

Tao Zhang

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/6174577/tao-zhang-publications-by-year.pdf>

Version: 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	CRISPR-BETS: a base-editing design tool for generating stop codons. <i>Plant Biotechnology Journal</i> , 2021 ,	11.6	5
69	DEEP GREEN PANICLE1 suppresses GOLDEN2-LIKE activity to reduce chlorophyll synthesis in rice glumes. <i>Plant Physiology</i> , 2021 , 185, 469-477	6.6	1
68	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	11.6	10
67	A cis-regulatory atlas in maize at single-cell resolution. <i>Cell</i> , 2021 , 184, 3041-3055.e21	56.2	37
66	Chorus2: design of genome-scale oligonucleotide-based probes for fluorescence in situ hybridization. <i>Plant Biotechnology Journal</i> , 2021 , 19, 1967-1978	11.6	8
65	Improved plant cytosine base editors with high editing activity, purity, and specificity. <i>Plant Biotechnology Journal</i> , 2021 , 19, 2052-2068	11.6	14
64	Genome- and transcriptome-wide off-target analyses of an improved cytosine base editor. <i>Plant Physiology</i> , 2021 , 187, 73-87	6.6	9
63	Single Copy Oligonucleotide Fluorescence In Situ Hybridization Probe Design Platforms: Development, Application and Evaluation. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	2
62	An efficient Oligo-FISH painting system for revealing chromosome rearrangements and polyploidization in Triticeae. <i>Plant Journal</i> , 2021 , 105, 978-993	6.9	19
61	Analysis of Off-Target Mutations in CRISPR-Edited Rice Plants Using Whole-Genome Sequencing. <i>Methods in Molecular Biology</i> , 2021 , 2238, 145-172	1.4	3
60	Targeting -Regulatory Elements for Rice Grain Quality Improvement. <i>Frontiers in Plant Science</i> , 2021 , 12, 705834	6.2	4
59	Single-cell analysis of cis-regulatory elements. <i>Current Opinion in Plant Biology</i> , 2021 , 65, 102094	9.9	4
58	Epigenomic Features of DNA G-Quadruplexes and Their Roles in Regulating Rice Gene Transcription. <i>Plant Physiology</i> , 2021 ,	6.6	4
57	A universal chromosome identification system for maize and wild Zea species. <i>Chromosome Research</i> , 2020 , 28, 183-194	4.4	15
56	Chromosome Painting Based on Bulked Oligonucleotides in Cotton. <i>Frontiers in Plant Science</i> , 2020 , 11, 802	6.2	3
55	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	4.4	9
54	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	18.3	14

53	Dual-color oligo-FISH can reveal chromosomal variations and evolution in <i>Oryza</i> species. <i>Plant Journal</i> , 2020 , 101, 112-121	6.9	24
52	An extraordinarily stable karyotype of the woody <i>Populus</i> species revealed by chromosome painting. <i>Plant Journal</i> , 2020 , 101, 253-264	6.9	21
51	Computational approaches for effective CRISPR guide RNA design and evaluation. <i>Computational and Structural Biotechnology Journal</i> , 2020 , 18, 35-44	6.8	59
50	Bidirectional Promoter-Based CRISPR-Cas9 Systems for Plant Genome Editing. <i>Frontiers in Plant Science</i> , 2019 , 10, 1173	6.2	28
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> , 2019 , 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> , 2019 , 20, 123	18.3	49
47	Improving Plant Genome Editing with High-Fidelity xCas9 and Non-canonical PAM-Targeting Cas9-NG. <i>Molecular Plant</i> , 2019 , 12, 1027-1036	14.4	113
46	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	14.4	16
45	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	5.8	7
44	Application of CRISPR-Cas12a temperature sensitivity for improved genome editing in rice, maize, and <i>Arabidopsis</i> . <i>BMC Biology</i> , 2019 , 17, 9	7.3	102
43	Widespread long-range cis-regulatory elements in the maize genome. <i>Nature Plants</i> , 2019 , 5, 1237-1249	11.5	127
42	The prevalence, evolution and chromatin signatures of plant regulatory elements. <i>Nature Plants</i> , 2019 , 5, 1250-1259	11.5	107
41	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	11.6	75
40	Proliferation of Regulatory DNA Elements Derived from Transposable Elements in the Maize Genome. <i>Plant Physiology</i> , 2018 , 176, 2789-2803	6.6	49
39	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	2.8	26
38	Amplification and adaptation of centromeric repeats in polyploid switchgrass species. <i>New Phytologist</i> , 2018 , 218, 1645-1657	9.8	18
37	Transcriptional and epigenetic adaptation of maize chromosomes in Oat-Maize addition lines. <i>Nucleic Acids Research</i> , 2018 , 46, 5012-5028	20.1	14
36	Plant Genome Editing Using FnCpf1 and LbCpf1 Nucleases at Redefined and Altered PAM Sites. <i>Molecular Plant</i> , 2018 , 11, 999-1002	14.4	92

