

# Tao Zhang

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

70  
papers

4,538  
citations

29  
h-index

67  
g-index

81  
ext. papers

5,897  
ext. citations

9.3  
avg. IF

5.66  
L-index

#	Paper	IF	Citations
70	ChIP-seq accurately predicts tissue-specific activity of enhancers. <i>Nature</i> , <b>2009</b> , 457, 854-8	50.4	1301
69	ChIP-Seq identification of weakly conserved heart enhancers. <i>Nature Genetics</i> , <b>2010</b> , 42, 806-10	36.3	343
68	A CRISPR-Cpf1 system for efficient genome editing and transcriptional repression in plants. <i>Nature Plants</i> , <b>2017</b> , 3, 17018	11.5	308
67	Genome-wide identification of regulatory DNA elements and protein-binding footprints using signatures of open chromatin in Arabidopsis. <i>Plant Cell</i> , <b>2012</b> , 24, 2719-31	11.6	164
66	A large-scale whole-genome sequencing analysis reveals highly specific genome editing by both Cas9 and Cpf1 (Cas12a) nucleases in rice. <i>Genome Biology</i> , <b>2018</b> , 19, 84	18.3	155
65	Widespread long-range cis-regulatory elements in the maize genome. <i>Nature Plants</i> , <b>2019</b> , 5, 1237-1249	11.5	127
64	Improving Plant Genome Editing with High-Fidelity xCas9 and Non-canonical PAM-Targeting Cas9-NG. <i>Molecular Plant</i> , <b>2019</b> , 12, 1027-1036	14.4	113
63	Chromosome-Specific Painting in Cucumis Species Using Bulked Oligonucleotides. <i>Genetics</i> , <b>2015</b> , 200, 771-9	4	109
62	The prevalence, evolution and chromatin signatures of plant regulatory elements. <i>Nature Plants</i> , <b>2019</b> , 5, 1250-1259	11.5	107
61	CRISPR-Cas9 Based Genome Editing Reveals New Insights into MicroRNA Function and Regulation in Rice. <i>Frontiers in Plant Science</i> , <b>2017</b> , 8, 1598	6.2	105
60	Application of CRISPR-Cas12a temperature sensitivity for improved genome editing in rice, maize, and Arabidopsis. <i>BMC Biology</i> , <b>2019</b> , 17, 9	7.3	102
59	Plant Genome Editing Using FnCpf1 and LbCpf1 Nucleases at Redefined and Altered PAM Sites. <i>Molecular Plant</i> , <b>2018</b> , 11, 999-1002	14.4	92
58	Maize LAZY1 mediates shoot gravitropism and inflorescence development through regulating auxin transport, auxin signaling, and light response. <i>Plant Physiology</i> , <b>2013</b> , 163, 1306-22	6.6	88
57	Genome-Wide Prediction and Validation of Intergenic Enhancers in Arabidopsis Using Open Chromatin Signatures. <i>Plant Cell</i> , <b>2015</b> , 27, 2415-26	11.6	87
56	Single transcript unit CRISPR 2.0 systems for robust Cas9 and Cas12a mediated plant genome editing. <i>Plant Biotechnology Journal</i> , <b>2019</b> , 17, 1431-1445	11.6	75
55	Next-generation sequencing, FISH mapping and synteny-based modeling reveal mechanisms of decreasing dysploidy in Cucumis. <i>Plant Journal</i> , <b>2014</b> , 77, 16-30	6.9	72
54	Comparative Oligo-FISH Mapping: An Efficient and Powerful Methodology To Reveal Karyotypic and Chromosomal Evolution. <i>Genetics</i> , <b>2018</b> , 208, 513-523	4	69

