

# Tao Zhang

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6174577/publications.pdf>

Version: 2024-02-01

74  
papers

6,885  
citations

94433

37  
h-index

82547

72  
g-index

81  
all docs

81  
docs citations

81  
times ranked

8668  
citing authors

#	ARTICLE	IF	CITATIONS
1	ChIP-seq accurately predicts tissue-specific activity of enhancers. <i>Nature</i> , 2009, 457, 854-858.	27.8	1,526
2	A CRISPR-Cpf1 system for efficient genome editing and transcriptional repression in plants. <i>Nature Plants</i> , 2017, 3, 17018.	9.3	425
3	ChIP-Seq identification of weakly conserved heart enhancers. <i>Nature Genetics</i> , 2010, 42, 806-810.	21.4	395
4	Widespread long-range cis-regulatory elements in the maize genome. <i>Nature Plants</i> , 2019, 5, 1237-1249.	9.3	250
5	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> , 2018, 19, 84.	8.8	230
6	The prevalence, evolution and chromatin signatures of plant regulatory elements. <i>Nature Plants</i> , 2019, 5, 1250-1259.	9.3	219
7	Genome-Wide Identification of Regulatory DNA Elements and Protein-Binding Footprints Using Signatures of Open Chromatin in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2012, 24, 2719-2731.	6.6	204
8	Chromosome-Specific Painting in <i>Cucumis</i> Species Using Bulked Oligonucleotides. <i>Genetics</i> , 2015, 200, 771-779.	2.9	192
9	A cis-regulatory atlas in maize at single-cell resolution. <i>Cell</i> , 2021, 184, 3041-3055.e21.	28.9	176
10	Application of CRISPR-Cas12a temperature sensitivity for improved genome editing in rice, maize, and <i>Arabidopsis</i> . <i>BMC Biology</i> , 2019, 17, 9.	3.8	172
11	Improving Plant Genome Editing with High-Fidelity xCas9 and Non-canonical PAM-Targeting Cas9-NG. <i>Molecular Plant</i> , 2019, 12, 1027-1036.	8.3	159
12	CRISPR-Cas9 Based Genome Editing Reveals New Insights into MicroRNA Function and Regulation in Rice. <i>Frontiers in Plant Science</i> , 2017, 8, 1598.	3.6	150
13	Comparative Oligo-FISH Mapping: An Efficient and Powerful Methodology To Reveal Karyotypic and Chromosomal Evolution. <i>Genetics</i> , 2018, 208, 513-523.	2.9	146
14	Genome-Wide Prediction and Validation of Intergenic Enhancers in <i>Arabidopsis</i> Using Open Chromatin Signatures. <i>Plant Cell</i> , 2015, 27, 2415-2426.	6.6	136
15	Plant Genome Editing Using FnCpf1 and LbCpf1 Nucleases at Redefined and Altered PAM Sites. <i>Molecular Plant</i> , 2018, 11, 999-1002.	8.3	136
16	Maize LAZY1 Mediates Shoot Gravitropism and Inflorescence Development through Regulating Auxin Transport, Auxin Signaling, and Light Response. <i>Plant Physiology</i> , 2013, 163, 1306-1322.	4.8	131
17	Single transcript unit CRISPR 2.0 systems for robust Cas9 and Cas12a mediated plant genome editing. <i>Plant Biotechnology Journal</i> , 2019, 17, 1431-1445.	8.3	120
18	Cold stress induces enhanced chromatin accessibility and bivalent histone modifications H3K4me3 and H3K27me3 of active genes in potato. <i>Genome Biology</i> , 2019, 20, 123.	8.8	119