35	Chromosome painting and its applications in cultivated and wild rice. <i>BMC Plant Biology</i> , 2018 , 18, 110	5.3	28
34	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	18.3	155
33	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	11.2	28
32	Comparative Oligo-FISH Mapping: An Efficient and Powerful Methodology To Reveal Karyotypic and Chromosomal Evolution. <i>Genetics</i> , 2018 , 208, 513-523	4	69
31	De novo genome assembly of reveals rapid genome expansion and adaptive evolution. <i>Communications Biology</i> , 2018 , 1, 84	6.7	12
30	Towards genome-wide prediction and characterization of enhancers in plants. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2017 , 1860, 131-139	6	29
29	A CRISPR-Cpf1 system for efficient genome editing and transcriptional repression in plants. <i>Nature Plants</i> , 2017 , 3, 17018	11.5	308
28	Meiotic crossovers are associated with open chromatin and enriched with Stowaway transposons in potato. <i>Genome Biology</i> , 2017 , 18, 203	18.3	31
27	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	4	60
26	Segmental Duplication of Chromosome 11 and its Implications for Cell Division and Genome-wide Expression in Rice. <i>Scientific Reports</i> , 2017 , 7, 2689	4.9	3
25	CRISPR-Cas9 Based Genome Editing Reveals New Insights into MicroRNA Function and Regulation in Rice. <i>Frontiers in Plant Science</i> , 2017 , 8, 1598	6.2	105
24	PlantDHS: a database for DNase I hypersensitive sites in plants. <i>Nucleic Acids Research</i> , 2016 , 44, D1148-53	5.1	44
23	Chromosome-Specific Painting in Cucumis Species Using Bulkied Oligonucleotides. <i>Genetics</i> , 2015 , 200, 771-9	4	109
22	Genome-Wide Prediction and Validation of Intergenic Enhancers in Arabidopsis Using Open Chromatin Signatures. <i>Plant Cell</i> , 2015 , 27, 2415-26	11.6	87
21	Genome-Wide Nucleosome Occupancy and Positioning and Their Impact on Gene Expression and Evolution in Plants. <i>Plant Physiology</i> , 2015 , 168, 1406-16	6.6	57
20	Next-generation sequencing, FISH mapping and synteny-based modeling reveal mechanisms of decreasing dysploidy in Cucumis. <i>Plant Journal</i> , 2014 , 77, 16-30	6.9	72
19	Open chromatin in plant genomes. <i>Cytogenetic and Genome Research</i> , 2014 , 143, 18-27	1.9	15
18	Adaptive evolution of duplicated hsp17 genes in wild barley from microclimatically divergent sites of Israel. <i>Genetics and Molecular Research</i> , 2014 , 13, 1220-32	1.2	5

17	Transcriptional abundance is not the single force driving the evolution of bacterial proteins. <i>BMC Evolutionary Biology</i> , 2013 , 13, 162	3	5
16	Maize LAZY1 mediates shoot gravitropism and inflorescence development through regulating auxin transport, auxin signaling, and light response. <i>Plant Physiology</i> , 2013 , 163, 1306-22	6.6	88
15	Copy number variation in potato - an asexually propagated autotetraploid species. <i>Plant Journal</i> , 2013 , 75, 80-89	6.9	35
14	Transcriptome comparative profiling of barley eibi1 mutant reveals pleiotropic effects of HvABCG31 gene on cuticle biogenesis and stress responsive pathways. <i>International Journal of Molecular Sciences</i> , 2013 , 14, 20478-91	6.3	8
13	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> , 2013 , 110, E4875-83	11.5	60
12	Genome-wide identification of regulatory DNA elements and protein-binding footprints using signatures of open chromatin in Arabidopsis. <i>Plant Cell</i> , 2012 , 24, 2719-31	11.6	164
11	Adaptive microclimatic evolution of the dehydrin 6 gene in wild barley at "Evolution Canyon", Israel. <i>Genetica</i> , 2011 , 139, 1429-38	1.5	10
10	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, 955-64	5.1	17
9	Diversity and evolution of four dispersed repetitive DNA sequences in the genus <i>Secale</i> . <i>Genome</i> , 2011 , 54, 285-300	2.4	7
8	ChIP-Seq identification of weakly conserved heart enhancers. <i>Nature Genetics</i> , 2010 , 42, 806-10	36.3	343
7	Identification of gliadin genes in <i>Dasypyrum</i> in relation to evolution and breeding. <i>Euphytica</i> , 2009 , 165, 155-163	2.1	13
6	Molecular cytogenetic characterization of wheat <i>Triticum aestivum</i> amphiploids and derived introgression lines with stripe rust resistance. <i>Euphytica</i> , 2009 , 167, 197-202	2.1	19
5	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, 2063-75	5.7	24
4	ChIP-seq accurately predicts tissue-specific activity of enhancers. <i>Nature</i> , 2009 , 457, 854-8	50.4	1301
3	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	3.2	1
2	A cis-regulatory atlas in maize at single-cell resolution		5
1	A large-scale whole-genome sequencing analysis reveals highly specific genome editing by both Cas9 and Cpf1 nucleases in rice		2