53	Self-cleaving ribozymes enable the production of guide RNAs from unlimited choices of promoters for CRISPR/Cas9 mediated genome editing. <i>Journal of Genetics and Genomics</i> , <b>2017</b> , 44, 469-472	4	60
52	The CentO satellite confers translational and rotational phasing on cenH3 nucleosomes in rice centromeres. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, E4875-83	11.5	60
51	Computational approaches for effective CRISPR guide RNA design and evaluation. <i>Computational and Structural Biotechnology Journal</i> , <b>2020</b> , 18, 35-44	6.8	59
50	Genome-Wide Nucleosome Occupancy and Positioning and Their Impact on Gene Expression and Evolution in Plants. <i>Plant Physiology</i> , <b>2015</b> , 168, 1406-16	6.6	57
49	Whole-chromosome paints in maize reveal rearrangements, nuclear domains, and chromosomal relationships. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2019</b> , 116, 1679-1685	11.5	55
48	Cold stress induces enhanced chromatin accessibility and bivalent histone modifications H3K4me3 and H3K27me3 of active genes in potato. <i>Genome Biology</i> , <b>2019</b> , 20, 123	18.3	49
47	Proliferation of Regulatory DNA Elements Derived from Transposable Elements in the Maize Genome. <i>Plant Physiology</i> , <b>2018</b> , 176, 2789-2803	6.6	49
46	PlantDHS: a database for DNase I hypersensitive sites in plants. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, D1148-53	53.1	44
45	A cis-regulatory atlas in maize at single-cell resolution. <i>Cell</i> , <b>2021</b> , 184, 3041-3055.e21	56.2	37
44	Copy number variation in potato - an asexually propagated autotetraploid species. <i>Plant Journal</i> , <b>2013</b> , 75, 80-89	6.9	35
43	Meiotic crossovers are associated with open chromatin and enriched with Stowaway transposons in potato. <i>Genome Biology</i> , <b>2017</b> , 18, 203	18.3	31
42	Towards genome-wide prediction and characterization of enhancers in plants. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , <b>2017</b> , 1860, 131-139	6	29
41	Bidirectional Promoter-Based CRISPR-Cas9 Systems for Plant Genome Editing. <i>Frontiers in Plant Science</i> , <b>2019</b> , 10, 1173	6.2	28
40	Chromosome painting and its applications in cultivated and wild rice. <i>BMC Plant Biology</i> , <b>2018</b> , 18, 110	5.3	28
39	CRISPRMatch: An Automatic Calculation and Visualization Tool for High-throughput CRISPR Genome-editing Data Analysis. <i>International Journal of Biological Sciences</i> , <b>2018</b> , 14, 858-862	11.2	28
38	Chromosome painting and comparative physical mapping of the sex chromosomes in <i>Populus tomentosa</i> and <i>Populus deltoides</i> . <i>Chromosoma</i> , <b>2018</b> , 127, 313-321	2.8	26
37	Adaptive microclimatic structural and expressional dehydrin 1 evolution in wild barley, <i>Hordeum spontaneum</i> , at Evolution Canyon, Mount Carmel, Israel. <i>Molecular Ecology</i> , <b>2009</b> , 18, 2063-75	5.7	24
36	Dual-color oligo-FISH can reveal chromosomal variations and evolution in <i>Oryza</i> species. <i>Plant Journal</i> , <b>2020</b> , 101, 112-121	6.9	24

35	An extraordinarily stable karyotype of the woody <i>Populus</i> species revealed by chromosome painting. <i>Plant Journal</i> , <b>2020</b> , 101, 253-264	6.9	21
34	Molecular cytogenetic characterization of wheat <i>Triticum aestivum</i> amphiploids and derived introgression lines with stripe rust resistance. <i>Euphytica</i> , <b>2009</b> , 167, 197-202	2.1	19
33	An efficient Oligo-FISH painting system for revealing chromosome rearrangements and polyploidization in Triticeae. <i>Plant Journal</i> , <b>2021</b> , 105, 978-993	6.9	19
32	Amplification and adaptation of centromeric repeats in polyploid switchgrass species. <i>New Phytologist</i> , <b>2018</b> , 218, 1645-1657	9.8	18
31	The chromosome number, karyotype and genome size of the desert plant diploid <i>Reaumuria soongorica</i> (Pall.) Maxim. <i>Plant Cell Reports</i> , <b>2011</b> , 30, 955-64	5.1	17
30	Local Changes in Chromatin Accessibility and Transcriptional Networks Underlying the Nitrate Response in <i>Arabidopsis</i> Roots. <i>Molecular Plant</i> , <b>2019</b> , 12, 1545-1560	14.4	16
29	A universal chromosome identification system for maize and wild <i>Zea</i> species. <i>Chromosome Research</i> , <b>2020</b> , 28, 183-194	4.4	15
28	Open chromatin in plant genomes. <i>Cytogenetic and Genome Research</i> , <b>2014</b> , 143, 18-27	1.9	15
27	Genome-wide MNase hypersensitivity assay unveils distinct classes of open chromatin associated with H3K27me3 and DNA methylation in <i>Arabidopsis thaliana</i> . <i>Genome Biology</i> , <b>2020</b> , 21, 24	18.3	14
26	Transcriptional and epigenetic adaptation of maize chromosomes in Oat-Maize addition lines. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, 5012-5028	20.1	14
25	Improved plant cytosine base editors with high editing activity, purity, and specificity. <i>Plant Biotechnology Journal</i> , <b>2021</b> , 19, 2052-2068	11.6	14
24	Identification of gliadin genes in <i>Triticum aestivum</i> in relation to evolution and breeding. <i>Euphytica</i> , <b>2009</b> , 165, 155-163	2.1	13
23	De novo genome assembly of <i>Arabidopsis thaliana</i> reveals rapid genome expansion and adaptive evolution. <i>Communications Biology</i> , <b>2018</b> , 1, 84	6.7	12
22	Adaptive microclimatic evolution of the dehydrin 6 gene in wild barley at "Evolution Canyon", Israel. <i>Genetica</i> , <b>2011</b> , 139, 1429-38	1.5	10
21	Genomic editing of intronic enhancers unveils their role in fine-tuning tissue-specific gene expression in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , <b>2021</b> , 33, 1997-2014	11.6	10
20	Development and application of oligonucleotide-based chromosome painting for chromosome 4D of <i>Triticum aestivum</i> L. <i>Chromosome Research</i> , <b>2020</b> , 28, 171-182	4.4	9
19	Genome- and transcriptome-wide off-target analyses of an improved cytosine base editor. <i>Plant Physiology</i> , <b>2021</b> , 187, 73-87	6.6	9
18	Transcriptome comparative profiling of barley <i>eibi1</i> mutant reveals pleiotropic effects of HvABCG31 gene on cuticle biogenesis and stress responsive pathways. <i>International Journal of Molecular Sciences</i> , <b>2013</b> , 14, 20478-91	6.3	8

