and Multi-Locus Genome-Wide Association Studies Identify QTNs Controlling Soybean Plant Height. <i>Frontiers in Plant Science</i> , 2020, 11, 9.	3.6	20
52	Comprehensive analyses of <i>microRNA</i> gene evolution in paleopolyploid soybean genome. <i>Plant Journal</i> , 2013, 76, 332-344.	5.7	19
53	The antagonistic MYB paralogs <i>RH1</i> and <i>RH2</i> govern anthocyanin leaf markings in <i>Medicago truncatula</i> . <i>New Phytologist</i> , 2021, 229, 3330-3344.	7.3	18
54	Exceptional lability of a genomic complex in rice and its close relatives revealed by interspecific and intraspecific comparison and population analysis. <i>BMC Genomics</i> , 2011, 12, 142.	2.8	14

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55	Chloroplast DNA Underwent Independent Selection from Nuclear Genes during Soybean Domestication and Improvement. <i>Journal of Genetics and Genomics</i> , 2016, 43, 217-221.	3.9	14
56	From one linear genome to a graph-based pan-genome: a new era for genomics. <i>Science China Life Sciences</i> , 2020, 63, 1938-1941.	4.9	14
57	Identification of QTL and genes for pod number in soybean by linkage analysis and genome-wide association studies. <i>Molecular Breeding</i> , 2020, 40, 1.	2.1	14
58	Mutation of YL Results in a Yellow Leaf with Chloroplast RNA Editing Defect in Soybean. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4275.	4.1	12
59	GenoBaits Soy40K: a highly flexible and low-cost SNP array for soybean studies. <i>Science China Life Sciences</i> , 2022, 65, 1898-1901.	4.9	10
60	FED: a web tool for foreign element detection of genome-edited organism. <i>Science China Life Sciences</i> , 2021, 64, 167-170.	4.9	8
61	Fine mapping QTL and mining genes for protein content in soybean by the combination of linkage and association analysis. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1095-1122.	3.6	8
62	QNE1 is a key flowering regulator determining the length of the vegetative period in soybean cultivars. <i>Science China Life Sciences</i> , 2022, 65, 2472-2490.	4.9	8
63	Quantitative Trait Locus Analysis of Protein and Oil Content in Response to Planting Density in Soybean (<i>Glycine max</i> [L.] Merri.) Seeds Based on SNP Linkage Mapping. <i>Frontiers in Genetics</i> , 2020, 11, 563.	2.3	7
64	Genome-wide expression analysis in a dwarf soybean mutant. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2014, 12, S70-S73.	0.8	4
65	Oil crops: From the classical traits to genetic improvement. <i>Journal of Integrative Plant Biology</i> , 2021, 63, 979-980.	8.5	2
66	Nested miRNA Secondary Structure Is a Unique Determinant of miR159 Efficacy in Arabidopsis. <i>Frontiers in Plant Science</i> , 2022, 13, .	3.6	2
67	Super graph-based pan-genome: bring rice functional genomic study into a new dawn. <i>Molecular Plant</i> , 2022, , .	8.3	1
68	Convergent selection of a gene in cereals leads to grain yield upgradation. <i>Science China Life Sciences</i> , 2022, , 1.	4.9	0