#	ARTICLE	IF	CITATIONS
19	Computational approaches for effective CRISPR guide RNA design and evaluation. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 35-44.	4.1	119
20	Genome-Wide Nucleosome Occupancy and Positioning and Their Impact on Gene Expression and Evolution in Plants. <i>Plant Physiology</i> , 2015, 168, 1406-1416.	4.8	98
21	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> , 2019, 116, 1679-1685.	7.1	95
22	Next-generation sequencing, FISH mapping and synteny-based modeling reveal mechanisms of decreasing dysploidy in <i>Cucumis</i> . <i>Plant Journal</i> , 2014, 77, 16-30.	5.7	90
23	PlantDHS: a database for DNase I hypersensitive sites in plants. <i>Nucleic Acids Research</i> , 2016, 44, D1148-D1153.	14.5	86
24	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> , 2017, 44, 469-472.	3.9	82
25	The <i>CentO</i> 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> , 2013, 110, E4875-83.	7.1	80
26	Proliferation of Regulatory DNA Elements Derived from Transposable Elements in the Maize Genome. <i>Plant Physiology</i> , 2018, 176, 2789-2803.	4.8	71
27	Meiotic crossovers are associated with open chromatin and enriched with Stowaway transposons in potato. <i>Genome Biology</i> , 2017, 18, 203.	8.8	62
28	An efficient Oligo-FISH painting system for revealing chromosome rearrangements and polyploidization in Triticeae. <i>Plant Journal</i> , 2021, 105, 978-993.	5.7	58
29	Improved plant cytosine base editors with high editing activity, purity, and specificity. <i>Plant Biotechnology Journal</i> , 2021, 19, 2052-2068.	8.3	55
30	Towards genome-wide prediction and characterization of enhancers in plants. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2017, 1860, 131-139.	1.9	53
31	CRISPRMatch: An Automatic Calculation and Visualization Tool for High-throughput CRISPR Genome-editing Data Analysis. <i>International Journal of Biological Sciences</i> , 2018, 14, 858-862.	6.4	53
32	Chromosome painting and its applications in cultivated and wild rice. <i>BMC Plant Biology</i> , 2018, 18, 110.	3.6	48
33	An extraordinarily stable karyotype of the woody <i>Populus</i> species revealed by chromosome painting. <i>Plant Journal</i> , 2020, 101, 253-264.	5.7	46
34	Dual-color oligo-FISH can reveal chromosomal variations and evolution in <i>Oryza</i> species. <i>Plant Journal</i> , 2020, 101, 112-121.	5.7	44
35	Chromosome painting and comparative physical mapping of the sex chromosomes in <i>Populus tomentosa</i> and <i>Populus deltoides</i> . <i>Chromosoma</i> , 2018, 127, 313-321.	2.2	43
36	Genomic editing of intronic enhancers unveils their role in fine-tuning tissue-specific gene expression in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2021, 33, 1997-2014.	6.6	43

#	ARTICLE	IF	CITATIONS
37	Copy number variation in potato “an asexually propagated autotetraploid species. <i>Plant Journal</i> , 2013, 75, 80-89.	5.7	39
38	Bidirectional Promoter-Based CRISPR-Cas9 Systems for Plant Genome Editing. <i>Frontiers in Plant Science</i> , 2019, 10, 1173.	3.6	39
39	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> , 2020, 21, 24.	8.8	35
40	Local Changes in Chromatin Accessibility and Transcriptional Networks Underlying the Nitrate Response in <i>Arabidopsis</i> Roots. <i>Molecular Plant</i> , 2019, 12, 1545-1560.	8.3	31
41	Chorus2: design of genome-scale oligonucleotide-based probes for fluorescence <i>in situ</i> hybridization. <i>Plant Biotechnology Journal</i> , 2021, 19, 1967-1978.	8.3	31
42	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> , 2009, 18, 2063-2075.	3.9	30
43	Amplification and adaptation of centromeric repeats in polyploid switchgrass species. <i>New Phytologist</i> , 2018, 218, 1645-1657.	7.3	30
44	A universal chromosome identification system for maize and wild <i>Zea</i> species. <i>Chromosome Research</i> , 2020, 28, 183-194.	2.2	26
45	Genome- and transcriptome-wide off-target analyses of an improved cytosine base editor. <i>Plant Physiology</i> , 2021, 187, 73-87.	4.8	25
46	De novo genome assembly of <i>Oryza granulata</i> reveals rapid genome expansion and adaptive evolution. <i>Communications Biology</i> , 2018, 1, 84.	4.4	24
47	Genome-wide analyses of PAM-relaxed Cas9 genome editors reveal substantial off-target effects by ABE8e in rice. <i>Plant Biotechnology Journal</i> , 2022, 20, 1670-1682.	8.3	23
48	Epigenomic features of DNA G-quadruplexes and their roles in regulating rice gene transcription. <i>Plant Physiology</i> , 2022, 188, 1632-1648.	4.8	22
49	Molecular cytogenetic characterization of wheat “ <i>Secale africanum</i> amphiploids and derived introgression lines with stripe rust resistance. <i>Euphytica</i> , 2009, 167, 197-202.	1.2	21
50	Development and application of oligonucleotide-based chromosome painting for chromosome 4D of <i>Triticum aestivum</i> L.. <i>Chromosome Research</i> , 2020, 28, 171-182.	2.2	21
51	Single-cell analysis of cis-regulatory elements. <i>Current Opinion in Plant Biology</i> , 2022, 65, 102094.	7.1	21
52	CRISPR-CBETS: a base-editing design tool for generating stop codons. <i>Plant Biotechnology Journal</i> , 2022, 20, 499-510.	8.3	21
53	The chromosome number, karyotype and genome size of the desert plant diploid <i>Reaumuria soongorica</i> (Pall.) Maxim. <i>Plant Cell Reports</i> , 2011, 30, 955-964.	5.6	20
54	Open Chromatin in Plant Genomes. <i>Cytogenetic and Genome Research</i> , 2014, 143, 18-27.	1.1	19