17	Chorus2: design of genome-scale oligonucleotide-based probes for fluorescence in situ hybridization. <i>Plant Biotechnology Journal</i> , <b>2021</b> , 19, 1967-1978	11.6	8
16	Diversity and evolution of four dispersed repetitive DNA sequences in the genus <i>Secale</i> . <i>Genome</i> , <b>2011</b> , 54, 285-300	2.4	7
15	Genome-wide Profiling of Histone Lysine Butyrylation Reveals its Role in the Positive Regulation of Gene Transcription in Rice. <i>Rice</i> , <b>2019</b> , 12, 86	5.8	7
14	Transcriptional abundance is not the single force driving the evolution of bacterial proteins. <i>BMC Evolutionary Biology</i> , <b>2013</b> , 13, 162	3	5
13	Adaptive evolution of duplicated hsp17 genes in wild barley from microclimatically divergent sites of Israel. <i>Genetics and Molecular Research</i> , <b>2014</b> , 13, 1220-32	1.2	5
12	CRISPR-BETS: a base-editing design tool for generating stop codons. <i>Plant Biotechnology Journal</i> , <b>2021</b> ,	11.6	5
11	A cis-regulatory atlas in maize at single-cell resolution		5
10	Targeting -Regulatory Elements for Rice Grain Quality Improvement. <i>Frontiers in Plant Science</i> , <b>2021</b> , 12, 705834	6.2	4
9	Single-cell analysis of cis-regulatory elements. <i>Current Opinion in Plant Biology</i> , <b>2021</b> , 65, 102094	9.9	4
8	Epigenomic Features of DNA G-Quadruplexes and Their Roles in Regulating Rice Gene Transcription. <i>Plant Physiology</i> , <b>2021</b> ,	6.6	4
7	Chromosome Painting Based on Bulked Oligonucleotides in Cotton. <i>Frontiers in Plant Science</i> , <b>2020</b> , 11, 802	6.2	3
6	Segmental Duplication of Chromosome 11 and its Implications for Cell Division and Genome-wide Expression in Rice. <i>Scientific Reports</i> , <b>2017</b> , 7, 2689	4.9	3
5	Analysis of Off-Target Mutations in CRISPR-Edited Rice Plants Using Whole-Genome Sequencing. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2238, 145-172	1.4	3
4	A large-scale whole-genome sequencing analysis reveals highly specific genome editing by both Cas9 and Cpf1 nucleases in rice		2
3	Single Copy Oligonucleotide Fluorescence In Situ Hybridization Probe Design Platforms: Development, Application and Evaluation. <i>International Journal of Molecular Sciences</i> , <b>2021</b> , 22,	6.3	2
2	Molecular cloning of cDNAs for 14-3-3 and its protein interactions in a white-rot fungus <i>Phanerochaete chrysosporium</i> . <i>Annals of Microbiology</i> , <b>2006</b> , 56, 191-196	3.2	1
1	DEEP GREEN PANICLE1 suppresses GOLDEN2-LIKE activity to reduce chlorophyll synthesis in rice glumes. <i>Plant Physiology</i> , <b>2021</b> , 185, 469-477	6.6	1