

Zhixi Tian

List of Publications by Year in descending order

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Version: 2024-02-01

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 | Progress in soybean functional genomics over the past decade. <i>Plant Biotechnology Journal</i> , 2022, 20, 256-282. | 8.3 | 76 |
| 2 | Omics-based interdisciplinarity is accelerating plant breeding. <i>Current Opinion in Plant Biology</i> , 2022, 66, 102167. | 7.1 | 26 |
| 3 | 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 |
| 4 | Convergent selection of a gene in cereals leads to grain yield upgradation. <i>Science China Life Sciences</i> , 2022, , 1. | 4.9 | 0 |
| 5 | 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 |
| 6 | 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 |
| 7 | Nested miRNA Secondary Structure Is a Unique Determinant of miR159 Efficacy in Arabidopsis. <i>Frontiers in Plant Science</i> , 2022, 13, . | 3.6 | 2 |
| 8 | Super graph-based pan-genome: bring rice functional genomic study into a new dawn. <i>Molecular Plant</i> , 2022, , . | 8.3 | 1 |
| 9 | 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 |
| 10 | 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 |
| 11 | Designing future crops: challenges and strategies for sustainable agriculture. <i>Plant Journal</i> , 2021, 105, 1165-1178. | 5.7 | 110 |
| 12 | 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 |
| 13 | 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 |
| 14 | A route to de novo domestication of wild allotetraploid rice. <i>Cell</i> , 2021, 184, 1156-1170.e14. | 28.9 | 259 |
| 15 | Oil crops: From the classical traits to genetic improvement. <i>Journal of Integrative Plant Biology</i> , 2021, 63, 979-980. | 8.5 | 2 |
| 16 | <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 |
| 17 | A Pd1 β -Ps β -P1 Feedback Loop Controls Pubescence Density in Soybean. <i>Molecular Plant</i> , 2020, 13, 1768-1783. | 8.3 | 22 |
| 18 | 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 |

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|----|---|------|-----------|
| 19 | 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 |
| 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 | Pan-Genome of Wild and Cultivated Soybeans. <i>Cell</i> , 2020, 182, 162-176.e13. | 28.9 | 508 |
| 22 | 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 |
| 23 | Stepwise selection on homeologous PRR genes controlling flowering and maturity during soybean domestication. <i>Nature Genetics</i> , 2020, 52, 428-436. | 21.4 | 229 |
| 24 | Toward a "Green Revolution" for Soybean. <i>Molecular Plant</i> , 2020, 13, 688-697. | 8.3 | 162 |
| 25 | 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 |
| 26 | 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 |
| 27 | 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 |
| 28 | Update soybean Zhonghuang 13 genome to a golden reference. <i>Science China Life Sciences</i> , 2019, 62, 1257-1260. | 4.9 | 65 |
| 29 | 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 |
| 30 | Decrease of gene expression diversity during domestication of animals and plants. <i>BMC Evolutionary Biology</i> , 2019, 19, 19. | 3.2 | 42 |
| 31 | Elevation of soybean seed oil content through selection for seed coat shininess. <i>Nature Plants</i> , 2018, 4, 30-35. | 9.3 | 75 |
| 32 | 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 |
| 33 | Parallel selection on a dormancy gene during domestication of crops from multiple families. <i>Nature Genetics</i> , 2018, 50, 1435-1441. | 21.4 | 168 |
| 34 | DNA methylation footprints during soybean domestication and improvement. <i>Genome Biology</i> , 2018, 19, 128. | 8.8 | 61 |
| 35 | 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 |
| 36 | De novo assembly of a Chinese soybean genome. <i>Science China Life Sciences</i> , 2018, 61, 871-884. | 4.9 | 122 |

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|----|--|------|-----------|
| 37 | 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 |
| 38 | Rational design of high-yield and superior-quality rice. <i>Nature Plants</i> , 2017, 3, 17031. | 9.3 | 293 |
| 39 | An R2R3-type MYB transcription factor, GmMYB29, regulates isoflavone biosynthesis in soybean. <i>PLoS Genetics</i> , 2017, 13, e1006770. | 3.5 | 128 |
| 40 | Adaptation of <i>Arabidopsis thaliana</i> to the Yangtze River basin. <i>Genome Biology</i> , 2017, 18, 239. | 8.8 | 44 |
| 41 | Genome-wide association studies dissect the genetic networks underlying agronomical traits in soybean. <i>Genome Biology</i> , 2017, 18, 161. | 8.8 | 363 |
| 42 | 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 |
| 43 | 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 |
| 44 | Functional conservation and divergence of <i>GmCHLI</i> genes in polyploid soybean. <i>Plant Journal</i> , 2016, 88, 584-596. | 5.7 | 20 |
| 45 | Genome-wide association study of 12 agronomic traits in peach. <i>Nature Communications</i> , 2016, 7, 13246. | 12.8 | 202 |
| 46 | Global investigation of the co-evolution of <i>MIRNA</i> genes and microRNA targets during soybean domestication. <i>Plant Journal</i> , 2016, 85, 396-409. | 5.7 | 36 |
| 47 | Functional Evolution of Phosphatidylethanolamine Binding Proteins in Soybean and <i>Arabidopsis</i> . <i>Plant Cell</i> , 2015, 27, 323-336. | 6.6 | 113 |
| 48 | 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 |
| 49 | Protomer Roles in Chloroplast Chaperonin Assembly and Function. <i>Molecular Plant</i> , 2015, 8, 1478-1492. | 8.3 | 33 |
| 50 | Genomics progress will facilitate molecular breeding in soybean. <i>Science China Life Sciences</i> , 2015, 58, 813-815. | 4.9 | 28 |
| 51 | 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 |
| 52 | Genome-wide expression analysis in a dwarf soybean mutant. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2014, 12, S70-S73. | 0.8 | 4 |
| 53 | Global Dissection of Alternative Splicing in Paleopolyploid Soybean. <i>Plant Cell</i> , 2014, 26, 996-1008. | 6.6 | 273 |
| 54 | 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 |

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|----|--|------|-----------|
| 55 | <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 |
| 56 | Comprehensive analyses of microRNA gene evolution in paleopolyploid soybean genome. <i>Plant Journal</i> , 2013, 76, 332-344. | 5.7 | 19 |
| 57 | 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 |
| 58 | 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 |
| 59 | Genome-Wide Characterization of Nonreference Transposons Reveals Evolutionary Propensities of Transposons in Soybean. <i>Plant Cell</i> , 2012, 24, 4422-4436. | 6.6 | 51 |
| 60 | 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 |
| 61 | Development of gene-tagged molecular markers for starch synthesis-related genes in rice. <i>Science Bulletin</i> , 2010, 55, 3768-3777. | 1.7 | 20 |
| 62 | SoyTEdb: a comprehensive database of transposable elements in the soybean genome. <i>BMC Genomics</i> , 2010, 11, 113. | 2.8 | 122 |
| 63 | 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 |
| 64 | Genome sequence of the palaeopolyploid soybean. <i>Nature</i> , 2010, 463, 178-183. | 27.8 | 3,854 |
| 65 | Bifurcation and Enhancement of Autonomous-Nonautonomous Retrotransposon Partnership through LTR Swapping in Soybean. <i>Plant Cell</i> , 2010, 22, 48-61. | 6.6 | 42 |
| 66 | 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 |
| 67 | 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 |
| 68 | 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 |