#	ARTICLE	IF	CITATIONS
55	Transcriptional and epigenetic adaptation of maize chromosomes in Oat-Maize addition lines. <i>Nucleic Acids Research</i> , 2018, 46, 5012-5028.	14.5	19
56	Identification of $\alpha$ -gliadin genes in <i>Dasypyrum</i> in relation to evolution and breeding. <i>Euphytica</i> , 2009, 165, 155.	1.2	15
57	Genome-wide Profiling of Histone Lysine Butyrylation Reveals its Role in the Positive Regulation of Gene Transcription in Rice. <i>Rice</i> , 2019, 12, 86.	4.0	15
58	Adaptive microclimatic evolution of the dehydrin 6 gene in wild barley at "Evolution Canyon", Israel. <i>Genetica</i> , 2011, 139, 1429-1438.	1.1	13
59	Targeting Cis-Regulatory Elements for Rice Grain Quality Improvement. <i>Frontiers in Plant Science</i> , 2021, 12, 705834.	3.6	13
60	Quality control and evaluation of plant epigenomics data. <i>Plant Cell</i> , 2022, 34, 503-513.	6.6	13
61	Single-Cell Transcriptome and Network Analyses Unveil Key Transcription Factors Regulating Mesophyll Cell Development in Maize. <i>Genes</i> , 2022, 13, 374.	2.4	13
62	Single Copy Oligonucleotide Fluorescence In Situ Hybridization Probe Design Platforms: Development, Application and Evaluation. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7124.	4.1	12
63	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> , 2013, 14, 20478-20491.	4.1	9
64	Diversity and evolution of four dispersed repetitive DNA sequences in the genus <i>Secale</i> . <i>Genome</i> , 2011, 54, 285-300.	2.0	8
65	Adaptive evolution of duplicated <i>hsp17</i> genes in wild barley from microclimatically divergent sites of Israel. <i>Genetics and Molecular Research</i> , 2014, 13, 1220-1232.	0.2	8
66	Chromosome Painting Based on Bulk Oligonucleotides in Cotton. <i>Frontiers in Plant Science</i> , 2020, 11, 802.	3.6	7
67	DEEP GREEN PANICLE1 suppresses GOLDEN2-LIKE activity to reduce chlorophyll synthesis in rice glumes. <i>Plant Physiology</i> , 2021, 185, 469-477.	4.8	6
68	Transcriptional abundance is not the single force driving the evolution of bacterial proteins. <i>BMC Evolutionary Biology</i> , 2013, 13, 162.	3.2	5
69	Segmental Duplication of Chromosome 11 and its Implications for Cell Division and Genome-wide Expression in Rice. <i>Scientific Reports</i> , 2017, 7, 2689.	3.3	4
70	Analysis of Off-Target Mutations in CRISPR-Edited Rice Plants Using Whole-Genome Sequencing. <i>Methods in Molecular Biology</i> , 2021, 2238, 145-172.	0.9	4
71	<i>De novo</i> centromere formation in pericentromeric region of rice chromosome 8. <i>Plant Journal</i> , 0, , .	5.7	4
72	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> , 2006, 56, 191-196.	2.6	1

#	ARTICLE	IF	CITATIONS
73	Molecular Characterization and Evolutionary Analysis of Alpha-gliadin Genes from <i>Eremopyrum bonaepartis</i> (Triticeae). <i>Journal of Agricultural Science</i> , 2010, 2, .	0.2	0
74	Identification, Classification and Phylogenetic Analysis of SET Domain Gene in Barley. <i>International Conference on Bioinformatics and Biomedical Engineering: [proceedings] International Conference on Bioinformatics and Biomedical Engineering</i> , 2010, , .	0.0	0